

**O'Bryen, Barbara**

---

**From:** Seharaseyon, Jegatheesan  
**Sent:** Tuesday, December 21, 2004 1:33 PM  
**To:** O'Bryen, Barbara  
**Subject:** RE: PR01550

Hi,

Please search SEQ ID NOs: 121 (NA) and 122 (AA) in 10/063734,  
In issued and commercial databases.

Also,

Please search the nucleotide encoding SEQ ID NO: 122.

Please do a word search of the nucleic acid with a word size of 10 nucleotides and  
a word search of the prtein, with a word size of 6 amino acids.

AND on the EST databases, in particular, I need enough hits to get at old art (~50).

Thanks,  
Seyon.

J. Seharaseyon  
Art Unit 1647  
Remsen 4C61  
Mailbox 4C70  
Phone: (571)-272-0892  
Fax: (571)-273-0892

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 22:49:14 ; Search time 5526 Seconds  
(without alignments)  
10756.995 Million cell updates/sec

Title: US-10-063-734-121

Perfect score: 1257

Sequence: 1 ggaagagagcgcgcggtcga.....aataaaattattccacaa 1257

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenBank1:\*  
1: gb\_bai:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
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8: gb\_pl:\*  
9: gb\_pr:\*  
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11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1257	100.0	1257	6	AX376298 Sequence
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5	1257	100.0	1257	6	AX491138 Sequence
6	1257	100.0	1257	6	AX697362 Sequence
7	1257	100.0	1257	6	AY358914 Sequence
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## ALIGNMENTS

SOURCE	Homo sapiens (human)
ODONTOMYX	

## REFERENCE 1

Wood, W. I.

JOURNAL  
Patent: WO 0116318-A 121 08-MAR-2001;  
Genentech, Inc. (US)

source 1. .1257

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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## ORIGIN

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Dp	481	ATTATGCAATGATCTTGGAAAAATTGCGAGTGTACATTTACAAGATGCGTTCAAATA	540
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RESULT 2	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
AX376298	AX376298	Sequence 365 from Patent WO0168848.	AX376298	AX376298.1	GI:19170540		Homo sapiens (human)	1 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and Zhang, Z.	Secreated and transmembrane polypeptides and nucleic acids encoding the same	Patent: WO 0168848-A 365 20-SEP-2001.	



Genentech, Inc. (US)  
 Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1257; DB 6; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-213;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGAGAGAGCGCGCGGGTAAAGCGCATTGATGACGCTCGCGCGGCTCGAGCGCG 60  
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 DEFINITION AX454660  
 ACCESSION AX454660  
 VERSION AX454660.1 GI:21713954  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,  
 Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,  
 Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.

TITLE  
 JOURNAL  
 Compositions and methods for the diagnosis and treatment of  
 disorders involving angiogenesis  
 Patent: WO 0208284-A 245 31-JAN-2002;

Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
 (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
 Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
 Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
 ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
 Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
 I. (US)

FEATURES  
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ORIGIN

Query Match 100.0%; Score 1257; DB 6; Length 1257;  
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 121 CCGCGAGCGCGGAGCGATGCAACCCCAAGGCGCGCGCTCGCGCGAGCGGCTCGCG 180  
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VERSION	AX491138.1	GI:22323906		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthera; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Masters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.			
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis			
JOURNAL	Patent: WO 0200690-A 245 03-JAN-2002;			
FEATURES	Genentech, Inc. (US)			
source	1..1257 Location/Qualifiers			
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Query Match	100.0%	Score 1257	DB 6	Length 1257
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AUTHORS	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Curell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimelid,C., Gu,Q., Haase,P.E., Helgens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagstad,A., Vanden,R., Watanabe,C., Wiand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,				

TITLE  
Goddard, A., Wood, W.I. and Godowski, P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment

JOURNAL  
Genome Res. 13 (10), 2265-2270 (2003)

PUBMED  
12975309

REFERENCE  
2 (bases 1 to 1257)

AUTHORS  
Clark, H.F.

TITLE  
Direct Submission

JOURNAL  
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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ORIGIN

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REFERENCE  
1  
Mack, D.H., Gish, K.C. and Afari, D.  
Methods of diagnosis of breast cancer, compositions and methods of  
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 TANG, T. Y., Lal, P., Baughn, M. R., Yue, H., Young, J. A., Lu, D. A. M. and Azimzal, Y.  
 Human secretory proteins  
 Patent: JP 2002537805-A 5 12-NOV-2002;  
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 PN JP 2002537805-A/5  
 PD 12-NOV-2002  
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 PR 05-MAR-1999 US 60/123117  
 PI TOM Y TANG, PREETI LAL, MARIAM R BAUGHN, HENRY YUE, JANICE AU YOUNG.

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 ACCESSION BD223153  
 VERSION BD223153.1 GI:31032923  
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 REFERENCE 1 (bases 1 to 1342)  
 Komatsu, G.A., Rosen, C.A., Ruben, S.M., Duan, R., Moore, P.A.,  
 Shi, Y., Lafleur, D., Wei, Y.F., Ni, J., Florence, K.A., Young, P.E.,  
 Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H.S. and  
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 TITLE 98 human secretory proteins  
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 ORGANISM Unknown.  
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 AUTHORS Komatsoulis, G., Rosen, C.A., Ruben, S.M., Duan, R.D., Moore, P.A., Shi, Y., LaFleur, D.W., Wei, Y.-F., Ni, J., Florence, K.A., Young, P., Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H. and Mucenki, M.  
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VERSION BD223185.1 GI:33032955
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Komatsu, S., G. A., Rosen, C. A., Ruben, S. M., Duan, R., Moore, P. A.,
Shi, Y., Lafleur, D., Wei, Y. F., N. J., Florence, K. A., Young, P. E.,
Breuer, L. A., Soppet, D. R., Endress, G. A., Ebner, R., Olsen, H. S. and
Mucenski, M.
98 human secretory proteins
Patent: JP 2002521055-A 120 16-JUL-2002;
HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002521055-A/120
PD 16-JUL-2002
PF 29-JUL-1999 JP 2000562480
PR 30-JUL-1998 US 60/094657, 05-AUG-1998 US 60/095486 PR
06-AUG-1998 US 60/095455, 06-AUG-1998 US 60/095454 PR
12-AUG-1998 US 60/096319
PI GEORGE A. KOMATSU, CRAIG A. ROSEN, STEVEN
M. RUBEN, ROXANNE DUAN,
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KIMBERLY A. FLORENCE, PAUL E. YOUNG, LARIE A. BREWER, DANIEL R.
SOPPET,
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Qy	488	CATAGATCTTGGGAAATTCGGGAGTGCATTTTCAAAAGATGCGTTCAATATGAGTCT	547
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RESULT 14			
LOCUS	BC014245		
DEFINITION	Homo sapiens collagen triple helix repeat containing 1, mRNA (CDNA clone MGC:20766 IMAGE:586039), complete cds.		
ACCESSION	BC014245		
VERSION	BC014245.2	GI:33878497	
KEYWORDS	MG.		
ORGANISM	Homo sapiens (human)		
SOURCE	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homino.		
AUTHORS	1 (bases 1 to 1236)		
	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L., Steplton T.E., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.M., Brownstein M.J., Udell T.B., Toshiyuki S., Canciani P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Holys S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S., Krzywinski M.I., Skalka U., Smalls D.E., Scherth A., Schein J.E., Jones S.J. and Marra M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99 (26), 16899-16903	(2002)
PIBMD	12477932		
REFERENCES	2 (bases 1 to 1236)		
AUTHORS	Strausberg R.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-SEP-2001)	National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	On Aug 19, 2003 this sequence version replaced gi:15559789.		
	Contact: MGC help desk		
	Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a>		
	Tissue Procurement: DCTD/DP		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),		
	Galtherberg, Maryland;		
	Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>		
	Contact: <a href="mailto:nisc_mgc@nhgri.nih.gov">nisc_mgc@nhgri.nih.gov</a>		
	Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Bren, K., Brinkley, C., Brooke, S., Dietrich, N.L., Granite, S., Gunn, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Machado, Q.L., Maestello, C., Masker, B., Mastrian, S.D., McCloskey, J.C., McQuell, J., Pearson, R., Stantirip, S., Thomas, P.J., Touchman, J.W., Tsurenge, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Series: IRAL Place: 30 Row 1 Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: GenomesScan gene prediction.

FEATURES	Location/Qualifiers
source	1. .1236

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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Kidney, renal cell adenocarcinoma"
/clone_lib="KIDNEY_MGC_14"
/lab_host="DH10B-R"
/submitter="NCBI"

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CDS	100. .831

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/gene="CtHRC1"
/codon_start=1
/product="collagen triple helix repeat containing 1"

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## ORIGIN

Query match 96.7%; Score 1215.8; DB 9; Length 1236;

Best Local Similarity 99.8%; Pred. No. 4.9e-206;  
Matches 1217; Conservative 0; Mismatches 2; Indels 0; Gaps 0

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Db 1 CTGCGGCGGCTCGGAGCGCGGGAGGCCAGACGCTCCTCCTCGGTCTC 60

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Db 61 CTCCGCTCCAGCTCCGCGCTGCCCGGAGCCATGCGACCCAGGGCCCCGCC 12

159 GCCTCCCCGACGGCTCCGGGCTCTGCTGCTCCCTGCTGCAAGCTGCCCGCCG 21

D<sub>b</sub> 121 GCCTCCCCGACGGCGTCCGGCGGCCTCCTGCTCCCTGCTGACGTGCCCGCCG 186

219 TCGAGCGCCCTCTGAGATCCCAAGGGAGCAAAAGCGCAGCTCCGCGAGGGAGGTC Z

D5 181 TCGAGCGCCCTCTGAGATCCCAAGGGAGCAAAAGGCGCAGCTCCGCGAGGGAAGTIG 2:

219 G T G A C C T G T A T A A T G G A A T G C C T A C A G G C C A G C A G A T G C C T G G T C A G A C G G 3'

DB 241 GGGACCTGTATATGGAAIGTCTTACAGGGCCAGCAGAGTGCCTGGTCGAGACGGG 30

339 AGCLCIGGCLAAIGIIMILCGGIAACLCGGALCCAGGICGGGAAGAAICAA 3

UD 301 AGCCCGGCGCAAGCAIICGGGAAACACIUGGAIICCAAGIICGGGAGGAIICAA 302

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QY	1239	ATAAAATTTATTTTCCACA	1257
Db	1201	ATAAAATTTATTTTCCACA	1219
RESULT 15			
LOCUS	AR405953	1220 bp	DNA
DEFINITION	Sequence 3 from patent US 6630325.	linear	PAT 18-DEC-2003
ACCESSION	AR405953		
VERSION	AR405953.1	GI:40155009	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (baes 1 to 1220)		
TITLE	Lindner,V. and Friesel,R.E.		
JOURNAL	Compositions, methods and kits relating to remodel		
FEATURES	Patent: US 6630325-A 3 07-OCT-2003;		
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Best Local Similarity	99.8%	Pred. No.	3.4e-203				
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QY	163	CCCGCAGCGAGCTCGCGCGCTCTGCTGCTCTGCTGCTGAGCTGCGCGCGCTGCA	222
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QY	403	AAAAGGGGGAATGTCTGAGGGGAAGCTTTGAGGATCTCTGCAACCCAACTACAGCAGT	462
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AY136825 1221 bp mRNA linear PRI 01-DEC-2002  
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ACCESSION AY136825  
VERSION AY136825.1 GI:25989620  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 1221)  
AUTHORS Lehnert, W., Moore, D.P., Harmon, K.J., Mancini, M.L. and Lindner, V.  
TITLE Expression of the novel collagen triple helix repeat-containing gene (Chrc1) suggests functions in multiple organ systems  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1221)  
AUTHORS Lindner, V.  
TITLE Direct Submission  
JOURNAL Submitted (29-JUL-2002) Center for Molecular Medicine, Maine Medical Center Research Institute, 81 Research Drive, Scarborough, ME 04074, USA

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ORIGIN  
Query Match 95.4%; Score 1198.8; DB 9; Length 1221;  
Best Local Similarity 99.8%; Pred. No. 5.1e-203;  
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RESULT 17

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DEFINITION 207 human secreted proteins.  
ACCESSION BD193030  
VERSION BD193030.1 GI:33002769  
KEYWORDS JP 2002516573-A/124.  
SOURCE  
ORGANISM  
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artificial sequences.  
1 (bases 1 to 1288)  
REFERENCE  
AUTHORS Young, P., Olsen, H.S., Ferrie, A.M., Ruben, S.M., Rosen, C.A.,  
Hu, J.S., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y.,  
Florence, C., Florence, K., Lafleur, D.W., Ni, U., Fan, P., Wei, Y.F.,  
Fischer, C.L., Soppet, D.R., Li, Y., Ze, Z., Kyaw, H., Yu, G.L., Fang, P.,  
Dillon, P.J., Andrews, G.A. and Carter, K.C.  
207 human secreted proteins  
Patent: JP 2002516573-A 124 04-JUN-2002;  
TITLE  
JOURNAL HUMAN GENOME SCIENCES INC  
PN JP 2002516573-A/124  
PD 04-JUN-2002  
PR 04-JUN-1998 JP 1999502815  
PR 06-JUN-1997 US 60/048915, 06-JUN-1997 US 60/048882 PR  
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PI PAUL, YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A  
PI ROSEN,  
PI JING SHAN HU, HENRIK S OLSEN, REINHARD EBNER, LAURIE A BREWER, PI  
PI YANGGU SHI, CHARLES FLORENCE, KIMBERLY FLORENCE, DAVID W LAFLAUR,  
PI JIAN NI,  
PI PING FAN, YING FEI WEI, CARRIE L FISCHER, DANIEL R SOPPET, YI LI,  
PI ZHIHENG ZENG,  
PI HLA KYAW, GUO LIANG YU, PING FENG, PATRICK J DILLON, GREGORY A PI  
PI HLA KYAW, GUO LIANG YU, PING FENG, PATRICK J DILLON, GREGORY A PI  
PI KENNETH C CARTER  
PC A01N37/18, A01N43/04, C12Q1/00, C12Q1/02, C12Q1/68, C12N5/00 PC  
C12N5/06, C12N15/00,  
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Best Local Similarity 99.3%; Pred. No. 1.1e-202;  
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AUTHORS	Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A., Hu, J.S., Olsen, H.S., Eber, R., Brewer, L.A., More, P.A., Shi, Y., Florence, K., Florence, K., Lafleur, D.W., Ni, J., Fan, P., Wei, Y.F., Fischer, C.L., Soppet, D.R., Li, Y., Zeng, Z., Kyaw, H., Yu, G.L., Feng, P., Dillon, P.V., Endres, G.A. and Carter, K.C.		
TITLE	207 human secreted proteins		
JOURNAL	Patent: EP 1428833-A 125 16-JUN-2004;		
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Best Local Similarity	99.3%	Pred. No. 1.1e-202;	Length 1288;
Matches 1242;	Conservative	2;	Mismatches 2;
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QY	728	GGAAGACTTTGTGAGGAATTTGGTGTCTGATTTGTGATGTGTCTATCTGGGTGGCAC	787
Db	718	GGAAGACTTTGTGAGGAATTTGGTGTCTGATTTGTGATGTGTCTATCTGGGTGGCAC	777
QY	788	TTTGTCAGATTACCCCAAGAGAGATGCTTCACTACAGATGGAATTCAGTTTCTGCATCAT	847
Db	778	TTTGTCAGATTACCCCAAGAGAGATGCTTCACTACAGATGGAATTCAGTTTCTGCATCAT	837
QY	848	TATTTGAAAGACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTTTTATTAAT	907
Db	838	TATTTGAAAGACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTTTTATTAAT	897
QY	908	GCCTTGGAAATGCTTCACTTAATATGACATTTTAAATTAAGTTTATGTATATACATCTGAATGA	967
Db	898	GCCTTGGAAATGCTTCACTTAATATGACATTTTAAATTAAGTTTATGTATATACATCTGAATGA	957
QY	968	AAGCAAGACTTAATATGTATTACAGACCAAGATGATTTCAACAGTGTTTTAAATCTAGC	1027
Db	958	AAGCAAGACTTAATATGTATTACAGACCAAGATGATTTCAACAGTGTTTTAAATCTAGC	1016
QY	1028	ATTATTCATTTTGGCTTCATATCAATAAGTGTTCATATATTTTTTTAGTGGTTAGAAATAC	1087
Db	1017	ATTATTCATTTTGGCTTCATATCAATAAGTGTTCATATATTTTTTTAGTGGTTAGAAATAC	1076
QY	1088	TTTTTTTCATATGTCATTTCTCTCAACCTATAATTTTGGAAATATGTTGTGTCTTTTGT	1146
Db	1077	TTTTTTTCATATGTCATTTCTCTCAACCTATAATTTTGGAAATATGTTGTGTCTTTTGT	1136
QY	1147	TTTTCTCTTGTATAGCAATTTTTTAAAAAAATATATAAGCTCCCAATCTTTGTACAAATTTG	1206
Db	1137	TTTTCTCTTGTATAGCAATTTTTTAAAAAAATATATAAGCTCCCAATCTTTGTACAAATTTG	1196
QY	1207	TAAATGTATAAGAAATTTTTTTTTTATATCTGTATAATTAATAATATATTTCCACACA	1257
Db	1197	TAAATGTATAAGAAATTTTTTTTTTATATCTGTATAATTAATAATATATTTCCMACA	1247
RESULT 19			
AKI30063			
AKI30063			
1190 bp			
mRNA			
linear			
PRI 10-SEP-2003			



DEFINITION Homo sapiens cDNA FLJ26553 fis, clone LNF01690.  
ACCESSION AK130063  
VERSION AK130063.1 GI:34526801  
KEYWORDS oligo cloning; fis (Full insert sequence).  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S.,  
Fukuzumi, Y., Fujimori, Y., Komiyama, M., Suzuki, Y., Hata, H.,  
Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T.,  
Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A.,  
Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.  
TITLE NEDO human cDNA sequencing project  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1190)  
AUTHORS Sugano, S. and Suzuki, Y.  
JOURNAL Direct Submission  
TITLE Submitted (31-JUN-2003) Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Laboratory of Genome Structure, Human Genome  
Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
(E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,  
Fax:81-3-5449-5416)  
COMMENT NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing;  
Research Association for Biotechnology (RAB); cDNA library  
construction and 5'-end one pass sequencing; Institute of Medical  
Science, University of Tokyo, Laboratory of Genome Structure, Human  
Genome Center; 3'-end one pass sequencing; RAB; clone selection for  
full insert sequencing; RAB and Helix Research Institute.  
FEATURES  
source  
1..1190  
/organism="Homo sapiens"  
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/clone="LNF01690"  
/cell\_type="fibroblast"  
/tissue\_type="lung"  
/clone\_1ib="LNF"  
/note="Cloning vector: pME18FLA"  
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Query Match 85.1%; Score 1069.8; DB 9; Length 1190;  
Best Local Similarity 92.9%; Pred. No. 4,3e-180;  
Matches 1168; Conservative 0; Mismatches 2; Indels 87; Gaps 1;  
QY 1 GGAGGAGGCGCGCGGTGAAGGCGCATGTATGACCTGGCGGCGCTCGAGCGCGG 60  
DB 16 GGAGGAGGCGCGCGGTGAAGGCGCATGTATGACCTGGCGGCGCTCGAGCGCGG 75  
QY 61 CGAGGCCAGAGCGCTGACCACTTCTCTCTCGTCTCTCGGCTTCAGCTCGCGGCTG 120  
DB 76 CGAGGCCAGAGCGCTGACCACTTCTCTCTCGTCTCTCGGCTTCAGCTCGCGGCTG 135  
QY 121 CGCGGACGCGGAGCCATGCGACCCCAAGGCGCGCGCTCCCGCAGCGGCTCGCGG 180  
DB 136 CGCGGACGCGGAGCCATGCGACCCCAAGGCGCGCGCTCCCGCAGCGG----- 187  
QY 181 GCTCTCTGCTGCTCTGCTGCTGCAAGTCCCGCGCGCGCTCGAGCGCTCTGAGATCCCA 240  
DB 188 ----- 187  
QY 241 AGGGGAACAAAGCGCAGCTCCCGCAGAGAGGAGTGTGACCTGTATAATGAAATGT 300  
DB 188 -----GCTCGGCGCAGAGGAGGAGTGTGACCTGTATAATGAAATGT 228  
QY 301 GCTTACAAGGCGCCAGCAGAGAGTGTCTGTGAGACGGAGACCTTGCGGCGCAATGTTATTC 360  
DB 229 GCTTACAAGGCGCCAGCAGAGAGTGTCTGTGAGACGGAGACCTTGCGGCGCAATGCGATTC 288  
QY 361 CGGTTACACCTGGGATCCAGGTCGGGATGGAATTAAGAGGAGAAAGGGGGAATTCCTGA 420  
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DB 289 CGGTTACACCTGGGATCCAGGTCGGGATGGAATTAAGAGGAGAAAGGGGAAATGTCGA 348  
QY 421 GGGAAAGCTTTGAGGAGTCTGAGACCCCACTCAAGCAGTGTTCATGAGTTCATTTGA 480  
DB 349 GGGAAAGCTTTGAGGAGTCTGAGACCCCACTCAAGCAGTGTTCATGAGTTCATTTGA 408  
QY 481 ATTATGAGATGATCTTGGGAAATTTGGAGGTGATGATTTACCAAGATCGTTCAATA 540  
DB 409 ATTATGAGATGATCTTGGGAAATTTGGAGGTGATGATTTACCAAGATCGTTCAATA 468  
QY 541 GTGCTCTAAGGATTTTGTTCAGTGTGCTGATCTCGGCTTAAATGCAAAATGATGCTGTC 600  
DB 469 GTGCTCTAAGGATTTTGTTCAGTGTGCTGATCTCGGCTTAAATGCAAAATGATGCTGTC 528  
QY 601 AGCGTTGATTTTCAATTCATGAGAGTGAATTTGAGAGCCCTTCCCATGAGCTGA 660  
DB 529 AGCGTTGATTTTCAATTCATGAGAGTGAATTTGAGAGCCCTTCCCATGAGCTGA 588  
QY 661 TAATTTATTTGAGACCAAGAGCCCTGAAATGAAATTCACAAATTAATTAATTCAGCACTT 720  
DB 589 TAATTTATTTGAGACCAAGAGCCCTGAAATGAAATTCACAAATTAATTAATTCAGCACTT 648  
QY 721 CTTCGTGGAAGACCTTTGTGAAGAAATGGTGTGATTAAGTGAATGTTGCTATCTGGG 780  
DB 649 CTTCGTGGAAGACCTTTGTGAAGAAATGGTGTGATTAAGTGAATGTTGCTATCTGGG 708  
QY 781 TTGGCAGCTTGTTCAGATTAACCAAGAGAGTGTCTTACCTGAGTGAATTCAGTTCTTC 840  
DB 709 TTGGCAGCTTGTTCAGATTAACCAAGAGAGTGTCTTACCTGAGTGAATTCAGTTCTTC 768  
QY 841 GCATCATTTATGGAAGACCTTGAAGAAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900  
DB 769 GCATCATTTATGGAAGACCTTGAAGAAATGCTTTAATTTTCAATTTGCTACCTCTTTT 828  
QY 901 TTATTAAGCTTGTGAAGTGTCTCATTTAAAGACATTTTAATTAAGTGAATTAATCATCT 960  
DB 829 TTATTAAGCTTGTGAAGTGTCTCATTTAAAGACATTTTAATTAAGTGAATTAATCATCT 888  
QY 961 GAATGAAGAGCAAGCTTAATATGTTTATACAGACCAAGTGTGATTCACACTGTTTAA 1020  
DB 889 GAATGAAGAGCAAGCTTAATATGTTTATACAGACCAAGTGTGATTCACACTGTTTAA 948  
QY 1021 ATTTCAGTATTAATCAATTTTGGTCAATCAAAAGTGTTCATATTTTAAATTTTAA 1080  
DB 949 ATTTCAGTATTAATCAATTTTGGTCAATCAAAAGTGTTCATATTTTAAATTTTAA 1008  
QY 1081 AGAATACCTTCTTATATGATCATTTCTCTCAACCTTAATTTTGAATTTGTTGCTCT 1140  
DB 1009 AGAATACCTTCTTATATGATCATTTCTCTCAACCTTAATTTTGAATTTGTTGCTCT 1068  
QY 1141 TTTGTTTTTCTCTTATATGATCATTTTAAATTAATTAAGTCAATCTTTGTATC 1200  
DB 1069 TTTGTTTTTCTCTTATATGATCATTTTAAATTAATTAAGTCAATCTTTGTATC 1128  
QY 1201 AATTTGTAATGTTAAGAAATTTTAAATCTGTTAAATTAATTAATTTTTCACA 1257  
DB 1129 AATTTGTAATGTTAAGAAATTTTAAATCTGTTAAATTAATTAATTTTTCACA 1185  
RESULT 20  
AF395488  
LOCUS AF395488 1215 bp mRNA linear PRI 07-JUN-2003  
DEFINITION Homo sapiens NTWC1 mRNA, complete cds.  
ACCESSION AF395488  
VERSION AF395488.1 GI:27525623  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS Sanuki, N., Fujiki, K., Kanai, A., Tanaka, Y. and Iwata, T.  
TITLE Novel polypeptide found in human cornea cDNA library



JOURNAL Unpublished  
REFERENCES 2 (bases 1 to 1215)  
AUTHORS Sanki N., Fujiki, K., Kanai, A., Tanaka, Y. and Iwata, T.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-2001) National Center for Sensor Organs,  
National Tokyo Medical Center, 2-5-1 Higashi-agaoka, Meguro, Tokyo  
152-8902, Japan

FEATURES Location/Qualifiers  
source 1..1215

CDS

/organism="Homo sapiens"  
/mol\_type="mRNA"  
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121..819  
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/product="NTMCI"  
/protein\_id="AA017919.1"  
/db\_xref="GI:27525624"  
/translation="MMPGRSIVKUREKTVSRKLEMPSPAFQGLICGRNGMCLQG  
PAGVPGRDSPGANGIPGTGIPGRDGPKEGECLESFEESWTENYKQGSISLNY  
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VSRILEELPYML"

ORIGIN

Query Match 76.7%; Score 964.6; DB 9; Length 1215;  
Best Local Similarity 99.6%; Pred. No. 2,1e-161;  
Matches 967; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 287 GTATAATGGAATGCTTACAGAGCCAGCAGAGTGCCTGTGAGACGGAGCCCTGG 346  
DB 228 GTATAATGGAATGCTTACAGAGCCAGCAGAGTGCCTGTGAGACGGAGCCCTGG 287  
QY 347 GGGCAATGTTATCCGGGTACACCTGGATCCCAAGTCCGAGATGATTTCAAGAGAAAA 406  
DB 288 GGGCAATGCTTACAGAGCCAGCAGAGTGCCTGTGAGACGGAGCCCTGG 347  
QY 407 GGGGGAATGCTGAGGGAAGCTTTGAGAGTCTGGAACACCACTACAGAGAGTTC 466  
DB 348 GGGGGAATGCTGAGGGAAGCTTTGAGAGTCTGGAACACCACTACAGAGAGTTC 407  
QY 467 ATGAGATTCATTAATTAATGAGATTAATGAGATTAATGAGATTAATGAGATTA 526  
DB 408 ATGAGATTCATTAATTAATGAGATTAATGAGATTAATGAGATTAATGAGATTA 467  
QY 527 GATGCGTCAAAATGCTCTTAAGAGTTCCTGAGTCTGAGTCTGAGTCTGAGTCT 586  
DB 468 GATGCGTCAAAATGCTCTTAAGAGTTCCTGAGTCTGAGTCTGAGTCTGAGTCT 527  
QY 587 AAATGCAATGCTGAGGCTGATTAATTAATTAATTAATTAATTAATTAATTAAT 646  
DB 528 AAATGCAATGCTGAGGCTGATTAATTAATTAATTAATTAATTAATTAATTAAT 587  
QY 647 TCCCATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 706  
DB 588 TCCCATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 647  
QY 707 TATTCATTCGACATTCCTGCTGAGAGACCTTTGAGAGAAATGCTGCTGAGTGA 766  
DB 648 TATTCATTCGACATTCCTGCTGAGAGACCTTTGAGAGAAATGCTGCTGAGTGA 707  
QY 767 TGTTCATTCGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 826  
DB 708 TGTTCATTCGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 767  
QY 827 GAATTCAGTTCGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 886  
DB 768 GAATTCAGTTCGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 827  
QY 887 TGTTCATTCGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 946  
DB 828 TGTTCATTCGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 887  
QY 947 TTATGATATCATCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1006

DB 888 TTATGATATCATCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 947  
QY 1007 CACACGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1066  
DB 948 CACACGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1007  
QY 1067 TTTTTCATTCGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1126  
DB 1008 TTTTTCATTCGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1067  
QY 1127 TATTCATTCGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1186  
DB 1068 TATTCATTCGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1127  
QY 1187 ACCAATCTTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1246  
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QY 1247 TATTCATTCGAGGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1246  
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RESULT 21

AR454024 837 bp DNA linear PAT 20-FEB-2004

LOCUS AR454024 Sequence 512 from patent US 6680197.

DEFINITION AR454024

ACCESSION AR454024

VERSION AR454024.1 GI:42686814

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match 65.7%; Score 826; DB 6; Length 837;

Best Local Similarity 99.9%; Pred. No. 8,6e-137;

Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 332 ATGCACTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 91  
DB 1 ATGCACTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 59  
QY 92 CGGTCCTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 151  
DB 60 CGGTCCTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 119  
QY 152 CCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 211  
DB 120 CCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 179  
QY 212 CCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 271  
DB 180 CCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 239  
QY 272 GAGAGTGTGAGCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 331  
DB 240 GAGAGTGTGAGCTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 299  
QY 332 AGACGGAGCCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 391  
DB 300 AGACGGAGCCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 359



[illegible]

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ORIGIN		
Query Match	58.2%; Score 732; DB 6; Length 732;	
Best Local Similarity	100.0%; Pred. No. 4.3e-120;	
Matches 732; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	138 ATGCGACCCCAAGGGCCCCGCCGCTCCCCCGAGCGGCTCCCGGGCCTTCGTGCTCTG	197
Db	1 ATGGGACCCCAGGGCCCCGCCGCTCCCCCGAGGGCTCCGGGCCTTCGTGCTCTG	60
OY	198 CTGCTGCAAGCTGCCCCGGCGCGTCTGAGGCGCTTGAGATCCCAAGGGGAACAAGAAGCG	257
Db	61 CTGCTGCAAGCTGCCCCGGCGCGTCTGAGGCGCTTGAGATCCCAAGGGGAACAAGAAGCG	120
OY	258 CAGCTCCGCGAGAGGAGTGTGTGAACTCTGATTAATGGAATGTGCTTACAAGGCGCACGA	317
Db	121 CAGCTCCGCGAGAGGAGTGTGTGAACTCTGATTAATGGAATGTGCTTACAAGGCGCACGA	180
OY	318 GGAGTGCTCGTGTGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGGTACACTGGGATC	377
Db	181 GGAGTGCTCGTGTGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGGTACACTGGGATC	240
OY	378 CCAGGTGGGATGTGATTCAAAGGAGAAAAGGGGAATGTCTGAGGAAAGCTTTGAGAG	437
Db	241 CCAGGTGGGATGTGATTCAAAGGAGAAAAGGGGAATGTCTGAGGAAAGCTTTGAGAG	300
OY	438 TCCTGGAACCAACTCAAGCAGTGTTCATGAGATTCATTGAATTATGCGATAGATCTT	497
Db	301 TCCTGGAACCAACTCAAGCAGTGTTCATGAGATTCATTGAATTATGCGATAGATCTT	360
OY	498 GGGAAAAATTGGGAGGTGACATTTACAAAGATGCGTTCAAAVTAGTGTCTAAGAAGTTTG	557
Db	361 GGGAAAAATTGGGAGGTGACATTTACAAAGATGCGTTCAAAVTAGTGTCTAAGAAGTTTG	420
OY	558 TTCAGTGGCTCACTTCGGCTAAAATGCAAGAAATGCATGCTGTCAAGCCTTGGTATTTCACA	617
Db	421 TTCAGTGGCTCACTTCGGCTAAAATGCAAGAAATGCATGCTGTCAAGCCTTGGTATTTCACA	480
OY	618 TTCATGAGAGCTGAAATGTTTCAGAACCTCTTCCCATTTGAAGCTATAATTTATTTGGACCA	677
Db	481 TTCATGAGAGCTGAAATGTTTCAGAACCTCTTCCCATTTGAAGCTATAATTTATTTGGACCA	540
OY	678 GGAAGCCCTGAATGAATTCACAATTAATATTCATGCACTTCTTGTGGAAGACTT	737
Db	541 GGAAGCCCTGAATGAATTCACAATTAATATTCATGCACTTCTTGTGGAAGACTT	600
OY	738 TGTGAGGAATTTGTTGCTGGAATTATGTGGAATGTTGCTATCTGGGTTGGCACTTGTTCAGAT	797
Db	601 TGTGAGGAATTTGTTGCTGGAATTATGTGGAATGTTGCTATCTGGGTTGGCACTTGTTCAGAT	660
OY	798 TAACCAAAAGGAGATGCTTCTACGAGATGGAATTCAAGTTCTGCAGATCATTTATGAAGAA	857
Db	661 TAACCAAAAGGAGATGCTTCTACGAGATGGAATTCAAGTTCTGCAGATCATTTATGAAGAA	720
OY	858 CTACCAAAATAA 869	
Db	721 CTACCAAAATAA 732	
RESULT 25		
LOCUS	AR454023	729 bp DNA linear PAT 20-FEB-2004
DEFINITION	Sequence 511 from patent US 6680197.	
ACCESSION	AR454023	
VERSION	AR454023.1 GI:42686813	
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 729)	

AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L.,  
Hepler, W.T. and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of breast  
cancer  
JOURNAL Patent: US 6680197-A 511 20-JAN-2004;  
FEATURES Location/Qualifiers  
source 1..729  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 58.0%; Score 729; DB 6; Length 729;  
Best Local Similarity 100.0%; Pred. No. 1.5e-119;  
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 ATGCCACCCGAGGGGCCCCCGCTCTCCCGCAGCGGCTCCGGGCTCTCTGCTCTG 197  
Db 1 ATGCCACCCGAGGGGCCCCCGCTCTCCCGCAGCGGCTCCGGGCTCTCTGCTCTG 60  
QY 198 CTGCTGACAGCTCCCGCGCGCTGAGCGGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 257  
Db 61 CTGCTGACAGCTCCCGCGCGCTGAGCGGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 120  
QY 258 CAGCTCCGCGAGAGGAGGAGTGTGACCTGTATATATGATGATGTCTTACAGGCGCAGCA 317  
Db 121 CAGCTCCGCGAGAGGAGGAGTGTGACCTGTATATATGATGATGTCTTACAGGCGCAGCA 180  
QY 318 GAGAGGCTGTGTCAGACGGGAGCCCTGGGGCCAAATTTATCCGGGTACACTTGGAGTC 377  
Db 181 GAGAGGCTGTGTCAGACGGGAGCCCTGGGGCCAAATTTATCCGGGTACACTTGGAGTC 240  
QY 378 CCAGGTCCGGATGATTTCAAGAGAGAGAGGAGGATGTCTGAGGAAAGCTTTGAGAG 437  
Db 241 CCAGGTCCGGATGATTTCAAGAGAGAGAGGAGGATGTCTGAGGAAAGCTTTGAGAG 300  
QY 438 TCCTGGACACCACTACAGAGAGTGTCTGAGATCTTGAATTAATGAGATCTT 497  
Db 301 TCCTGGACACCACTACAGAGAGTGTCTGAGATCTTGAATTAATGAGATCTT 360  
QY 498 GGGAAATTTGGGAGTGTATCTTCAAGAGATGCTTCAAGAGCTTAAAGATTTG 557  
Db 361 GGGAAATTTGGGAGTGTATCTTCAAGAGATGCTTCAAGAGCTTAAAGATTTG 420  
QY 558 TTCAGTGGCTCACTTCGGCTAAATATGCAAAATGATGCTGTGAGGTTGATTTTACA 617  
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QY 618 TTCATGAGAGTGTATGTCAGAGCTCTTCCATTTGAAGCTATTAATTTTGAACCA 677  
Db 481 TTCATGAGAGTGTATGTCAGAGCTCTTCCATTTGAAGCTATTAATTTTGAACCA 540  
QY 678 GGAAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 737  
Db 541 GGAAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 600  
QY 738 TGTGAAGGAATTTGCTGATTAATGATGATGATGATGATGATGATGATGATGATG 797  
Db 601 TGTGAAGGAATTTGCTGATTAATGATGATGATGATGATGATGATGATGATGATG 660  
QY 798 TACCCAAAGAGAGATGCTTTCTATCTGATGATGATGATGATGATGATGATGATG 857  
Db 661 TACCCAAAGAGAGATGCTTTCTATCTGATGATGATGATGATGATGATGATGATG 720  
QY 858 CTACCAAAA 866  
Db 721 CTACCAAAA 729

RESULT 26  
BD006704  
LOCUS BD006704 732 bp DNA linear PAT 31-JAN-2002  
DEFINITION Novel polypeptide.  
ACCESSION BD006704

VERSION BD006704.1 GI:18635075  
KEYWORDS JP 2001029090-A/7.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 732)  
AUTHORS Ito, Y., Mogi, S., Tanaka, H., Okubo, S. and Ogi, K.  
TITLE Novel polypeptide  
JOURNAL Patent: JP 2001029090-A 7 06-FEB-2001;  
COMMENT TAKEDA CHEMICAL INDUSTRIES LTD  
OS Homo sapiens (human)  
PN JP 2001029090-A/7  
PD 06-FEB-2001  
PF 19-MAY-2000 JP 2000147530  
PR  
PI YASUAKI ITO, SHINICHI MOGI, HIDEYUKI TANAKA, SHOICHI OKUBO, PI  
KAZUHIRO OGI  
PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,  
PC A61P1/00  
PC A61P5/00, A61P9/00, A61P11/00, A61P25/00, A61P25/18, A61P31/00, PC  
A61P35/00,  
PC A61P37/00, C07K14/47, C07K16/18, C12P21/02, G01N33/15, G01N33/50,  
PC G01N33/56//  
PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12P21/02, PC  
C12R1.91)  
PC C12N5/10, C12R1.91), (C12P21/08, C12R1.91), C12N15/00, A61K37/02,  
PC C12N5/00,  
PC (C12N5/00, C12R1.91)  
CC  
FH Key Location/Qualifiers  
FT source 1..732  
FT /organism="Homo sapiens (human)".  
FEATURES  
source 1..732  
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ORIGIN

Query Match 58.0%; Score 728.8; DB 6; Length 732;  
Best Local Similarity 99.7%; Pred. No. 1.6e-119;  
Matches 730; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 138 ATGCCACCCGAGGGGCCCCCGCTCTCCCGCAGCGGCTCCGGGCTCTCTGCTCTG 197  
Db 1 ATGCCACCCGAGGGGCCCCCGCTCTCCCGCAGCGGCTCCGGGCTCTCTGCTCTG 60  
QY 198 CTGCTGACAGCTCCCGCGCGCTGAGCGGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 257  
Db 61 CTGCTGACAGCTCCCGCGCGCTGAGCGGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 120  
QY 258 CAGCTCCGCGAGAGGAGTGTGACCTGTATATATGATGATGATGATGATGATGATG 317  
Db 121 CAGCTCCGCGAGAGGAGTGTGACCTGTATATATGATGATGATGATGATGATGATG 180  
QY 318 GGAAGGCTGTGTCAGACGGGAGCCCTGGGGCCAAATTTATTCGGGTACACTTGGATC 377  
Db 181 GGAAGGCTGTGTCAGACGGGAGCCCTGGGGCCAAATTTATTCGGGTACACTTGGATC 240  
QY 378 CCAGGTCCGGATGATTTCAAGAGAGAGAGGAGGATGTCTGAGGAAAGCTTTGAGAG 437  
Db 241 CCAGGTCCGGATGATTTCAAGAGAGAGAGGAGGATGTCTGAGGAAAGCTTTGAGAG 300  
QY 438 TCCTGGACACCACTACAGAGAGTGTCTGAGATCTTGAATTAATGAGATCTT 497  
Db 301 TCCTGGACACCACTACAGAGAGTGTCTGAGATCTTGAATTAATGAGATCTT 360  
QY 498 GGGAAATTTGGGAGTGTATCTTCAAGAGATGCTTCAAGAGCTTAAAGATTTG 557  
Db 361 GGGAAATTTGGGAGTGTATCTTCAAGAGATGCTTCAAGAGCTTAAAGATTTG 420  
QY 558 TTCAGTGGCTCACTTCGGCTAAATATGCAAAATGATGCTGTGAGGTTGATTTTACA 617

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Db 421 TTCAAGGCTCACTTGCGCTAAATATGCAAAATGACGCTGACGGTGTGATTTTCA 480  
Qy 618 TTCAATGAGCTGAATGTTTCAAGACCTCTTCCCATGAGCTATATTTATTTGACCA 677  
Db 481 TTCAATGAGCTGAATGTTTCAAGACCTCTTCCCATGAGCTATATTTATTTGACCA 540  
Qy 678 GGAAGCCCTGAATGATTTCAACAATTAATTCATGCACTTCTGTGAGAGACTT 737  
Db 541 GGAAGCCCTGAATGATTTCAACAATTAATTCATGCACTTCTGTGAGAGACTT 600  
Qy 738 TGTGAAGGATTTGCTGATTTAGTGAATGTTGCTATCTGGGTGCACTTGTTCAGAT 797  
Db 601 TGTGAAGGATTTGCTGATTTAGTGAATGTTGCTATCTGGGTGCACTTGTTCAGAT 660  
Qy 798 TACCCAAAAGAGATGCTTCTACTGATGAGATTCAGTTTCTGCACTTATTTAGAA 857  
Db 661 TACCCAAAAGAGATGCTTCTACTGATGAGATTCAGTTTCTGCACTTATTTAGAA 720  
Qy 858 CTACCAAAATTA 869  
Db 721 CTACCAAAATTA 732

RESULT 27  
LOCUS CQ714369 732 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 303 from Patent WO02068579.  
ACCESSION CQ714369  
VERSION CQ714369.1 GI:42275226  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W., and Myers, E.W.  
TITLE Kites, such as nucleic acid arrays, comprising a majority of humenexons or transcripts, for detecting expression and other uses thereof  
JOURNAL Patent: WO 02068579-A 303 06-SEP-2002;  
PE Corporation (NY) (US)  
LOCATION/Qualifiers  
1. 732  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

FEATURES  
source  
1. 732  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 57.9%; Score 727.2; DB 6; Length 732;  
Best Local Similarity 99.6%; Pred. No. 3.1e-119; Mismatches 3; Indels 0; Gaps 0;  
Matches 729; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 138 ATGCGAAGCCGAGGCGCCGCGCTCCGCGCAGCGGCTCCGCGCTCTGCTGCTCTG 197  
Db 1 ATGCGAAGCCGAGGCGCCGCGCTCCGCGCAGCGGCTCCGCGCTCTGCTGCTCTG 60  
Qy 198 CTGCTGCAAGTCCCGCGCGCTGAGCGGCTTGAATCCCAAGGAGGAAAGCGG 257  
Db 61 CTGCTGCAAGTCCCGCGCGCTGAGCGGCTTGAATCCCAAGGAGGAAAGCGG 120  
Qy 258 CAGCTCCGCGAGGAGGAGGCTGTGAGCTGTATTAAGTATGCTTACAGGCGCAGCA 317  
Db 121 CAGCTCCGCGAGGAGGAGGCTGTGAGCTGTATTAAGTATGCTTACAGGCGCAGCA 180  
Qy 318 GGAAGCTCTGCTGAGACGGAGCCCTGAGGCGCAATGTTATTCGGGTAACCTGGAGATC 377  
Db 181 GGAAGCTCTGCTGAGACGGAGCCCTGAGGCGCAATGTTATTCGGGTAACCTGGAGATC 240  
Qy 378 CCAAGTCTGGAGTGAATTTCAAGAGAAAGGGGAAATGTCTGAGGAGAAAGCTTTGAGAG 437  
Db 241 CCAAGTCTGGAGTGAATTTCAAGAGAAAGGGGAAATGTCTGAGGAGAAAGCTTTGAGAG 300

Qy 438 TCTTGACACCCCACTACAGCAGTGTTCATGAGTTCATTTGAATTAATGATAGTCT 497  
Db 301 TCTTGACACCCCACTACAGCAGTGTTCATGAGTTCATTTGAATTAATGATAGTCT 360  
Qy 498 GGGAAATTTGGGAGTGTACATTTTACAAAGATGCGTTCAAAATAGCTTCTAGAGTTTG 557  
Db 361 GGGAAATTTGGGAGTGTACATTTTACAAAGATGCGTTCAAAATAGCTTCTAGAGTTTG 420  
Qy 558 TTCAAGGCTCACTTCCGCTAAATATGCAAAATGATGATGCTGAGGTTGATTTTCA 617  
Db 421 TTCAAGGCTCACTTCCGCTAAATATGCAAAATGATGATGCTGAGGTTGATTTTCA 480  
Qy 618 TTCAATGAGCTGAATGTTTCAAGACCTCTTCCCATGAGCTATATTTATTTGACCA 677  
Db 481 TTCAATGAGCTGAATGTTTCAAGACCTCTTCCCATGAGCTATATTTATTTGACCA 540  
Qy 678 GGAAGCCCTGAATGATTTCAACAATTAATTCATGCACTTCTGTGAGAGACTT 737  
Db 541 GGAAGCCCTGAATGATTTCAACAATTAATTCATGCACTTCTGTGAGAGACTT 600  
Qy 738 TGTGAAGGATTTGCTGATTTAGTGAATGTTGCTATCTGGGTGCACTTGTTCAGAT 797  
Db 601 TGTGAAGGATTTGCTGATTTAGTGAATGTTGCTATCTGGGTGCACTTGTTCAGAT 660  
Qy 798 TACCCAAAAGAGATGCTTCTACTGATGAGATTCAGTTTCTGCACTTATTTAGAA 857  
Db 661 TACCCAAAAGAGATGCTTCTACTGATGAGATTCAGTTTCTGCACTTATTTAGAA 720  
Qy 858 CTACCAAAATTA 869  
Db 721 CTACCAAAATTA 732

RESULT 28  
LOCUS AX375790/c 683 bp DNA linear PAT 01-MAR-2002  
DEFINITION Sequence 3 from Patent WO0173031.  
ACCESSION AX375790  
VERSION AX375790.1 GI:19170293  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Xu, J., and Stolk, J.A.  
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer  
JOURNAL Patent: WO 0173031-A 3 04-OCT-2001;  
CORIXA CORPORATION (US)  
LOCATION/Qualifiers  
1. 683  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

FEATURES  
source  
1. 683  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 54.3%; Score 682.2; DB 6; Length 683;  
Best Local Similarity 99.7%; Pred. No. 3e-111; Mismatches 2; Indels 0; Gaps 0;  
Matches 681; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 516 AATTTTCAAAATAGCTTCAATATGCTCTTAAGAGTTTCTTCAAGGCTCACTTGG 575  
Db 683 AATTTTCAAAATAGCTTCAATATGCTCTTAAGAGTTTCTTCAAGGCTCACTTGG 624  
Qy 576 CTAAATGAGAAATGATGCTGTGAGCGTTGGTATTTTCAATTCATGAGCTGATGT 635  
Db 623 CTAAATGAGAAATGATGCTGTGAGCGTTGGTATTTTCAATTCATGAGCTGATGT 564  
Qy 636 TGAAGCTCTTCCCATTTGAAGCTATATTTATTTGACCAAGAAAGCCCTGAATGAT 695  
Db 563 TGAAGCTCTTCCCATTTGAAGCTATATTTATTTGACCAAGAAAGCCCTGAATGAT 504

QY 696 TCAACATTAATATTCATGCACTTCTCTGTGGAAGACCTTGTGAAGAAATTGGTCT 755  
DB 503 TCAACATTAATATTCATGCACTTCTCTGTGGAAGACCTTGTGAAGAAATTGGTCT 444  
QY 756 GGATTAGTGAATGTTGCTATCTGGGTGGCACTTGTTCAGTTAACCCAAAAGAGATGCT 815  
DB 443 GGATTAGTGAATGTTGCTATCTGGGTGGCACTTGTTCAGTTAACCCAAAAGAGATGCT 384  
QY 816 TCTACTGATGGAATTCAGTTCTCGCATCATTAATGAAGAACTAACAAATTAATGCTT 875  
DB 383 TCTACTGATGGAATTCAGTTCTCGCATCATTAATGAAGAACTAACAAATTAATGCTT 324  
QY 876 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAAGTGTCTCAATTAATGCAAT 935  
DB 323 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAAGTGTCTCAATTAATGCAAT 264  
QY 936 TTTAAATAGTTTATGATATACATCTGAATGAAGAAAGCAAGCTAAATATGTTACAGCA 995  
DB 263 TTTAAATAGTTTATGATATACATCTGAATGAAGAAAGCAAGCTAAATATGTTACAGCA 204  
QY 996 AAGTGTGATTCACACTGTTTTTAAATCTAGCATTAATCAATTTGGCTTCATCAAAAGTG 1055  
DB 203 AAGTGTGATTCACACTGTTTTTAAATCTAGCATTAATCAATTTGGCTTCATCAAAAGTG 144  
QY 1056 GTTTCATATTTTTTTTATGTTAGTGTGAATATCTTTCTTATGTCACATTTCTCAACT 1115  
DB 143 GTTTCATATTTTTTTTATGTTAGTGTGAATATCTTTCTTATGTCACATTTCTCAACT 84  
QY 1116 ATAATTTGGAATATGTTGTGCTTTTGTCTTCTAGTATGCAATTTTAAATAA 1175  
DB 83 ATAATTTGGAATATGTTGTGCTTTTGTCTTCTAGTATGCAATTTTAAATAA 24  
QY 1176 ATATTAAGCTACCAATCTTGT 1198  
DB 23 ATATTAAGCTACCAATCTTGT 1

RESULT 29  
AR280558/c  
LOCUS AR280558 683 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 63 from patent US 6518237.  
ACCESSION AR280558  
VERSION AR280558.1 GI:29716028  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Yugiu,J., Dillon,D.C., Mitcham,J.L. and Xu,J.  
TITLE Compositions for treatment and diagnosis of breast cancer and methods for their use  
JOURNAL Patent: US 6518237-A 63 11-FEB-2003;  
FEATURES  
LOCATION/Qualifiers  
1..683  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 54.2%; Score 681.8; DB 6; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.5e-111;  
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTCACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 575  
DB 683 ACATTTCACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624  
QY 576 CTAATAATGCAAGATGCAATGCTGAGGTTGTATTCACATTTCAATGAAGGCTGAATGT 635  
DB 623 CTAATAATGCAAGATGCAATGCTGAGGTTGTATTCACATTTCAATGAAGGCTGAATGT 564  
QY 636 TCAGGACCTCTTCCCATTTGAAGCTAATATTTATTTGACCAAGAGGCTGAATGAT 695  
DB 563 TCAGGACCTCTTCCCATTTGAAGCTAATATTTATTTGACCAAGAGGCTGAATGAT 504

QY 696 TCAACATTAATATTCATGCACTTCTCTGTGGAAGACCTTGTGAAGAAATTGGTCT 755  
DB 503 TCAACATTAATATTCATGCACTTCTCTGTGGAAGACCTTGTGAAGAAATTGGTCT 444  
QY 756 GGATTAGTGAATGTTGCTATCTGGGTGGCACTTGTTCAGTTAACCCAAAAGAGATGCT 815  
DB 443 GGATTAGTGAATGTTGCTATCTGGGTGGCACTTGTTCAGTTAACCCAAAAGAGATGCT 384  
QY 816 TCTACTGATGGAATTCAGTTCTCGCATCATTAATGAAGAACTAACAAATTAATGCTT 875  
DB 383 TCTACTGATGGAATTCAGTTCTCGCATCATTAATGAAGAACTAACAAATTAATGCTT 324  
QY 876 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAAGTGTCTCAATTAATGCAAT 935  
DB 323 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAAGTGTCTCAATTAATGCAAT 264  
QY 936 TTTAAATAGTTTATGATATACATCTGAATGAAGAAAGCAAGCTAAATATGTTACAGCA 995  
DB 263 TTTAAATAGTTTATGATATACATCTGAATGAAGAAAGCAAGCTAAATATGTTACAGCA 204  
QY 996 AAGTGTGATTCACACTGTTTTTAAATCTAGCATTAATCAATTTGGCTTCATCAAAAGTG 1055  
DB 203 AAGTGTGATTCACACTGTTTTTAAATCTAGCATTAATCAATTTGGCTTCATCAAAAGTG 144  
QY 1056 GTTTCATATTTTTTTTATGTTAGTGTGAATATCTTTCTTATGTCACATTTCTCAACT 1115  
DB 143 GTTTCATATTTTTTTTATGTTAGTGTGAATATCTTTCTTATGTCACATTTCTCAACT 84  
QY 1116 ATAATTTGGAATATGTTGTGCTTTTGTCTTCTAGTATGCAATTTTAAATAA 1175  
DB 83 ATAATTTGGAATATGTTGTGCTTTTGTCTTCTAGTATGCAATTTTAAATAA 24  
QY 1176 ATATTAAGCTACCAATCTTGT 1198  
DB 23 ATATTAAGCTACCAATCTTGT 1

RESULT 30  
AR283054/c  
LOCUS AR283054 683 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 63 from patent US 6528054.  
ACCESSION AR283054  
VERSION AR283054.1 GI:29719881  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.  
TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
JOURNAL Patent: US 6528054-A 63 04-MAR-2003;  
FEATURES  
LOCATION/Qualifiers  
1..683  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 54.2%; Score 681.8; DB 6; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.5e-111;  
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTCACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 575  
DB 683 ACATTTCACAAAGATGCGTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624  
QY 576 CTAATAATGCAAGATGCAATGCTGAGGTTGTATTCACATTTCAATGAAGGCTGAATGT 635  
DB 623 CTAATAATGCAAGATGCAATGCTGAGGTTGTATTCACATTTCAATGAAGGCTGAATGT 564  
QY 636 TCAGGACCTCTTCCCATTTGAAGCTAATATTTATTTGACCAAGAGGCTGAATGAT 695

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Db 563 TCAGACCTCTCCCATTTGAGCTATATTTATTTGGACCAAGAGCCCTGAAATGAAT 504
Qy 696 TCACCAATTAATATTCATGCGACTCTTCTGTGGAGAGACTTTGAGGAATGGTGCT 755
Db 503 TCACCAATTAATATTCATGCGACTCTTCTGTGGAGAGACTTTGAGGAATGGTGCT 444
Qy 756 GGATTAGGAGAGTGTCTATCTGGGTGGCACTTGTTCAGATTAACCAAGAGAGATGCT 815
Db 443 GGATTAGGAGAGTGTCTATCTGGGTGGCACTTGTTCAGATTAACCAAGAGAGATGCT 384
Qy 816 TCTACTGATGAGAAATTCAGTTTCTCCGATCATTAATGAGAACTACCAAAATTAATGCTT 875
Db 383 TCTACTGATGAGAAATTCAGTTTCTCCGATCATTAATGAGAACTACCAAAATTAATGCTT 324
Qy 876 TAATTTTCATTTGCTACCTCTTTTATTTATTTAGCCCTGGAGATGCTCACTTAATGACAT 935
Db 323 TAATTTTCATTTGCTACCTCTTTTATTTATTTAGCCCTGGAGATGCTCACTTAATGACAT 264
Qy 936 TTTAAATTAAGTTTATGATATACCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 995
Db 263 TTTAAATTAAGTTTATGATATACCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 204
Qy 996 AAGTGTGATTTTCACACTGTTTTTAAATCTAGCATTAATTCATTTGGCTTCAATCAAAAGTG 1055
Db 203 AAGTGTGATTTTCACACTGTTTTTAAATCTAGCATTAATTCATTTGGCTTCAATCAAAAGTG 144
Qy 1056 GTTTCAAATATTTTTTTTATGTTGTTAGGTAGAAATACCTTCTTCATAGTCAATCTCAACCT 1115
Db 143 GTTTCAAATATTTTTTTTATGTTGTTAGGTAGAAATACCTTCTTCATAGTCAATCTCAACCT 84
Qy 1116 ATAAATTTGAATATGTTGTGCTTTGTTTCTCTAGATAGCATTTTAAATTA 1175
Db 83 ATAAATTTGAATATGTTGTGCTTTGTTTCTCTAGATAGCATTTTAAATTA 24
Qy 1176 ATATAAAGCTACCAATCTTTGT 1198
Db 23 ATATAAAGCTACCAATCTTTGT 1
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RESULT 31
AR341827/c 683 bp DNA linear PAT 17-AUG-2003
LOCUS AR341827 Sequence 63 from patent US 6573368.
DEFINITION AR341827
ACCESSION AR341827 GI:33736404
VERSION AR341827.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 683)
TITLES Yugi,J., Dillon,D.C., Mitcham,J.L. and Xu,J.
JOURNAL Compositions for the treatment and diagnosis of breast cancer and
FEATURES methods for their use
source Patent: US 6573368-A 63 03-JUN-2003;
1. .683 Location/Qualifiers
/mol_type="genomic DNA"
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ORIGIN
Query Match 54.2%; Score 681.8; DB 6; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.5e-111;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 636 TCAGACCTCTCCCATTTGAGCTATATTTATTTGGACCAAGAGCCCTGAAATGAAT 695
Db 563 TCAGACCTCTCCCATTTGAGCTATATTTATTTGGACCAAGAGCCCTGAAATGAAT 504
Qy 696 TCACCAATTAATATTCATGCGACTCTTCTGTGGAGAGACTTTGAGGAATGGTGCT 755
Db 503 TCACCAATTAATATTCATGCGACTCTTCTGTGGAGAGACTTTGAGGAATGGTGCT 444
Qy 756 GGATTAGGAGAGTGTCTATCTGGGTGGCACTTGTTCAGATTAACCAAGAGAGATGCT 815
Db 443 GGATTAGGAGAGTGTCTATCTGGGTGGCACTTGTTCAGATTAACCAAGAGAGATGCT 384
Qy 816 TCTACTGATGAGAAATTCAGTTTCTCCGATCATTAATGAGAACTACCAAAATTAATGCTT 875
Db 383 TCTACTGATGAGAAATTCAGTTTCTCCGATCATTAATGAGAACTACCAAAATTAATGCTT 324
Qy 876 TAATTTTCATTTGCTACCTCTTTTATTTATTTAGCCCTGGAGATGCTCACTTAATGACAT 935
Db 323 TAATTTTCATTTGCTACCTCTTTTATTTATTTAGCCCTGGAGATGCTCACTTAATGACAT 264
Qy 936 TTTAAATTAAGTTTATGATATACCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 995
Db 263 TTTAAATTAAGTTTATGATATACCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 204
Qy 996 AAGTGTGATTTTCACACTGTTTTTAAATCTAGCATTAATTCATTTGGCTTCAATCAAAAGTG 1055
Db 203 AAGTGTGATTTTCACACTGTTTTTAAATCTAGCATTAATTCATTTGGCTTCAATCAAAAGTG 144
Qy 1056 GTTTCAAATATTTTTTTTATGTTGTTAGGTAGAAATACCTTCTTCATAGTCAATCTCAACCT 1115
Db 143 GTTTCAAATATTTTTTTTATGTTGTTAGGTAGAAATACCTTCTTCATAGTCAATCTCAACCT 84
Qy 1116 ATAAATTTGAATATGTTGTGCTTTGTTTCTCTAGATAGCATTTTAAATTA 1175
Db 83 ATAAATTTGAATATGTTGTGCTTTGTTTCTCTAGATAGCATTTTAAATTA 24
Qy 1176 ATATAAAGCTACCAATCTTTGT 1198
Db 23 ATATAAAGCTACCAATCTTTGT 1
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RESULT 32
AR343822/c 683 bp DNA linear PAT 17-AUG-2003
LOCUS AR343822 Sequence 63 from patent US 6579973.
DEFINITION AR343822
ACCESSION AR343822
VERSION AR343822.1
KEYWORDS GI:33739722
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 683)
TITLES Yugi,J., Dillon,D.C., Mitcham,J.L., Xu,J. and Harlocker,S.L.
JOURNAL Compositions for the treatment and diagnosis of breast cancer and
FEATURES methods for their use
source Patent: US 6579973-A 63 17-JUN-2003;
1. .683 Location/Qualifiers
/mol_type="genomic DNA"
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ORIGIN
Query Match 54.2%; Score 681.8; DB 6; Length 683;
Best Local Similarity 99.6%; Pred. No. 3.5e-111;
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 636 TCAGGACCTCTTCCCATGGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 695  
DB 563 TCAGGACCTCTTCCCATGGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 504  
QY 636 TCAGGACCTCTTCCCATGGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 755  
DB 503 TCAGGACCTCTTCCCATGGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 444  
QY 756 GGATGATGAGATGCTATCTGAGTGGGTTGGACCTGTTGATGATGATGATGATGATGAT 815  
DB 443 GGATGATGAGATGCTATCTGAGTGGGTTGGACCTGTTGATGATGATGATGATGATGAT 384  
QY 816 TCTACTGATGAGATGCTATCTGAGTGGGTTGGACCTGTTGATGATGATGATGATGATGAT 875  
DB 383 TCTACTGATGAGATGCTATCTGAGTGGGTTGGACCTGTTGATGATGATGATGATGATGAT 324  
QY 876 TTAATTTTCAATTTTGTCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 935  
DB 323 TTAATTTTCAATTTTGTCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 264  
QY 936 TTTAATAATGTTTATGATATCATCTGATGAGAAAGCAAGCTAATATGTTTACAGACCA 995  
DB 263 TTTAATAATGTTTATGATATCATCTGATGAGAAAGCAAGCTAATATGTTTACAGACCA 204  
QY 996 AAGTGTGATTTTCAACCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1055  
DB 203 AAGTGTGATTTTCAACCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 144  
QY 1056 GTTTCAATATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1115  
DB 143 GTTTCAATATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 84  
QY 1116 ATAAATTTGGAATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1175  
DB 83 ATAAATTTGGAATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 24  
QY 1176 ATATAAAGCTACCAATCTTTGT 1198  
DB 23 ATATAAAGCTACCAATCTTTGT 1

RESULT 33  
AR351023/c 683 bp DNA linear PAT 17-AUG-2003  
LOCUS AR351023  
DEFINITION Sequence 63 from patent US 6586572.  
ACCESSION AR351023  
VERSION AR351023.1 GI:33752702  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Hepler, W.T.  
TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
JOURNAL Patent: US 6586572-A 63 01-JUN-2003;  
FEATURES  
1. 683 Location/Qualifiers  
source /organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 54.2%; Score 681.8; DB 6; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.5e-111;  
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCAGCTTGG 575  
DB 683 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCAGCTTGG 624  
QY 576 CTAAATAGCAAAATGCAATGCTGCTGCAAGGCTTGATTTTCACTTCAATGAGAGCTGAATGT 635

DB 623 CTAAATAGCAAAATGCAATGCTGCTGCAAGGCTTGATTTTCACTTCAATGAGAGCTGAATGT 564  
QY 636 TCAGGACCTCTTCCCATGGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 695  
DB 563 TCAGGACCTCTTCCCATGGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 504  
QY 696 TCAGGACCTCTTCCCATGGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 755  
DB 503 TCAGGACCTCTTCCCATGGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 444  
QY 756 GGATGATGAGATGCTATCTGAGTGGGTTGGACCTGTTGATGATGATGATGATGATGAT 815  
DB 443 GGATGATGAGATGCTATCTGAGTGGGTTGGACCTGTTGATGATGATGATGATGATGAT 384  
QY 816 TCTACTGATGAGATGCTATCTGAGTGGGTTGGACCTGTTGATGATGATGATGATGATGAT 875  
DB 383 TCTACTGATGAGATGCTATCTGAGTGGGTTGGACCTGTTGATGATGATGATGATGATGAT 324  
QY 876 TTAATTTTCAATTTTGTCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 935  
DB 323 TTAATTTTCAATTTTGTCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 264  
QY 936 TTTAATAATGTTTATGATATCATCTGATGAGAAAGCAAGCTAATATGTTTACAGACCA 995  
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QY 996 AAGTGTGATTTTCAACCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1055  
DB 203 AAGTGTGATTTTCAACCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 144  
QY 1056 GTTTCAATATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1115  
DB 143 GTTTCAATATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 84  
QY 1116 ATAAATTTGGAATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1175  
DB 83 ATAAATTTGGAATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 24  
QY 1176 ATATAAAGCTACCAATCTTTGT 1198  
DB 23 ATATAAAGCTACCAATCTTTGT 1

RESULT 34  
AR352789/c 683 bp DNA linear PAT 17-AUG-2003  
LOCUS AR352789  
DEFINITION Sequence 63 from patent US 6590076.  
ACCESSION AR352789  
VERSION AR352789.1 GI:33758194  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Yudin, J., Dillon, D.C., Mitcham, J.L. and Xu, J.  
TITLE Compositions for the treatment and diagnosis of breast cancer and methods for their use  
JOURNAL Patent: US 6590076-A 63 08-JUL-2003;  
FEATURES  
1. 683 Location/Qualifiers  
source /organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 54.2%; Score 681.8; DB 6; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.5e-111;  
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCAGCTTGG 575  
DB 683 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCAGCTTGG 624



QY 576 CTAAATGAGAAATGCATGCTGTGACGGTGGTATTCACATTCATGAGAGCTGANTGT 635  
DB 623 CTAAATGAGAAATGCATGCTGTGACGGTGGTATTCACATTCATGAGAGCTGANTGT 564  
QY 636 TCAGGACCTCTCCCATTTGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 695  
DB 563 TCAGGACCTCTCCCATTTGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 504  
QY 696 TCACAAATTAATATTCATGCACTCTCTGTGGAAGAGCTTGTGAAGAAATGGTGCT 755  
DB 503 TCACAAATTAATATTCATGCACTCTCTGTGGAAGAGCTTGTGAAGAAATGGTGCT 444  
QY 756 GGATTAAGGAGATGCTATCTGGGTGGACCTTGTTCAGATTACCAAGAGAGATGCT 815  
DB 443 GGATTAAGGAGATGCTATCTGGGTGGACCTTGTTCAGATTACCAAGAGAGATGCT 384  
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DB 383 TCTACTGATGGAATTCAGTTCTCGCATCATTTATTTGAAGAACTACCAAAATTAATGCTT 324  
QY 876 TAATTTTCATTTGCTACCTCTTTTATTTATGAGCTTGAAGAGCTTCACTTAATGACAT 935  
DB 323 TAATTTTCATTTGCTACCTCTTTTATTTATGAGCTTGAAGAGCTTCACTTAATGACAT 264  
QY 936 TTTAAATTAAGTTATGTATATCATCTGAATGAAAGCAAGCTAATATGTTTACAGACCA 995  
DB 263 TTTAAATTAAGTTATGTATATCATCTGAATGAAAGCAAGCTAATATGTTTACAGACCA 204  
QY 996 AAGTGATTTTCACTGCTTTTAAATCTAGCATTTATCAATTTGCTTCATCAAAAGTG 1055  
DB 203 AAGTGATTTTCACTGCTTTTAAATCTAGCATTTATCAATTTGCTTCATCAAAAGTG 144  
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DB 143 GTTTCAAATTTTTTTAGTGGTTGAATATCTTCTCACTCATCTCTCAACT 84  
QY 1116 ATAAATTTGGAATATGTGTGCTTTTGTGTTTCTCTAGATATGCAATTTTAAAAA 1175  
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QY 1176 ATATAAAGCTACCAATCTTTGT 1198  
DB 23 ATATAAAGCTACCAATCTTTGT 1

RESULT 35  
AR453603/c 683 bp DNA linear PAT 20-FEB-2004  
LOCUS AR453603  
DEFINITION Sequence 63 from patent US 6680197.  
ACCESSION AR453603  
VERSION AR453603.1 GI:42686393  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L.,  
Hepler,W.T. and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of breast  
cancer  
JOURNAL Patent: US 6680197-A 63 20-JAN-2004;  
FEATURES Location/Qualifiers  
source 1..683  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 54.2%; Score 681.8; DB 6; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.5e-111;  
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 516 ACATTTACAAAGATGCTTCAATATGCTCTAAGATTTTGTTCAGTGCTCACTTCG 575  
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DB 683 ACATTTACAAAGATGCTTCAATATGCTCTAAGATTTTGTTCAGTGCTCACTTCG 624  
QY 576 CTAAATGAGAAATGCATGCTGTGACGGTGGTATTCACATTCATGAGAGCTGANTGT 635  
DB 623 CTAAATGAGAAATGCATGCTGTGACGGTGGTATTCACATTCATGAGAGCTGANTGT 564  
QY 636 TCAGGACCTCTCCCATTTGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 695  
DB 563 TCAGGACCTCTCCCATTTGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 504  
QY 696 TCACAAATTAATATTCATGCACTCTCTGTGGAAGAGCTTGTGAAGAAATGGTGCT 755  
DB 503 TCACAAATTAATATTCATGCACTCTCTGTGGAAGAGCTTGTGAAGAAATGGTGCT 444  
QY 756 GGATTAAGGAGATGCTATCTGGGTGGACCTTGTTCAGATTACCAAGAGAGATGCT 815  
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QY 876 TAATTTTCATTTGCTACCTCTTTTATTTATGAGCTTGAAGAGCTTCACTTAATGACAT 935  
DB 323 TAATTTTCATTTGCTACCTCTTTTATTTATGAGCTTGAAGAGCTTCACTTAATGACAT 264  
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DB 143 GTTTCAAATTTTTTTAGTGGTTGAATATCTTCTCACTCATCTCTCAACT 84  
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DB 83 ATAAATTTGGAATATGTGTGCTTTTGTGTTTCTCTAGATATGCAATTTTAAAAA 24  
QY 1176 ATATAAAGCTACCAATCTTTGT 1198  
DB 23 ATATAAAGCTACCAATCTTTGT 1

RESULT 36  
AX302743/c 683 bp DNA linear PAT 30-NOV-2001  
LOCUS AX302743  
DEFINITION Sequence 63 from Patent WO0179286.  
ACCESSION AX302743  
VERSION AX302743.1 GI:17383244  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and  
Hepler,W.T.  
TITLE Compositions and methods for the therapy and diagnosis of breast  
cancer  
JOURNAL Patent: WO 0179286-A 63 25-OCT-2001;  
FEATURES Location/Qualifiers  
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/organism="Homo sapiens"  
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ORIGIN  
Query Match 54.2%; Score 681.8; DB 6; Length 683;  
QY 516 ACATTTACAAAGATGCTTCAATATGCTCTAAGATTTTGTTCAGTGCTCACTTCG 575  
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Best Local Similarity 99.6%; Pred. No. 3.5e-111;  
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 516 ACATTACAAAGAGGTTCAAAATAGTGTCTAAAGAGTTTGTGCGGTGCTCACTTCGG 575
Db 683 ACATTACAAAGAGGTTCAAAATAGTGTCTAAAGAGTTTGTGCGGTGCTCACTTCGG 624
QY 576 CTAAATACAGAAATGACATGCTGTCAGCGTGGATTTTCAATTCAGAGCTGAATGT 635
Db 623 CTAAATACAGAAATGACATGCTGTCAGCGTGGATTTTCAATTCAGAGCTGAATGT 564
QY 636 TCAGAGACTCTTCCCATTTGAAGCTAATTTATTGACCAAGAAAGCCCTGAATGAAT 695
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Db 323 TAAATTTGATTTGTCACCTCTTTTATTTATGACCTGGAAGGTTCACTTAAATGACAT 264
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QY 996 AAGGTGATTTTCACTGTTTAAATCTAGACATATTTGTTGTTAAATCAAAAGTG 1055
Db 203 AAGGTGATTTTCACTGTTTAAATCTAGACATATTTGTTGTTAAATCAAAAGTG 144
QY 1056 GTTTCATATTTTGTAGTTGTTAGTAATACTTCTTCATGTCATCTCTCAACT 1115
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QY 1116 ATAAATTTGGAATATGTTGTGCTTTGTTTCTCTTAAGTATAGCAATTTTAAAAA 1175
Db 83 ATAAATTTGGAATATGTTGTGCTTTGTTTCTCTTAAGTATAGCAATTTTAAAAA 24
QY 1176 ATATTAAGCTACCAATCTTTGT 1198
Db 23 ATATTAAGCTACCAATCTTTGT 1

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RESULT 37  
AY136824  
LOCUS AY136824 1217 bp mRNA linear ROD 01-DEC-2002  
DEFINITION Rattus norvegicus collagen triple helix repeat-containing protein 1  
(Chrc1) mRNA, complete cds.  
ACCESSION AY136824  
VERSION AY136824.1 GI:25989618  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 1217)  
AUTHORS Lehner, W., Moore, D.P., Harmon, K.J., Mancini, M.L. and Lindner, V.  
TITLE Expression of the novel collagen triple helix repeat-containing  
gene (Chrc1) suggests functions in multiple organ systems  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1217)  
AUTHORS Lindner, V.  
TITLE Direct Submission

JOURNAL Submitted (29-JUN-2002) Center for Molecular Medicine, Maine  
Medical Center Research Institute, 81 Research Drive, Scarborough,  
ME 04074, USA

FEATURES  
source Location/Qualifiers  
1..1217  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/cblseq\_type="8 day balloon-injured carotid artery"  
1..1217  
/gene="Chrc1"  
117..854  
/gene="Chrc1"  
/note="matrix protein"  
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/product="collagen triple helix repeat-containing protein  
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gene  
CDS  
1..1217  
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## ORIGIN

Query Match 52.8%; Score 664.2; DB 10; Length 1217;  
Best Local Similarity 81.0%; Pred. No. 5.2e-108;  
Matches 869; Conservative 0; Mismatches 173; Indels 31; Gaps 7;

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QY 17 GTGAAGGCGCATGATGATGACCTCGGCGGCTCGAGCGGCGGAGCCAGACGCTGA 76
Db 6 GTGAAGGCGCATGATGATGACCTCGGCGGCTCGAGCGGCGGAGCCAGACGCTGA 54
QY 77 CCAGCTTC-CTCTCTCGGTCTCTCTCGGCTTCAGCTCCGCTGCGCGGACCGGAG 135
Db 55 GCAGGCGCGGCTTCGCGACCCCTTGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCT 114
QY 136 CCATGCGACCCGAGGCGCGCGCGCTCCCGGAGCGGCTCCGCGGCTC-----CTGC 169
Db 115 CGATGACCCCGAGAGCGCGCGCGCTCCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 174
QY 190 TGTCTCTGCTCTGAGCTGCGCGCGCTCGAGCGCTCGAGATCCCAAGGGAAGC 249
Db 175 TACTGCTGCTCTGAGCTGCTGCGCGCTGCTGAGATCCCAAGGGAAGC 234
QY 250 AAAAGCGCGAGCTCCGCGAGAGGAGGTGTGAAGCTGTATATGATGATGATGCTTACAG 309
Db 235 AAAAGCGCGATCCGCGAGAGGAGGTGTGAAGCTGTATATGATGATGATGCTTACAG 284
QY 310 GGCACGAGAGTCTGCTGCTGAGAGAGGAGCCCTGGGCGCAATGTTATCCCGGTACAC 369
Db 295 GACGACGAGAGTCTGCTGCTGAGAGAGGAGCCCTGGGCGCAATGTTATCCCGGTACAC 354
QY 370 CTGGATCCCGAGTCTGCGATGATTTCAAGAGGAGGAGATGCTGAGGGAAGCT 429
Db 355 CGGGAATCCGAGTCTGCGATGATTTCAAGAGGAGGAGATGCTTAAAGGGAAGCT 414
QY 430 TTGAGAGTCTGGAACACCACTAACAGAGTGTTCATGAGATTCATTGAATTATGCA 489
Db 415 TTGAGAGTCTGGAACACCACTAACAGAGTGTTCATGAGATTCATTGAATTATGCA 474
QY 490 TAGATCTTGGGAAATTTGGAGGTGATTAATTAAGAGTGGTCAAAATGAGTCTTA 549
Db 475 TAGATCTTGGGAAATTTGGAGGTGATTAATTAAGAGTGGTCAAAATGAGTCTTA 534
QY 550 GAGTTTGTTCAGTGTCTCACTTGGCTTAAATGACAAATGATGATGCTGACGTTGT 609
Db 535 GAGTTTGTTCAGTGTCTGCTTGGCTTAAATGACAAATGATGATGCTGACGTTGT 594
QY 610 ATTTCATTAATGAGAGTGAATGTTGAGAGCTCTTCCCATTTGAAGTATATTTATT 669

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Db 595 ATTTTACCTTTAATGAGCTGAATGTTCAAGACCTCTTCCCATTTGAAGATCATCTATC 654  
Qy 670 TGGACCAAGAGAGCCCTGAATTAATTCACATTAATATTCATCCGACCTCTTCTGTG 729  
Db 655 TGGACCAAGAGAGCCCTGAATTAATTCACATTAATATTCATCCGACCTCTTCTGTG 714  
Qy 730 AAGGACTTTGTGAAGAAATGTCGTGATTAAGTGTGATTTGCTATCTGGGGTGGACCT 789  
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Qy 790 GTTCAGATTACCCAAAGAGATGCTTCACTGATGGAATTCAGTTTCTGACATTA 849  
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Qy 850 TTGAAGACTACCAAAATA-----ATGCTTAATTTTCATTTGCTACCTCTTTT 901  
Db 835 TTGAAGACTACCAAAATAAGCCCTGAAGGTTTCATTTCTGCTCATTTACTGTGA 894  
Qy 902 TATTATGCTTGATGTTCACTTAATGACATTTTA--ATAAGTTTATGATACATCT 960  
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Qy 961 GAATG-AAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTACACTGTTTTA 1019  
Db 955 AATGAAAAAGCAAGTAAATAGTTTACAGACCAAGTGTGATCTCAGAC--TTTAA 1011  
Qy 1020 AATTCGATTAATTTCTTCTTCAATCAAAAGTGTTCATTTTCTT 1072  
Db 1012 GATTCAGATTAATTCATTTTATTTTCAACCAAGATGTTTCAGATTTTATTT 1064

RESULT 38  
AR405952 1192 bp DNA linear PAT 18-DEC-2003  
LOCUS AR405952 Sequence 1 from patent US 6630325.  
DEFINITION AR405952  
ACCESSION AR405952  
VERSION AR405952.1 GI:40155008  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1192)  
AUTHORS Linder, V. and Friesel, R. E.  
TITLE Compositions, methods and kits relating to remodel  
JOURNAL Patent: US 6630325-A 1 07-OCT-2003;  
FEATURES  
source 1. 1192  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 52.6%; Score 661.4; DB 6; Length 1192;  
Best Local Similarity 81.5%; Pred. No. 1.6e-107;  
Matches 844; Conservative 0; Mismatches 171; Indels 20; Gaps 6;

Qy 55 GCGCGGCGAGCGAGCGTGAACAGCTTC-CTCTCCTGCTCTCTCCGCGCTCCAGCTC 113  
Db 13 GCGAGCTGGGCGAGCGTGAACAGCGCGCGCTCTGCGACCCCTTGTCTCTGCTC 72  
Qy 114 CCGGCTGCCGCGAGCGAGCGCATGCGACCCCGAGGCGCCGCGCTCCCGACGCG 173  
Db 73 TGGGCTTGGAGTACCGACAGATGCAACCCCAAGCGCGCGCTCCCGACGCTG 132  
Qy 174 CTCCGGCGGCTC-----CTGCTGCTCTGCTGCTGACGCTGCCGCGCGCTGAGCGCC 227  
Db 133 CTGCTGGGCTCTTCTTGTGCTACTGCTGCTCTGACGCTGTCGCGCGCTCCAGCGCC 192  
Qy 228 TCTGAGATCCCGAAGGGAAGCAAAAGCGGACCTCCGCGAGGAGGAGTGTGACCTG 287  
Db 193 TCTGAGATCCCGAAGGGAAGCAAAAGCGGACCTGATCCGCGAGGAGGAGTGTGACCTG 252  
Qy 288 TATATGGAATGTGCTTAAAGGCGCAGAGAGTGCCTGATCGAGCGGAGACCTGCGG 347

Db 253 TATATGGAATGTGCTTAAAGGAGCAGGAGAGATTTCTGTGCGAGTGGAGCCCTGGG 312  
Qy 348 GCCAATGTTATTCGCGGTACCTGGGATCCAGGTCGGGATGAGATTCGAAGGAGAAAG 407  
Db 313 GCCAATGGAATTCCTGGCACCGGGAATCCAGGTCGGGATGAGATTCGAAGGAGAAAG 372  
Qy 408 GGGGAATGTCTGAAGGAAAGCTTTGAGAGTCTCTGACACCCCAACTACAAGAGTGTCA 467  
Db 373 GGGGAGTGTCTTAAGGAAAGCTTTGAGAGATCTGAGACCCCAACTACAAGAGTGTCA 432  
Qy 468 TGAAGTTCATTAATTAATGAGATGATCTTGGGAAAATTCGAGAGTGAATTTACAAAG 527  
Db 433 TGAAGTTCATTAATTAATGAGATGATCTTGGGAAAATTCGAGAGTGAATTTACAAAG 492  
Qy 528 ATGCGTTCAATAGTCTCTTAAGATTTGTTCAAGGCTCCTCGGCTAAATGACAGA 587  
Db 493 ATGCGATCAAGACGCGCTTTCAGATCTGTTCAAGGCTCCTCGGCTCAAAATGACAG 552  
Qy 588 AATGATGCTGTGACGCTGTGATTTTCAATTCATGAGCTGAATGTTCAAGACCTCTT 647  
Db 553 AATGCTGTGTCAAGCTGTGATTTTCACTTAATGAGCTGAATGTTCAAGACCTCTT 612  
Qy 648 CCCATTAAGCTAATAATTAATTTTGAACCAAGAGCCCTGAATGATTAATCAATTAAT 707  
Db 613 CCCATTAAGCTAATCATCTATCTGACCAAGAGCCCTGAATTAATCAATTAAT 672  
Qy 708 AATTCAGCACTCTCTCTGTGAAGAGCTTTGTGAAGAAATGTGCTGATTAATGAGAT 767  
Db 673 AATTCAGTCACTCTCTCTGTGAAGAGCTTTGTGAAGAAATGTGCTGATTAATGAGAT 732  
Qy 768 GTTGCTATCTGGGTTGGCACTTGTGAGATTAACCAAGAGAGATCTCTGATGAGT 827  
Db 733 GTTGCTATCTGGGTTGGCACTTGTGAGATTAACCAAGAGAGATCTCTGATGAGT 792  
Qy 828 AATTCAGTCTCTGATCATTAATTAAGAGATCAACCAAAATA-----ATGCTTAAT 879  
Db 793 AATTCAGTCTCTGATCATTAATTAAGAGATCAACCAAAATAAGCCCTGAAGGTTTCAAT 852  
Qy 880 TTTCAATTTGCTACCTTTTTTTTATTAATGCTTGAATGTTCACTTAATGACATTTTA 939  
Db 853 TCCCTGCTCATTAATTTGTAATCAACCTGTGATGCTGATTAATGACATTTTA 912  
Qy 940 -ATAAGTTTATTAATTAATGATGATG-AAAAGCAAGCTAAATATGTTTACAGACCAA 997  
Db 913 GAGTACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 972  
Qy 998 GTGTGATTTCAACTGTTTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1057  
Db 973 GTGTGATTTCAACTGTTTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1029  
Qy 1058 TTCAATTTTCTTTT 1072  
Db 1030 TTCAAGATTTTATTT 1044

RESULT 39  
AX067343 687 bp DNA linear PAT 24-JAN-2001  
LOCUS AX067343 Sequence 47 from Patent WO0078960.  
DEFINITION AX067343  
ACCESSION AX067343  
VERSION AX067343.1 GI:12544967  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Yugu, J. and Mitcham, J. L.  
TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
JOURNAL Patent: WO 0078960-A 47 28-DEC-2000;  
CORIXA CORPORATION (US)  
FEATURES Location/Qualifiers

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/note="n = A,T,C or G"
ORIGIN

Query Match      51.0%; Score 640.8; DB 6; Length 687;
Best Local Similarity 97.5%; Pred. No. 6.9e-104;
Matches 659; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

QY 570 CTTCGGCTAAATGAGAAATGATGCTGTCAGCCGTTGATTTTCATTCATGAGAGCT 629
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QY 630 GAATGTTGAGAGCTCTTCCCATTTGAGCTATTAATTTGAGACCAAGAAAGCCCTGAA 689
Db 61 GAATGTTGAGAGCTCTTCCCATTTGAGCTATTAATTTGAGACCAAGAAAGCCCTGAA 120
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Db 181 GGTGCTGATTAAGTGAATGTCATCTGGTGGCACTTGTTCAGATTACCCAAAGAA 240
QY 810 GATGCTTCTACTGATGGAATTCAGTTTCTGCATCATTAATTTGAGAACTACCAAAATTA 869
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QY 870 ATGCTTAATTTTCACTTGTGCTACCTCTTTTATTTATGACCTTGAATGCTTCACTTAA 929
Db 301 ATGCTTAATTTTCACTTGTGCTACCTCTTTTATTTATGACCTTGAATGCTTCACTTAA 360
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Db 541 CAACCTATTAATTTGGAATATGTTGTGTCTTTTGTATTTTCTCTTATGATAGCAATTTT 599
QY 1170 AAAAAAATATAAAGCTACCAATCTTGTAGCAATTTGTAAGAAATGTTAAGAAATTTTAT 1229
Db 600 AAAAAAATATAAAGCTACCAATCTTGTAGCAATTTGTAAGAAATGTTAAGAAATTTTAT 659
QY 1230 ATCTGTAAATATAAAA 1245
Db 660 ATCTGTAAATATAAAA 675

RESULT 40
AR405955 734 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 9 from patent US 6630325.
ACCESSION AR405955
VERSION AR405955.1 GI:40155011
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 734)
AUTHORS Lindner,V. and Friesel,R.E.
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TITLE
JOURNAL Compositions, methods and kits relating to remodel
Patent: US 6630325-A 9 07-OCT-2003;
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ORIGIN

Query Match      45.1%; Score 566.6; DB 6; Length 734;
Best Local Similarity 87.0%; Pred. No. 1.1e-90;
Matches 636; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

QY 142 GACCCCAAGGCGCCGCGCTCCCGCAGCGGCTCCGCGGCTCC-----TGCTGCTCC 195
Db 4 GCCCCCAAGGCGCGCCGCTCCCGCAGCGGCTCCGCGGCTCCGCTTCTTGCTGCTGCTGC 63
QY 196 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
Db 64 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 123
QY 256 CGCAGCTCCGCGCAGAGGAGAGTGTGAGCACTGTATTAATGGAATGTCTTCAAGGCGCAG 315
Db 124 CGCTGATCCGCGCAGAGGAGAGTGTGAGCACTGTATTAATGGAATGTCTTCAAGGAGCAG 183
QY 316 CAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 375
Db 184 CAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
QY 376 TCCAGAGCTGCGGATGATTTCAAGAGAGAAAGGGGGAATGCTGAGAGGAAAGCTTTGAGG 435
Db 244 TCCAGAGCTGCGGATGATTTCAAGAGAGAAAGGGGGAATGCTTAAAGGAAAGCTTTGAGG 303
QY 436 AGTCTGGAACACCAACATCAACAGAGTGTATGATGATTTCAATTAATGAGCATATGATC 495
Db 304 AATCTGGAACCCCAACATCAACAGAGTGTATGATGATTTCAATTAATGAGCATATGATC 363
QY 496 TTGGGAAATATGCGGAGTGTACATTTTCAAAAGATGCTTCAAAATGATGCTCTAAGAGTT 555
Db 364 TTGGGAAATATGCGGAAATGTATCATTTCAAAAGATGCTTCAAAATGATGCTCTAAGAGTT 423
QY 556 TGTTCAGTGTCTCACTTGTGCTAAATATGAGAAATGCAATGCTGTGAGCGTTGATTTCA 615
Db 424 TGTTCAGTGTCTCTCTTGTGCTCAAAATGAGAAATGCTGTGCTGCAACGCTGATATTTTA 483
QY 616 CATTCAGAGGAGTGAATGTTGAGAGCTCTTCCCATTTGAGAGCTAATTAATTTGAGAC 675
Db 484 CATTAAATGAGAGTGAATGTTGAGAGCTCTTCCCATTTGAGAGCTAATTAATTTGAGAC 543
QY 676 AAGGAGCCCTGAATGATTTCAACATTAATTAATTCATGCACTTCTCTGTGGAAGAC 735
Db 544 AAGGAGCCCTGAATGATTTCAACATTAATTAATTCATGCACTTCTCTGTGGAAGAC 603
QY 736 TTTGTGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
Db 604 TCTGTGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
QY 796 ATTACCCCAAGAGAGTGTCTTCACTGAGATGGAATTCAGTTTCTCGCATCATTAATGAAG 855
Db 664 ATTACCCCAAGAGAGTGTCTTCACTGAGATGGAATTCAGTTTCTCGCATCATTAATGAAG 723
QY 856 AACTACCAAAA 866
Db 724 AACTACCAAAA 734

RESULT 41
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LOCUS
DEFINITION Homo sapiens genomic DNA, chromosome 8q23, clone: KB1896D3.
ACCESSION AP004221
VERSION AP004221.1 GI:15824052
KEYWORDS
SOURCE
Homo sapiens (human)
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QY	12316	CTGAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGGTGATTTTCAACAGCTTTT	1018
QY	959	CTGAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGGTGATTTTCAACAGCTTTT	1018
QY	1019	AAATTCAGCAATATTCATATTTGCTTCATCAATCAAAAGTGCTTCATATATTTTTTTAGTTGG	1078
QY	123376	AAATCTGACATTTATTCATATTTGCTTCATCAATCAAAAGTGCTTCATATATTTTTTTAGTTGG	123435
QY	1079	TTAATAATCTTCTTCATATGTCACATCTTCACACTTAATTTGGATATATTTGGTGTG	1138
QY	123436	TTAATAATCTTCTTCATATGTCACATCTTCACACTTAATTTGGATATATTTGGTGTG	123495
QY	1139	CTTTTGTTTTTCTCTAGATATGCAATTTTTTAAAAAAAATATMAAGCTACCAATCTTGT	1198
QY	123496	CTTTTGTTTTTCTCTAGATATGCAATTTTTTAAAAAAAATATMAAGCTACCAATCTTGT	123558
QY	1199	ACATTTGTTAAAGTTAAGATTTTTTTTTTATATCTGTTAATMAATTAATTTTCCACA	1257
QY	123556	ACATTTGTTAAAGTTAAGATTTTTTTTTTATATCTGTTAATMAATTAATTTTCCACA	123614
RESULT 42			
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DEFINITION			linear
ACCESSION	AC012213		PRI 07-FEB-2002
VERSION	AC012213.8	GI:18598769	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 176922)		
TITLE	Barren, B., Linton, L., Nusbaum, C. and Lander, E.		
JOURNAL	Homo sapiens chromosome, clone RP11-1C8		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 176922)		
TITLE	Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barua, N., Becker, J., Collins, J., Collymore, A., Cook, P., Dearlano, K., Dewar, K., Domini, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J., Johnson, R., Jones, C., Kam, L., Karatas, A., Klein, J., Lebeck, J., Lien, C., Locke, K., MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teefave, S., Titrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.		
JOURNAL	Direct Substation		
REFERENCE	Submitted (21-Oct-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
AUTHORS	3 (bases 1 to 176922)		
TITLE	Barren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barua, N., Baerlein, V., Boguslavsky, L., Boughalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J., Charazot, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., LaRoque, K., Lamazares, R., Landers, T., Lebeck, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menhus, L., Mihova, T., Mlewa, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,		

TITLE  
JOURNAL

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Topam, K., Travers, M., Travis, N., Triggilo, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zaitoun, J., Zembek, L., Zimmer, A. and Zody, M.  
Direct Submission

## COMMENT

Submitted (07-FEB-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Feb 7, 2002 this sequence version replaced gi:18129443.  
All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www.seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L1765

Center clone name: L\_C\_8

## FEATURES

source

Location/Qualifiers

1. 176922

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/clone="RP11-1C8"

/clone\_11b="RPC1-11 Human Male BAC"

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complement(314. .522)

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2072. .2115

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2121. .2132

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2165. .2183

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5119. .5414

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7906. .8368

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9603. .9668

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18650. .18660

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22145. .22311

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22318. .22624

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28335. .28731

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Best Local Similarity 93.8%; Pred. No. 1.4e-85;
Matches 562; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

659 TATAATTTATTTGGACCAAGAAAGCCCTGAATGAAATTCACCAATTAATTCATGCGAC 718
Db 136403 TAAATTTTACAAAGATTTGCTCTTGTCTTAAAGAAAGTGAACCTTCATCTTTG 136344

QY 719 TTTCTCTGGAAGACCTTTGTGAAGAAATGCTGCTGATTAAGATGTTGCTATCTG 778
Db 136343 TCTTGACATGGAAGACCTTTGTGAAGAAATGCTGCTGATTAAGATGTTGCTATCTG 136284

QY 779 GGTGGGCACTGTTGATGATTAACCAAGAGATGCTTCTACTGATGGAATTCAGTTTC 838
Db 136283 GGTGGGCACTGTTGATGATTAACCAAGAGATGCTTCTACTGATGGAATTCAGTTTC 136224

QY 839 TCGCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCACTGACCTCTT 898
Db 136223 TCGCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCACTGACCTCTT 136164

QY 899 TTTTATTTAGCTTGGAAATGTTCACTTAATGACATTTTAAATAGTTTATGATACAT 958
Db 136163 TTTTATTTAGCTTGGAAATGTTCACTTAATGACATTTTAAATAGTTTATGATACAT 136104

QY 959 CTGAATGAAAAGCAAGCTTAATATGTTTACAGACCAAGGTGATTTACACTGTTTTT 1018
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QY 1019 AAATTCACATTTATTCATTTTCTTCATCAATCAAAAGTGTTCATATTTTATTTAGTGG 1078
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QY 1079 TTAGAATACTTTCTTCATAGTCACATTTCTCAACCTATTAATTTGGAATTTGTTGTGT 1138
Db 135983 TTAGAATACTTTCTTCATAGTCACATTTCTCAACCTATTAATTTGGAATTTGTTGTGT 135924

QY 1139 CTTTGTGTTTTTCTCTAGTATAGATTTTAAATTAATTAAGCTTCCATCTTTGT 1198
Db 135923 CTTTGTGTTTTTCTCTAGTATAGATTTTAAATTAATTAAGCTTCCATCTTTGT 135864

QY 1199 ACAATTTGTAATGTTAAGATTTTATATCTGTAAATTAATTAATTTTCCAAACA 1257
Db 135863 ACAATTTGTAATGTTAAGATTTTATATCTGTAAATTAATTAATTTTCCAAACA 135805

RESULT 43
AX339938/C 560 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 185 from Patent WO0196388.
ACCESSION AX339938
VERSION AX339938.1 GI:18135919
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Jiang, Y., Harlocker, S.L. and Secrist, H.
Compositions and methods for the therapy and diagnosis of colon
cancer
Patent: WO 0196388-A 185 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
1..560
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
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Best Local Similarity 99.3%; Pred. No. 1.3e-84;
Matches 554; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

643 CTCCTCCCATTTGAAGCTATAA-TTATTTGGACCAAGAAAGCCCTGAATGAATTCACA 701
Db 558 HCTTCCCATTTGAAGCTATAATTTTATTTGGACCAAGAAAGCCCTGAATGAATTCACA 499

QY 702 ATTATATTCATCCGACCTCTTCTGTGAAGACCTTTGTGAAGAAATTTGTGCTGATTA 761
Db 498 ATTATATTCATCCGACCTCTTCTGTGAAGACCTTTGTGAAGAAATTTGTGCTGATTA 439

QY 762 GTGATGTTGCTATCTGCGGTTGGACCTTGTCAATTAACCAAGAGATGCTTCACT 821
Db 438 GTGATGTTGCTATCTGCGGTTGGACCTTGTCAATTAACCAAGAGATGCTTCACT 379

QY 822 GGATGGAATTAAGATTTCTCGCATCATTTTGAAGAACTACCAAAATAATGCTTTAATTT 881
Db 378 GGATGGAATTAAGATTTCTCGCATCATTTTGAAGAACTACCAAAATAATGCTTTAATTT 319

QY 882 TCATTTGCTACCTC-TTTTTTATATGCTTGAAGTTCATCTTAATGAATTTTAA 940
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QY 941 ATTAAGTTATGATACATCTGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGTG 1000
Db 258 ATTAAGTTATGATACATCTGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGTG 199

QY 1001 TGATTTCACTGTTTTTAAATCTAGACATTAATCTTTTCTTCATCAATCAAAAGTGTTC 1060
Db 198 TGATTTCACTGTTTTTAAATCTAGACATTAATCTTTTCTTCATCAATCAAAAGTGTTC 139

QY 1061 AATATTTTTTATGTTGTTGAATACCTTCTTCATGTCACATCTTCCTCACTTAAT 1120
Db 138 AATATTTTTTATGTTGTTGAATACCTTCTTCATGTCACATCTTCCTCACTTAAT 79

QY 1121 TTGAATATGTTGTTGCTTTTCTTTTCTCTTATGATAGCATTTTAAAAAATAA 1180
Db 78 TTGAATATGTTGTTGCTTTTCTTTTCTCTTATGATAGCATTTTAAAAAATAA 19

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Db 18 AAAGCTACCAATCTTTGT 1

RESULT 44
CQ463279 485 bp DNA linear PAT 30-JAN-2004
LOCUS CQ463279
DEFINITION Sequence 6057 from Patent WO0192581.
ACCESSION CQ463279
VERSION CQ463279.1 GI:41428898
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Algate, P.A., Harlocker, S.L. and Jones, R.
Compositions and methods for the therapy and diagnosis of
ovariancancer
Patent: WO 0192581-A 6057 06-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
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ORIGIN

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Best Local Similarity 99.6%; Pred. No. 1.2e-75;
Matches 483; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 794 AGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTCTCGCATTTATGA 853  
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QY 914 GAATGCTCACTAAATGACATTTTAATTAATGATTAATGATTAATGATTAATG 973  
DB 181 GAATGCTCACTAAATGACATTTTAATTAATGATTAATGATTAATGATTAATG 240  
QY 974 AGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTTTAAATCTAGCATTTAT 1033  
DB 241 AGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTTTAAATCTAGCATTTAT 300  
QY 1034 CATTTTGCTTCAATCAAAAGTGTGATTTTCAATATTTTGTGTTAGAAATCTTCTT 1093  
DB 301 CATTTTGCTTCAATCAAAAGTGTGATTTTCAATATTTTGTGTTAGAAATCTTCTT 360  
QY 1094 CATAGTCACATTCCTCAACCTTAATTTGGAATATGTTGGTCTTTGTTTTTCTC 1153  
DB 361 CATAGTCACATTCCTCAACCTTAATTTGGAATATGTTGGTCTTTGTTTTTCTC 420  
QY 1154 TTAGTATAGCATTTTAAATAATTAATTAAGTACCAATCTTTGTAATTTGTAATGT 1213  
DB 421 TTAGTATAGCATTTTAAATAATTAATTAAGTACCAATCTTTGTAATTTGTAATGT 480  
QY 1214 TAAGA 1218  
DB 481 TAAGA 485

RESULT 45  
CQ463299/c  
LOCUS CQ463299 464 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 6077 from Patent WO0192581.  
ACCESSION CQ463299  
VERSION CQ463299.1 GI:41428918  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
Aligate, P.A., Harlocker, S.L. and Jones, R.  
TITLE Compositions and methods for the therapy and diagnosis of  
ovariolancancer  
JOURNAL Patent: WO 0192581-A 6077 06-DEC-2001;  
CORIXA CORPORATION (US)  
FEATURES  
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Query Match: 36.5%; Score 459.2; DB 6; Length 464;  
Best Local Similarity 99.4%; Pred. No. 1.2e-71;  
Matches 461; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 853 AAGAATACCAAAATTAATGCTTTAATTTTCACTTGTCTTTTATTAATGCTTG 912  
DB 404 AAGAATACCAAAATTAATGCTTTAATTTTCACTTGTCTTTTATTAATGCTTG 345

QY 913 GGAATGTTCACTTAATGACATTTTAATTAAGTTATGATATACATCTGAATGAAGA 972  
DB 344 GGAATGTTCACTTAATGACATTTTAATTAAGTTATGATATACATCTGAATGAAGA 285  
QY 973 AAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTTTAAATCTAGCATTTAT 1032  
DB 284 AAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTTTAAATCTAGCATTTAT 225  
QY 1033 TCATTTTGCTCAATCAAAAGTGTGATTTTCAATTTTGTAGTTGATTAATCTTCT 1092  
DB 224 TCATTTTGCTCAATCAAAAGTGTGATTTTCAATTTTGTAGTTGATTAATCTTCT 165  
QY 1093 TCATGCTCACTTCTCAACCTTAATTTGGAATATGTTGGTCTTTGTTTTTCT 1152  
DB 164 TCATGCTCACTTCTCAACCTTAATTTGGAATATGTTGGTCTTTGTTTTTCT 105  
QY 1153 CTTAGTATAGCATTTTAAATAATTAATTAAGTACCAATCTTTGTAATTTGTAATG 1212  
DB 104 CTTAGTATAGCATTTTAAATAATTAATTAAGTACCAATCTTTGTAATTTGTAATG 45  
QY 1213 TTAAATTTTATTTTATCTGTTAAATTAATTTTCCAC 1256  
DB 44 TTAAATTTTATTTTATCTGTTAAATTAATTTTCCAC 1

RESULT 46  
CQ712169  
LOCUS CQ712169 466 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 57095 from Patent WO02070737.  
ACCESSION CQ712169  
VERSION CQ712169.1 GI:42273026  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
Liew, C.C., Marshall, W.B. and Zhang, H.  
TITLE Compositions and methods relating to osteoarthritis  
JOURNAL Patent: WO 02070737-A 57095 12-SEP-2002;  
Chondrogene Inc. (CA)  
FEATURES  
source 1..466  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match: 34.7%; Score 435.8; DB 6; Length 466;  
Best Local Similarity 98.9%; Pred. No. 1.7e-67;  
Matches 448; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 693 AATTCAACAATTAATTAATGACATTTCTGTTGGAAGACTTTGTAAGGAATTTG 752  
DB 14 AATTCAACAATTAATTAATGACATTTCTGTTGGAAGACTTTGTAAGGAATTTG 73  
QY 753 GCTGATTAAGTGAATGTTGCTATCTGGTGTGCACTTGTTCAGATTACCCAAAGAGAT 812  
DB 74 GCTGATTAAGTGAATGTTGCTATCTGGTGTGCACTTGTTCAGATTACCCAAAGAGAT 133  
QY 813 GCTTCACTGAGATGGAATTCAGTTTCTGCAATCATTAATGAAGAACTTACC-AAATTAAT 871  
DB 134 GCTTCACTGAGATGGAATTCAGTTTCTGCAATCATTAATGAAGAACTTACC-AAATTAAT 193  
QY 872 GCTTCACTGAGATGGAATTCAGTTTCTGCAATCATTAATGAAGAACTTACC-AAATTAAT 931  
DB 194 GCTTCACTGAGATGGAATTCAGTTTCTGCAATCATTAATGAAGAACTTACC-AAATTAAT 253  
QY 932 ACATTTTAATTAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 991  
DB 254 ACATTTTAATTAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 313

Query 992 ACCAAGTGTGATTTGACACTGTTTAAATCTAGCATTAATTTGCTTCATCAAA 1051  
Db 314 ACCAAGTGTGATTTGACACTGTTTAAATCTAGCATTAATTTGCTTCATCAAA 373  
Qy 1052 AGTGTGTTCAATTTTCTTTTGTGTTGAAATTAATTTCTTCAATGTCATCTCTCA 1111  
Db 374 AGTGTGTTCAATTTTCTTTTGTGTTGAAATTAATTTCTTCAATGTCATCTCTCA 433  
Qy 1112 ACCATTAATTTGGAATATTTGTTGCTTTTG 1144  
Db 434 ACCATTAATTTGGAATATTTGTTGCTTTTG 466

RESULT 47  
AX351434 460 bp DNA linear PAT 06-FEB-2002  
LOCUS AX351434  
DEFINITION Sequence 181 from Patent WO0196390.  
ACCESSION AX351434  
VERSION AX351434.1 GI:18616781  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 Jiang, Y., Hepler, W.T., Clapper, J.D., Wang, A. and Secrist, H.  
Compositions and methods for the therapy and diagnosis of colon  
cancer  
Patent: WO 0196390-A 181 20-DEC-2001;  
JOURNAL CORIXA CORPORATION (US)  
FEATURES  
source location/Qualifiers  
1..460  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 34.5%; Score 433.2; DB 6; Length 460;  
Best Local Similarity 98.9%; Pred. No. 5e-67;  
Matches 457; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Qy 737 TTGTAAGGAATTTGTCGTGATTTGATGATTTGCTATCTGCTGGTGGACATTTGTCACA 796  
Db 460 TTGTAAGGAATTTGTCGTGATTTGATGATTTGCTATCTGCTGGTGGACATTTGTCACA 403  
Qy 797 TTACCAAAAGAGATGCTTCTACTGATGATGATTCAGTTCTCGCATCATTTAGAGA 856  
Db 402 TTACCAAAAGAGATGCTTCTACTGATGATGATTCAGTTCTCGCATCATTTAGAGA 343  
Qy 857 ACTACCAAAATTAATGCTTTAATTTTCTGCTACCTCTTTTATTAATGCTTGGAA 916  
Db 342 ACTACCAAAATTAATGCTTTAATTTTCTGCTACCTCTTTTATTAATGCTTGGAA 283  
Qy 917 TGTTCACCTTAATGACATTTTAATTAATTAATGATATCATCTGAATGAAGAAAGC 976  
Db 282 TGTTCACCTTAATGACATTTTAATTAATTAATGATATCATCTGAATGAAGAAAGC 223  
Qy 977 TAAATATGTTTACAGACCAAGTGTGATTTCACTGTTTAAATCTAGCATTAATCAT 1036  
Db 222 TAAATATGTTTACAGACCAAGTGTGATTTCACTGTTTAAATCTAGCATTAATCAT 163  
Qy 1037 TTTGCTTCAATCAAAAGTGTTCATATTTTCTTGTGTTAGTTAGAAATACCTTCTCAT 1096  
Db 162 TTTGCTTCAATCAAAAGTGTTCATATTTTCTTGTGTTAGTTAGAAATACCTTCTCAT 103  
Qy 1097 AGTACATTTCTCTCAACCTAATTAATTTGGAATTTGTTGTCCTTTGTTTCTCTCA 1156  
Db 102 AGTACATTTCTCTCAACCTAATTTGGAATTTGTTGTCCTTTGTTTCTCTCA 43  
Qy 1157 GTATAGCATTTTAAAAAATATAAAGCTACCAATCTTGT 1198  
Db 42 GTATAGCATTTTAAAAAATATAAAGCTACCAATCTTGT 1

RESULT 48  
AX340025 471 bp DNA linear PAT 10-JAN-2002  
LOCUS AX340025  
DEFINITION Sequence 272 from Patent WO0196388.  
ACCESSION AX340025  
VERSION AX340025.1 GI:18136006  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 Jiang, Y., Harlocker, S.L. and Secrist, H.  
Compositions and methods for the therapy and diagnosis of colon  
cancer  
Patent: WO 0196388-A 272 20-DEC-2001;  
JOURNAL CORIXA CORPORATION (US)  
FEATURES  
source location/Qualifiers  
1..471  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 34.3%; Score 431.2; DB 6; Length 471;  
Best Local Similarity 98.9%; Pred. No. 1.1e-66;  
Matches 464; Conservative 1; Mismatches 1; Indels 3; Gaps 3;

Qy 516 ACATTTACAAAGATGCTTCAATTAATGCTCTAAGATTTTGTTCAGTGTGCTCACTTCG 575  
Db 1 ACATTTACAAAGATGCTTCAATTAATGCTCTAAGATTTTGTTCAGTGTGCTCACTTCG 60  
Qy 576 CTAAATGCAAAATGCAATGCTGTCAGCTGTTGTAATTTTCAATTCATGAGCTGAATGT 635  
Db 61 CTAAATGCAAAATGCAATGCTGTCAGCTGTTGTAATTTTCAATTCATGAGCTGAATGT 120  
Qy 636 TCAGACCTCTTCCCATTTGAAGCTATTAATTTATTTGACCAAGAACCTTGAATGAAT 695  
Db 121 TCAGACCTCTTCCCATTTGAAGCTATTAATTTATTTGACCAAGAACCTTGAATGAAT 180  
Qy 696 TCACCAATTAATTAATGATGCACTTCTTGTGTGAGAGACTTTGTGAGGAATGTGCT 755  
Db 181 TCACCAATTAATTAATGATGCACTTCTTGTGTGAGAGACTTTGTGAGGAATGTGCT 240  
Qy 756 GGAATTAAGATTTGCTATCTGCTGCTGCACTTGTTCATTAATTAATTAATTAATGCT 815  
Db 241 GGAATTAAGATTTGCTATCTGCTGCTGCACTTGTTCATTAATTAATTAATTAATGCT 300  
Qy 816 TCTACTGATGATTAATGATGCTTCTGCTGATTAATTAATTAATTAATTAATGCTT 875  
Db 301 TCTACTGATGATTAATGATGCTTCTGCTGATTAATTAATTAATTAATTAATGCTT 360  
Qy 876 TAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 934  
Db 361 TAAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 420  
Qy 935 TTTTAAATTAAG-TTATGTAATCA-TCTGAATGAAGCAAACTTAAT 981  
Db 421 TTTTAAATTAAGTTTATGTAATCACTTGAATGAAGCAAACTTAAD 469

RESULT 49  
BX935556 1009 bp mRNA linear VMT 30-MAR-2004  
LOCUS BX935556  
DEFINITION Gallus gallus finished cDNA, clone ChEST82313.  
ACCESSION BX935556  
VERSION BX935556.2 GI:46018669  
KEYWORDS  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;



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OM nucleic - nucleic search, using sw model

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(without alignments)  
10400.714 Million cell updates/sec

Title: US-10-063-734-121

Perfect score: 1257

Sequence: 1 ggaagagagcgcgcggtgta.....ataataattatcccaaca 1257

Scoring table: COLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size: 10

Total number of hits satisfying chosen parameters: 38449985

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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1: gb\_est1:  
2: gb\_est2:  
3: gb\_hnc:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gsa1:  
9: gb\_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1104	87.8	1288	3	BC021025 Homo sapi
2	1054	83.9	1207	3	CR605392 full-leng
3	1036	82.4	1189	3	CR596030 full-leng
4	958	76.2	1111	3	CR612318 full-leng
5	950	75.6	1103	3	CR594803 full-leng
6	700	55.7	1098	1	AL532456 full-leng
7	693	55.1	747	6	CA415410 full-leng
8	693	55.1	796	5	BQ008675 full-leng
9	691	55.0	1102	1	AL575307 full-leng
10	682	54.3	702	5	BQ010155 full-leng
11	668	53.1	1100	1	AL551834 full-leng
12	640	50.9	723	6	CA431413 full-leng
13	636	50.6	683	2	BE607414 full-leng
14	632	50.3	683	2	BE607414 full-leng
15	603	48.0	902	5	BQ424201 full-leng
16	602	47.9	827	1	AL544722 full-leng
17	595	47.3	922	5	BQ425098 full-leng
18	588	46.8	730	5	BU729033 full-leng
19	587	46.7	700	7	CN394776 full-leng
20	581	46.2	724	9	BQ009009 full-leng
21	579	46.1	732	9	AY399084 full-leng
22	572	44.7	610	5	BQ013605 full-leng
23	562	44.4	903	4	BT763235 full-leng
24	558	44.4	903	4	BT763235 full-leng

25	557	44.3	710	3	CR592899 full-leng
26	552	43.9	556	1	AT162109 full-leng
27	548	43.6	567	6	CAB68366 full-leng
28	538	42.8	671	5	BUG24465 full-leng
29	535	42.6	654	5	BUG24261 full-leng
30	532	42.3	549	1	A1085616 full-leng
31	532	42.3	1132	6	BMS60093 full-leng
32	531	42.2	716	6	CA413294 full-leng
33	518	41.2	569	2	AM071610 full-leng
34	512	40.7	512	4	BM887835 full-leng
35	508	40.4	723	5	BQ005403 full-leng
36	500	39.8	986	5	BQ648112 full-leng
37	476	37.9	1064	1	AL564395 full-leng
38	474	37.7	528	2	BES50475 full-leng
39	472	37.5	492	2	BF000103 full-leng
40	472	37.5	504	2	AW316980 full-leng
41	472	37.5	511	1	A1422726 full-leng
42	469	37.3	571	7	CN394775 full-leng
43	462	36.8	507	1	AI809642 full-leng
44	461	36.7	466	1	A1359844 full-leng
45	457	36.4	463	1	A1379443 full-leng

## ALIGNMENTS

RESULT 1	BC021025	1288 bp	mRNA	linear	HTC 04-AUG-2004
LOCUS	BC021025				
DEFINITION	Homo sapiens collagen triple helix repeat containing 1, mRNA (CDNA clone IMAGE:3617432).				
ACCESSION	BC021025				
VERSION	BC021025.1	GI:18045042			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Strasberg, R.L., Feingold, F.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marisano, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uebli, T.B., Toshimaki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Wallach, S.J., Bosak, S.A., McMan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richard, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, V.S., Krzywicki, M.I., Skalka, U., Smillie, D.E., Schermer, A., Schein, J.E., Jones, S.J., and Marra, M.A.				
TITLE	human and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 1288)				
AUTHORS	Director MGC Project.				
TITLE	Direct Submission				
JOURNAL	Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>				
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a> Tissue Procurement: ATCC/DCTD/DTF CDNA Library Preparation: Rubin Laboratory				

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 contact: amadan@systemsbiology.org  
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha  
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
 Series: IRAL Plate: 24 Row: 1 Column: 7  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 19923988  
 This clone has the following problem: no cloning site /  
 microdeletion.

FEATURES  
 source  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:3617432"  
 /tissue\_type="Skin, melanotic melanoma."  
 /clone\_lib="NIH MGC 20"  
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 /note="Vector: pOT37"

## ORIGIN

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 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1254; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GGAGGAGCGCGCGGGTGAAGGCGCATTTGACAGCTGGGCGGCTCGAGCGCG 60
Db 6 GGAGGAGCGCGCGGGTGAAGGCGCATTTGACAGCTGGGCGGCTCGAGCGCG 65
QY 61 CGAGCCAGACGCTGACCACTTCTCTCTGCTGCTCTCGGCTCGAGCTCGGCGCTG 120
Db 66 CGAGCCAGACGCTGACCACTTCTCTCTGCTGCTCTCGGCTCGAGCTCGGCGCTG 125
QY 121 CCCGCGACCGGAGCCATGCGACCCCGAGGCGCGCGCTCGGCGAGCGCTCGCG 180
Db 126 CCCGCGACCGGAGCCATGCGACCCCGAGGCGCGCGCTCGGCGAGCGCTCGCG 185
QY 181 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 186 GCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
QY 241 AGGGAGCAAAAGCGAGCTCCGCGAGAGGAGTGTGAGCTGTATTAATGAGATGT 300
Db 246 AGGGAGCAAAAGCGAGCTCCGCGAGAGGAGTGTGAGCTGTATTAATGAGATGT 305
QY 301 GCTTACAAGGCGCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 306 GCTTACAAGGCGCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
QY 361 CGGCTACACTGGAGTCCAGAGTGGAGTGAATCAAGAGGAGAAAGGGGAAATTCGGA 420
Db 366 CGGCTACACTGGAGTCCAGAGTGGAGTGAATCAAGAGGAGAAAGGGGAAATTCGGA 425
QY 421 GGGAAAGCTTTGAGAGTCTGACACCACTACAGAGTGTGATGAGATTCATTTGA 480
Db 426 GGGAAAGCTTTGAGAGTCTGACACCACTACAGAGTGTGATGAGATTCATTTGA 485
QY 481 ATTATGCAATGATCTGGGAAATTTGGGAGTGTACATTTTACAAGATGCGTTCAATA 540
Db 486 ATTATGCAATGATCTGGGAAATTTGGGAGTGTACATTTTACAAGATGCGTTCAATA 545
QY 541 GTGCTCAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGAGAAATGCAATGCTGTC 600
Db 546 GTGCTCAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGAGAAATGCAATGCTGTC 605
QY 601 AGCGTTGATTTTCAATTCATGAGAGTGTGATGATTCAGAGCTTTCCCATTTGAAGTA 660
Db 606 AGCGTTGATTTTCAATTCATGAGAGTGTGATGATTCAGAGCTTTCCCATTTGAAGTA 665

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QY 661 TAATTTATTTGGACCAAGAAAGCCCTGAATGAATTCACATTAATTCATGCACTT 720
Db 666 TAATTTATTTGGACCAAGAAAGCCCTGAATGAATTCACATTAATTCATGCACTT 725
QY 721 CTTCGTGGAAGAGCTTTGTGAAGAAATGGTGTGCTGATTAAGGATGTTGATCGGG 780
Db 726 CTTCGTGGAAGAGCTTTGTGAAGAAATGGTGTGCTGATTAAGGATGTTGATCGGG 785
QY 781 TTGGCACTTTGTACATTACCCAAAGAGAGTGTCTTACTGATGATGATTCAGTTCTC 840
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QY 841 GCATCATTAATGAAGAAATACCAAAATTAATGCTTTAATTTCTACTGCTACCTTTT 900
Db 846 GCATCATTAATGAAGAAATACCAAAATTAATGCTTTAATTTCTACTGCTACCTTTT 905
QY 901 TTATATGCTCTGGAATGTTCACTTAATGACATTTTAATTAATGATTAATGATCATCT 960
Db 906 TTATATGCTCTGGAATGTTCACTTAATGACATTTTAATTAATGATTAATGATCATCT 965
QY 961 GAATGAAAGCAAAAGCTTAATATGTTTACAGACCAAGTGTGATTCACATGTTTTAA 1020
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QY 1141 TTGTTTTTCTCTTATGATGATTTTAAATTAATTAAGCTAACATTTGTGAC 1200
Db 1146 TTGTTTTTCTCTTATGATGATTTTAAATTAATTAAGCTAACATTTGTGAC 1205
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Db 1206 AATTTGTAATGTTAAAGATTTTATATCTGTTAAATTAATTAATTTTCCAAAC 1262

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RESULT 2  
 CR605392 1207 bp mRNA linear HTC 21-JUL-2004  
 LOCUS CR605392  
 DEFINITION full-length cDNA clone CS0D1037YD19 of Placenta Cot 25-normalized  
 of Homo sapiens (human).  
 ACCESSION CR605392  
 VERSION CR605392.1 GI:50486199  
 KEYWORDS HTC; CNSLT cDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (Bases 1 to 1207)  
 AUTHORS Li, W.B., Gruber, C., Jessee, V. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 REMARK Contact: Feng Liang Email: [fliang@life.uchicago.edu](mailto:fliang@life.uchicago.edu) URL:  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
 Faraday Avenue  
 Carlsbad, CA 92008  
 REFERENCE 2 (Bases 1 to 1207)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr)  
 - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
 FEATURES  
 Location/Qualifiers



QY	105	CTCAGCTCCGGCGTGGCCGGCAGCTGGGAGCATTGGACCCCAAGGGCCCGCGCTCC	164
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QY	165	CCGAGCGGCTCCGGCGCTCTCTGCTGCTCTCTGCTGCACTGCCCGCGCTCGAGC	224
Db	121	CCCGAGCGGCTCCGGCGCTCTCTGCTGCTCTCTGCTGCACTGCCCGCGCTCGAGC	180
QY	225	GGCTCTGAGATCCCGAAGGGGAGCAAAAGCCGACCTCCGGCAGAGGAGTGTGGAC	284
Db	181	GGCTCTGAGATCCCGAAGGGGAGCAAAAGCCGACCTCCGGCAGAGGAGTGTGGAC	240
QY	285	CTGTATTAATGGAATGTGCTTACAGAGGCGCAGAGGATGCTGGTCCAGACGGAGCCT	344
Db	241	CTGTATTAATGGAATGTGCTTACAGAGGCGCAGAGGATGCTGGTCCAGACGGAGCCT	300
QY	345	GGGGCCAAATGTATTCGGGGTACACTGGGATCCAGGTGGATGGATTCAAAGAGAA	404
Db	301	GGGGCCAAATGTATTCGGGGTACACTGGGATCCAGGTGGATGGATTCAAAGAGAA	360
QY	405	AAGGGGAAATGTCTAGAGGAGAAAGCTTGAAGAGTCCAGACCCCAATCTAAGCACTGT	464
Db	361	AAGGGGAAATGTCTAGAGGAGAAAGCTTGAAGAGTCCAGACCCCAATCTAAGCACTGT	420
QY	465	TCATGAGTTCATTGAAATTATGCAATGATCTTGGGAAAATTCGGAGTGTACATTYAC	524
Db	421	TCATGAGTTCATTGAAATTATGCAATGATCTTGGGAAAATTCGGAGTGTACATTYAC	480
QY	525	AAGATCGTTCAATATAGTGTCTTAAGAGTTTGTTCAGTGGCTCACTGGCTAAATATG	584
Db	481	AAGATCGTTCAATATAGTGTCTTAAGAGTTTGTTCAGTGGCTCACTGGCTAAATATG	540
QY	585	AGAAATGCATGCTGTGACGCTGGTATTTGCATTCATGATGAGCTGATTTGAGACCT	644
Db	541	AGAAATGCATGCTGTGACGCTGGTATTTGCATTCATGATGAGCTGATTTGAGACCT	600
QY	645	CTTCCCATGAGACTPAATTTATTTTGGACCAAGGAAGCCCTGAATGAAATTCACAAAT	704
Db	601	CTTCCCATGAGACTPAATTTATTTTGGACCAAGGAAGCCCTGAATGAAATTCACAAAT	660
QY	705	AATATTCAATCGACTTCTCTGTGGAAGACTTGTGAAGAAATGGTGTGATTTAGTG	764
Db	661	AATATTCAATCGACTTCTCTGTGGAAGACTTGTGAAGAAATGGTGTGATTTAGTG	720
QY	765	GATGTGCTATCTGGGTTGGACCTGTTCAGATTACCAAGAGAGATGCTTCTACGTGA	824
Db	721	GATGTGCTATCTGGGTTGGATCTGTTCAGATTACCAAGAGAGATGCTTCTACGTGA	780
QY	825	TGGAATTCAGTTTCTGTGCAATCATTTATTTGAAGACTACCAAAATPAATGCTTAATTTGA	884
Db	781	TGGAATTCAGTTTCTGTGCAATCATTTATTTGAAGACTACCAAAATPAATGCTTAATTTGA	840
QY	885	TTTGTCACTCTTTTATTTATATGCTTGGATGTTCACCTTAATGACATTTTAATTA	944
Db	841	TTTGTCACTCTTTTATTTATATGCTTGGATGTTCACCTTAATGACATTTTAATTA	900
QY	945	GTTATGTATACATCTGATGAGAAAGCAAGCTPAATATGTTTACAGACCAAGTGTAT	1004
Db	901	GTTATGTATACATCTGATGAGAAAGCAAGCTPAATATGTTTACAGACCAAGTGTAT	960
QY	1005	TTCAACTGTCTTTTAATCTAGCATTATTCATTTGCTTCAATCAAAAGTGTCTCAAT	1064
Db	961	TTCAACTGTCTTTTAATCTAGCATTATTCATTTGCTTCAATCAAAAGTGTCTCAAT	1020
QY	1065	TTTTTTTAGTGGTTAGAAATCTTCTCAATAGTCAATTCCTCAACCTTAATTTGG	1124
Db	1021	TTTTTTTAGTGGTTAGAAATCTTCTCAATAGTCAATTCCTCAACCTTAATTTGG	1080
QY	1125	AATATTTGTGTGCTCTTTTGTCTTCTAGTATAGCATTTTAAAAAATATATAAG	1184
Db	1081	AATATTTGTGTGCTCTTTTGTCTTCTAGTATAGCATTTTAAAAAATATATAAG	1140
QY	1185	CTACCAATCTTTGTACAAATTTGTAAGATTTTATTAATCTT	1233

Db	1141	CTACCAATCTTGTGTACAAATTTGTAATGTAAGAATTTTTTATATCT	1189
RESULT 4			
CR612318			
LOCUS			
DEFINITION	CR612318	1111 bp	mRNA linear HTC 21-JUL-2004
ACCESSION	full-length cDNA clone CS0DM014YN20 of Fetal Liver of Homo sapiens (human).		
VERSION	CR612318.1	GI:50493125	
KEYWORDS	HTC; CNSLT cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.		
TITLE	1 (bases 1 to 1111)		
JOURNAL	Unpublished		
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1111)		
REFERENCE	Genoscope.		
AUTHORS	Direct Submission		
TITLE	Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage		
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
COMMENT	- Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.		
FEATURES	location/Qualifiers		
source	1..1111		
ORIGIN	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DM014YN20" /tissue.type="Fetal liver" /plasmid="pCMVSPORT_6"		
Query Match	76.2% ; Score 958 ; DB 3 ; Length 1111 ;		
Best Local Similarity	99.7% ; Pred. No. 0 ;		
Matches 1108 ;	Conservative 0 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;		
QY	140	GGCAGCCCAAGGGCCCCCGCGCCCTCCCGCAGCGGCTCCGCGGCTCCCTGCTGCT	199
DB	1	GGACCCCAAGGGCCCCCGCGCTCCCGCAGCGGCTCCGCGGCTCCCTGCTGCTGCT	60
QY	200	GCTGAGCTGCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAGCAAAAGCGCA	259
DB	61	GCTGAGCTGCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAGCAAAAGCGCA	120
QY	260	GCTCCGGAGAAGGGAGGCGTGTGACCTGTATATATGAAATGTGCTTACAGGGCCAGCAGG	319
DB	121	GCTCCGGAGAAGGGAGGCGTGTGACCTGTATATATGAAATGTGCTTACAGGGCCAGCAGG	180
QY	320	AGTGCCTGTGTGAGACGCGGAGCCCTCGGGGCCAATGTTATTCGCGGTACACCTGGATCCC	379
DB	181	AGTGCCTGTGTGAGACGCGGAGCCCTCGGGGCCAATGTTATTCGCGGTACACCTGGATCCC	240
QY	380	AGTCTGGGATGTGATTCAAAGGAAAGGGGGAATGTCTGAGGGAAGCTTTGAGAGTC	439
DB	241	AGTCTGGGATGTGATTCAAAGGAAAGGGGGAATGTCTGAGGGAAGCTTTGAGAGTC	300
QY	440	CTGGAACCCCACTACAAAGCAGTGTCTATGAGATTCATTGAATATGSCATAGATCTTGG	499
DB	301	CTGGAACCCCACTACAAAGCAGTGTCTATGAGATTCATTGAATATGSCATAGATCTTGG	360
QY	500	GAATAATTCGGAGTGTACATTACAAAGATGCTTCAATATAGTCTCTAAGAGTTTGT	559



Db	361	GAATATTCGGAGTGTACATTTACAAAGATGCGTTCAAAATAGTGTCTTAAGAGTTTGT	420
Qy	560	CAGTGGCTCAGTGGCTAAAATGCAAAATGCATGCTGTCAAGCTTGTATTTCAATT	619
Db	421	CAGTGGCTCAGTGGCTAAAATGCAAAATGCATGCTGTCAAGCTTGTATTTCAATT	480
Qy	620	CAATGAGACTGAATGTTTACGACCTCTTCCCATTTGAAGCTATTAATTTATTTGACCAAG	679
Db	481	CAATGAGACTGAATGTTTACGACCTCTTCCCATTTGAAGCTATTAATTTATTTGACCAAG	540
Qy	680	AAGCCCTGAATGAAATTCAGCAATTAATATTCATGCACTTCTCTGGAAGACCTTG	739
Db	541	AAGCCCTGAATGAAATTCAGCAATTAATATTCATGCACTTCTCTGGAAGACCTTG	600
Qy	740	TGAAGAAATTTGGTGTGATTAAGTGAATGTTGCTATCTGGGTGGCACTTGTACAGATTA	799
Db	601	TGAAGAAATTTGGTGTGATTAAGTGAATGTTGCTATCTGGGTGGCACTTGTACAGATTA	660
Qy	800	CCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTCTTGGCATCAATTATGAAAGACT	859
Db	661	CCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTCTTGGCATCAATTATGAAAGACT	720
Qy	860	ACCAAAATTAATGCTTAAATTTTCACTTGGCACTCTTTTAAATTAAGCTTGAATGG	919
Db	721	ACCAAAATTAATGCTTAAATTTTCACTTGGCACTCTTTTAAATTAAGCTTGAATGG	780
Qy	920	TTCACTTAAATGACATTTTAAATAAGTTATGATATACATCTGAATGAAACCAAGCTAA	979
Db	781	TTCACTTAAATGACATTTTAAATAAGTTATGATATACATCTGAATGAAACCAAGCTAA	840
Qy	980	ATATGTTTACAGACCAAAAGTGTGATTTCACTGTGTTTTAAATCTAGCAATTAATTCATTT	10399
Db	841	ATATGTTTACAGACCAAAAGTGTGATTTCACTGTGTTTTAAATCTAGCAATTAATTCATTT	900
Qy	1040	GCTTCAATCAAAAAGTGTTCATATTTTAAATAGTGTAGAAATCTTCTTCATAGT	10999
Db	901	GCTTCAATCAAAAAGTGTTCATATTTTAAATAGTGTAGAAATCTTCTTCATAGT	960
Qy	1100	CACATTTCTGCAACCTATTAATTTGGAAATTTGTTGTGCTCTTTGTTTTCTCTTAGTA	11599
Db	961	CACATTTCTGCAACCTATTAATTTGGAAATTTGTTGTGCTCTTTGTTTTCTCTTAGTA	10200
Qy	1160	TAGCATTTTAAATAAAATATATAAAGCTACCAATCTTTGTACAAATTTGTAAATGTTAAGA	12199
Db	1021	TAGCATTTTAAATAAAATATATAAAGCTACCAATCTTTGTACAAATTTGTAAATGTTAAGA	10800
Qy	1220	TTTTTTTTTATATCTGTTAATTAATAATTAAT	1250
Db	1081	TTTTTTTTTATATCTGTTAATTAATAATAATTAAT	1111
RESULT 5			
LOCUS	CR594803	1103 bp	mRNA linear HTC 21-JUN-2004
DEFINITION	Full-length cDNA clone CS0D1022YF04 of Placenta Cot 25-normalized		
ACCESSION	CR594803		
VERSION	CR594803.1	GI:50475610	
KEYWORDS	HTC; cNSLT_cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1103)		
JOURNAL	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.		
REMARK	Full-length cDNA libraries and normalization		
REFERENCE	Unpublished		
AUTHORS	Contact : Feng Liang Email : fliang@lifetech.com URL :		
REMARK	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600		
REFERENCE	Paradey Avenue		
AUTHORS	2 (bases 1 to 1103)		
	Genoscope.		

Query Match	75.6%	Score 950	DB 3	Length 1103
Best Local Similarity	99.7%	Pred. No. 0		
Matches 1100	Conservative 0	Mismatches 3	Indels 0	Gaps 0
69	GAGCGTACCAACGTTCCCTCTCTGAGTCTCTCCGCGCTCCGAGCTCCGCGCTCCGCGAG	128		
1	GAGCGTACCAACGTTCCCTCTCTGAGTCTCTCCGCGCTCCGAGCTCCGCGCTCCGCGAG	60		
129	CCGGAGAGCATACGACCCCGAGGGCCCGCGCTCCCGCGAGCGAGCTCCGCGCTCTG	188		
61	CCGGAGAGCATACGACCCCGAGGGCCCGCGCTCCCGCGAGCGAGCTCCGCGCTCTG	120		
189	CTGCTCTGCTGCTGACAGTCCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAGAG	248		
121	CTGCTCTGCTGCTGACAGTCCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAGAG	180		
249	CAAAAGGGGAGCTCCCGCAGAGGAGGTGTGACCTGTATATGAAATGTCCTTACAA	308		
181	CAAAAGGGGAGCTCCCGCAGAGGAGGTGTGACCTGTATATGAAATGTCCTTACAA	240		
309	GGGCGAGAGAGTGCCTGCTGAGACGGAGGCGCTGGGGCCAAATGTTATCCGGGTACA	368		
241	GGGCGAGAGAGTGCCTGCTGAGACGGAGGCGCTGGGGCCAAATGTTATCCGGGTACA	300		
369	CCTGGGATCCAGAGTCCGAGTGAATTCAAAGAGAAAAGGGGAAATGTCGAGGGAAA	428		
301	CCTGGGATCCAGAGTCCGAGTGAATTCAAAGAGAAAAGGGGAAATGTCGAGGGAAA	360		
429	TTTGAAGAGTCTTGAGACCCCACTACAGAGTGTTCATGAGATTCATGAAATATGCG	488		
361	TTTGAAGAGTCTTGAGACCCCACTACAGAGTGTTCATGAGATTCATGAAATATGCG	420		
489	ATAGATCTTGGGAAAATTGGGGAGGTGATTTTCAAAAGATGCGTCCAAATAGTCTGA	548		
421	ATAGATCTTGGGAAAATTGGGGAGGTGATTTTCAAAAGATGCGTCCAAATAGTCTGA	480		
549	AGAGTTTGTTCAGTGGCTCACTTCGCTAAATATGCAAAATGCAATGCTGACGGTGG	608		
481	AGAGTTTGTTCAGTGGCTCACTTCGCTAAATATGCAAAATGCAATGCTGACGGTGG	540		
609	TATTTACATTCATGAGCTGAATGTTGAGAGCTCTTCCCATTTGAAGCTATATATAT	668		
541	TATTTACATTCATGAGCTGAATGTTGAGAGCTCTTCCCATTTGAAGCTATATATAT	600		
669	TTGAGCAAGGAGCCCTGAATGATTTCAACATTTAATATTCATGCACTTCTTCTGG	728		
601	TTGAGCAAGGAGCCCTGAATGATTTCAACATTTAATATTCATGCACTTCTTCTGG	660		
729	GAAGGACTTTGTGAAGAAATGGTGTGATAGTGAATGTTGTATCTGGGTGGCACT	788		
661	GAAGGACTTTGTGAAGAAATGGTGTGATAGTGAATGTTGTATCTGGGTGGCACT	720		
789	TGTTCAATTCACCAAAAGAGATGCTTCTACTGAGATGAATTCAGTTTCTGCACTAT	848		

Db 721 TGTTCAGATTACCCAAAGAGATGCTTCTAGTGAATGCAATTCAGTTCTCCATCAT 780  
Qy 849 ATTGAAGAACTACCAAAATATATGCTTAATTTTCATTTGCTCACTCTTTTATATG 908  
Db 781 ATTGAAGAACTACCAAAATATATGCTTAATTTTCATTTGCTCACTCTTTTATATG 840  
Qy 909 CCTTGAATGCTTCACTTAATGACATTTTAAATTAAGTTATGATACATCTGAATGAA 968  
Db 841 CCTTGAATGCTTCACTTAATGACATTTTAAATTAAGTTATGATACATCTGAATGAA 900  
Qy 969 ACCAAAGCTAAATATGCTTACAGACCAAGTGTGATTTTCACTGTTTAAATCTAGCA 1028  
Db 901 ACCAAAGCTAAATATGCTTACAGACCAAGTGTGATTTTCACTGTTTAAATCTAGCA 960  
Qy 1029 TTATTCATTTGCTTCAATCAAAAGTGTTCATATATTTTCTAGTTGGTTAGAAATCT 1088  
Db 961 TTATTCATTTGCTTCAATCAAAAGTGTTCATATATTTTCTAGTTGGTTAGAAATCT 1020  
Qy 1089 TTCTTCATGTCATCTCTCACTATATATTTGGAATATTTGTGTGCTTTTGT 1148  
Db 1021 TTCTTCATGTCATCTCTCACTATATATTTGGAATATTTGTGTGCTTTTGT 1080  
Qy 1149 TTCTTCATGTCATCTCTCACTATATATTTGGAATATTTGTGTGCTTTTGT 1103  
Db 1081 TTCTTCATGTCATCTCTCACTATATATTTGGAATATTTGTGTGCTTTTGT 1103

RESULT 6  
AL532456 1098 bp mRNA linear EST 24-MAR-2004  
LOCUS AL532456 Homo sapiens FETAL LIVER Homo sapiens cDNA clone  
DEFINITION CS0DM014YN20 5-PRIME, mRNA sequence.  
ACCESSION AL532456  
VERSION AL532456.3 GI:45707373  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1098)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 13, 2001 this sequence version replaced gi:31070288.  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with NotI and cloned  
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 4941.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CS0DM014G10QPlc=4941.f.  
FEATURES  
source Location/Qualifiers  
1..1098  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DM014YN20"  
/tissue\_type="FETAL LIVER"  
/dev\_stage="fetal"  
/clone\_id="Homo sapiens FETAL LIVER"  
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with NotI and  
cloned into the NotI and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

ORIGIN  
Query Match 55.7%; Score 700; DB 1; Length 1098;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 700; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 ATTCGGGGTACCTCGGATCCAGTGGGATGATTCAAAGAGAAAGGGGAATGT 416  
Db 217 ATTCGGGGTACCTCGGATCCAGTGGGATGATTCAAAGAGAAAGGGGAATGT 276  
Qy 417 CTGAGGAAAGGCTTGAAGAGTCTGACACCAACTCAAGAGCTTATGAGATTC 476  
Db 277 CTGAGGAAAGGCTTGAAGAGTCTGACACCAACTCAAGAGCTTATGAGATTC 336  
Qy 477 TTGAATATGCAATGATCTTGGGAAATTCGGAGTGTACATTTCAAAAGATGCTTCA 536  
Db 337 TTGAATATGCAATGATCTTGGGAAATTCGGAGTGTACATTTCAAAAGATGCTTCA 336  
Qy 537 AATAGTGTCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTTAAATGCAAAATGATGC 596  
Db 397 AATAGTGTCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTTAAATGCAAAATGATGC 456  
Qy 597 TGTCAAGCTGGATTTTCACTCAATGAGCTGAATGTTCAAGACCTTCCCATTTGA 656  
Db 457 TGTCAAGCTGGATTTTCACTCAATGAGCTGAATGTTCAAGACCTTCCCATTTGA 516  
Qy 657 GCTATATTTATTTGAGCAAGAGAGCCCTGAATGATTCACATTAATTAATTCATCGC 716  
Db 517 GCTATATTTATTTGAGCAAGAGAGCCCTGAATGATTCACATTAATTAATTCATCGC 576  
Qy 717 ACTTCTTCTGGGAAAGACTTTTGAAGAAATGTGCTGATTTAGTGAATGCTTATC 776  
Db 577 ACTTCTTCTGGGAAAGACTTTTGAAGAAATGTGCTGATTTAGTGAATGCTTATC 636  
Qy 777 TGGGTTGCACTTGTTCAGATTTACCAAAAGAGATCTTCACTGATGGAATTCAGTT 836  
Db 637 TGGGTTGCACTTGTTCAGATTTACCAAAAGAGATCTTCACTGATGGAATTCAGTT 696  
Qy 837 TCTGCATCATTTATGAAAGACTACCAAAATTAATGCTTAAATTTTCATTTGCTACCTG 896  
Db 697 TCTGCATCATTTATGAAAGACTACCAAAATTAATGCTTAAATTTTCATTTGCTACCTG 756  
Qy 897 TTTTATTTATGACCTTGAATGCTTCAATTAATGATTTTAAATGATTAATGATTAAC 956  
Db 757 TTTTATTTATGACCTTGAATGCTTCAATTAATGATTTTAAATGATTAATGATTAAC 816  
Qy 957 ATCTGAATGAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTACACTGTT 1016  
Db 817 ATCTGAATGAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTACACTGTT 876  
Qy 1017 TTAATCTAGATTAATTCATTTTGTCTTCATCAAAAGTGG 1056  
Db 877 TTAATCTAGATTAATTCATTTTGTCTTCATCAAAAGTGG 916

RESULT 7  
CA415410/c 747 bp mRNA linear EST 07-NOV-2002  
LOCUS CA415410/c  
DEFINITION UI-H-E20-baw-n-12-0-UI.s1 NCI CGAP Chi Homo sapiens cDNA clone  
UI-H-E20-baw-n-12-0-UI 3', mRNA sequence.  
ACCESSION CA415410  
VERSION CA415410  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 747)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Straubeberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Orthopedics Dr. Steven Gitelis/ Rush Presbyterian, Dept. of



## ORIGIN

Query Match 55.1%; Score 693; DB 5; Length 796;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 653; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

565 GCTCAGTGGCTGAAATGAGAAATGATGCTGCTGAGCTGGTGGTATTTTCACTTCAATG 624  
 710 GCTCAGTGGCTGAAATGAGAAATGATGCTGCTGAGCTGGTGGTATTTTCACTTCAATG 651  
 625 GAGCTGAATGTTAGAGACCTCTTCCATGAGCTATTAATTTATTTGAGCAAGAGGCC 684  
 650 GAGCTGAATGTTAGAGACCTCTTCCATGAGCTATTAATTTATTTGAGCAAGAGGCC 591  
 685 CTGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 744  
 590 CTGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 531  
 745 GAATGCTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 804  
 530 GAATGCTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 471  
 805 AAGGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 864  
 470 AAGGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411  
 865 AATAATGCTTAAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 924  
 410 AATAATGCTTAAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 351  
 925 TTAATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 984  
 350 TTAATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 291  
 985 TTTACAGACCAAGTGTGATTTCACTGCTGTTTAAATTAATTAATTAATTAATTAATTAATTA 1044  
 290 TTTACAGACCAAGTGTGATTTCACTGCTGTTTAAATTAATTAATTAATTAATTAATTAATTA 231  
 1045 AATCAAAAGTGTGATTTCACTGCTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 1104  
 230 AATCAAAAGTGTGATTTCACTGCTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 171  
 1105 TCTCAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1164  
 170 TCTCAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 111  
 1165 TTTTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1224  
 110 TTTTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 51  
 1225 TTTATATCTGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1257  
 50 TTTATATCTGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 18

RESULT 9 AL575307/c 1102 bp mRNA linear EST 06-APR-2004  
 LOCUS AL575307 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 DEFINITION clone CS0D1061YA20 3-PRIME, mRNA sequence.  
 ACCESSION AL575307  
 VERSION AL575307.3 GI:46248266  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 16, 2001 this sequence version replaced gi:31313615.  
 Contact: Genoscope

## FEATURES

source

Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 4941.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna7s-CS0D1061YA20P1fc=4941.f.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1061YA20"  
 /cissue\_type="PLACENTA COT 25-NORMALIZED"  
 /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 55.0%; Score 691; DB 1; Length 1102;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 841; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

357 ATTCGGGTGACACCTGGGATCCAGTGGGATGATTAATTAATTAATTAATTAATTAATTAATTA 416  
 879 ATTCGGGTGACACCTGGGATCCAGTGGGATGATTAATTAATTAATTAATTAATTAATTAATTA 820  
 417 CTGAGGAAACCTTTGAGAGTCTGACACCCATCAAGAGTTCATGAGATTCA 476  
 819 CTGAGGAAACCTTTGAGAGTCTGACACCCATCAAGAGTTCATGAGATTCA 760  
 477 TTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 536  
 759 TTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 700  
 537 AATAGTCTTAAGATTTTGTTCAGTGGCTCACTTCGCTAAATTAATTAATTAATTAATTAATTA 596  
 699 AATAGTCTTAAGATTTTGTTCAGTGGCTCACTTCGCTAAATTAATTAATTAATTAATTAATTA 640  
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 VERSION BQ010155.1 GI:19735056  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 702)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgabs-rc@mail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 CDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Distribution: Clone distribution information can be found  
 through the I.M.A.G.E. Consortium/BLNI, at: http://image.llnl.gov  
 The following repetitive elements were found in this cDNA  
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 Seq primer: M13 FORWARD  
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 (Pharmacia) with a modified polylinker; Site 1: Scor I;  
 Site 2: Not I; NCI\_CGAP ED0 is a cDNA library containing  
 the following tissue(s): Chondrosarcoma cell line C5. The  
 library was constructed according to Bonaldo, Lennon and  
 Soares, Genome Research, 6:791-806, 1996. First strand  
 cDNA synthesis was primed with an oligo-dT primer  
 containing a Not I site. Double stranded cDNA was ligated  
 to an EcoR I adaptor, digested with Not I, and cloned  
 directionally into pTR73-Pac vector. The oligonucleotide  
 used to prime the synthesis of first-strand cDNA contains  
 a library tag sequence that is located between the Not I  
 site and the (dT)18 tail. The sequence tag for this  
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 TAG LIB=UI-H-ED0  
 TAG\_SEQ=CCTCAAGGCT"

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 DB 582 TCAACAAATTAATTAATTCATGCACTTCTGTGGAAGAGCTTTGGAAGAAATGGTGT 523  
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 QY 876 TAATTTTCAATTTGCTACCTCTTTTATTAATGCTTGAATGCTTCAATTAATGACAT 935  
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 DB 42 TTAATTAATTAATTTTCCACA 21  
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 ACCESSION AL551834  
 VERSION AL551834.3 GI:45856624  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1100)  
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:1273650.  
 CONTACT: Genoscope



ORIGIN TAG\_SEQ=CGGTCACTC"

Query Match 50.9%; Score 640; DB 6; Length 723;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 690; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 687 GAATGAATTTCAACATTAATTAATTCATTCGACCTCTTCTGTGAGAGACCTTTGTGAGGA 746  
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LOCUS BE607413  
DEFINITION col01ES0306c04 colon carcinoma tissue cDNA library Homo sapiens  
ACCESSION BE607413  
VERSION BE607413.1 GI:13123454  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Huang,Y.M., Wang,K., Zhang,J.Zh., Li,X.Y., Li,Y., Huang,D.Q.,  
Xie,Y., Mao,Y.M., Bao,L. and Sun,Zh.R.  
TITLE Identification of genes differentially over-expressed in human  
colon carcinoma using combination of SSH and cDNA microarray

JOURNAL analysis  
Unpublished (2000)  
CONTACT: Huang Y.M.  
COMMENT Department of Experimental Medicine  
Beijing 306 hospital, Beijing  
No.9, Anxiang Beilei Road, Beijing, 100101, P.R.China  
Tel: 8610-66356111  
Fax: +86-10-66356111  
Email: hybboy@sina.com.

FEATURES  
source location/Qualifiers

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/mol\_type="mRNA"  
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/clone\_lib="colon carcinoma tissue cDNA library"  
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Site\_2: EcoRI"

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Matches 636; Conservative 0; Mismatches 0;

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Db 456 AGGAATGTTGTTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 397  
Qy 803 AAAAGAGATGCTTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 862  
Db 396 AAAAGAGATGCTTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 337  
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LOCUS BQ425266  
DEFINITION AGENCOURT 7912803 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6150166  
5', mRNA sequence.



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ACCESSION      BQ425266
VERSION         BQ425266.1
KEYWORDS       GI:21120581
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      NIH-MGC http://mgs.nci.nih.gov/
                National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cga@bbs-rcmail.nih.gov
                Tissue Procurement: ATCC/DCPD/DRP
                CDNA Library Preparation: Life Technologies, Inc.
                CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                DNA Sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LNL at:
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                Average insert size 2 kb. Library constructed by Life
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ORIGIN
Query Match      50.6%; Score 636; DB 5; Length 851;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 736; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GAGGCGCGGCGGTGAAAGCGCATTTGATGACGCTCGCGCGGCGCTCGAGCGCGGCGAG 65
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QY      66 CGAAGCGGTGACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125
DB      96 CGAAGCGGTGACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 155
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DB      156 CAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCGCTCTCCGCGAGCGGCTCTCGCGGCTTC 215
QY      186 CTGCTGCTCTGCTCTGCTGAGCTGCGCGCGCGCGCTCGAGCGGCTCTGAGATCCCAAGGGG 245
DB      216 CTGCTGCTCTGCTCTGCTGAGCTGCGCGCGCGCGCTCTGAGATCCCAAGGGG 275
QY      246 AAGCAAAAGGCGGCACTCCGCGAGAGGAGGTGTGTGACCTGTATTAATGAATGTGCTTA 305
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QY      366 AACACTGGGATCCAGGTGCGGATGATTTCAAAAGAGAAAGGAGGAAATGTCTGAGGAA 425
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RESULT 15
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DEFINITION      colonEST0306c10 colon carcinoma tissue cDNA library Homo sapiens
ACCESSION      BE607414
VERSION      BE607414.1
KEYWORDS      BE607414.1 GI:13123455
SOURCE      EST.
ORGANISM      Homo sapiens (human)
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                1 (bases 1 to 683)
                Identification of genes differentially over-expressed in human
                colon carcinoma using combination of SSH and cDNA microarray
                analysis
                Unpublished (2000)
                Contact: Huang Y.W.
                Department of Experimental Medicine
                Beijing 306 hospital, Beijing
                No.9, Anxiang Beilei Road, Beijing, 100101, P.R.China
                Tel: 8610-66356111
                Fax: +86-10-66356111
                Email: hywboy@sina.com.
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      516 ACATTTCAGAAAGTGCCTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 575
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US-09-489-847-124
/ Sequence 124, Application US/09489847
/ Patent No. 647615
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al
/ TITLE OF INVENTION: 98 Human Secreted Proteins
/ FILE REFERENCE: P2031P1
/ CURRENT APPLICATION NUMBER: US/09/489, 847
/ CURRENT FILING DATE: 2000-01-24
/ EARLIER APPLICATION NUMBER: PCT/US99/17130
/ EARLIER FILING DATE: 1999-07-29
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ EARLIER APPLICATION NUMBER: 60/095,486
/ EARLIER FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: 60/096,319
/ EARLIER FILING DATE: 1998-08-12
/ EARLIER APPLICATION NUMBER: 60/095,454
/ EARLIER FILING DATE: 1998-08-06
/ EARLIER APPLICATION NUMBER: 60/095,455
/ EARLIER FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 376
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 124
/ LENGTH: 1286
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: SITE
/ LOCATION: (1284)
/ OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-124

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Query Match	77.0%	Score 968,	DB 4;	Length 1286;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 1188; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1;

QY	67	QY	127
QY	CAGAGCTGACCAAGTTCCTCTCCTCGGATCTCTCGGCTCCGCGCTGCGCGAC	QY	AGCCGGAGACCATGTCGACCCACGGGCCCCGCGCTCCCCGATGCGCTCCGCGGCTTC
Db	60	Db	120
Db	CAGAGCTGACCAAGTTCCTCTCTCTCGGATCTCTCGGCTCCGCGCTCCGCGCTGCGCGAC	Db	AGCCGGAGACCATGTCGACCCACGGGCCCCGCGCTCCCCGATGCGCTCCGCGGCTTC
			179

QY	187	TGCGTCTCTGCTGCTGAGGTGCGCGCGCGCTGAGAGGCTCTGAGATCCCCAAAGGGA	246
Db	180	TGCTGCTCTGCTGCTGAGCTGCGCGCGCGCTGAGAGGCTCTGAGATCCCCAAAGGGA	239
QY	247	AGCAAAAGGCGCACCTCCGCGAGAGGAGTGTGACCTGTATATGGAATGTCTTAC	306
Db	240	AGCAAAAGGCGCA-CTCCGCGAGAGGAGTGTGACCTGTATATGGAATGTCTTAC	298
QY	307	AAGGCGCAGCAGAGTGCCTGTGTGAGACGGAGACCTTGGGGCCAAATGTAATCCGGGTA	366
Db	299	AAGGCGCAGCAGAGTGCCTGTGTGAGACGGAGACCTTGGGGCCAAATGTCCTGGGTA	358
QY	367	CACCTGGGATCCAGAGTCGGGATGATTCAAAGAGAAAAAGGGGAATGTCTGAGGAAA	426
Db	359	CACCTGGGATCCAGAGTCCAGGTGCGGATTCGAAGAGAAAAAGGGGAATGTCTGAGGAAA	418
QY	427	GCTTTAGAGAGTCTCTGACACCCCACTACAGCAGTGTTCATGAGATTATTATG	486
Db	419	GCTTTAGAGAGTCTCTGACACCCCACTACAGCAGTGTTCATGAGATTATTATG	478
QY	487	GCATAGATCTTGGGAAAAATGCGGAGTGTACATTTACAAAGATGCGTTCAATAGTCTC	546
Db	479	GCATAGATCTTGGGAAAAATGCGGAGTGTACATTTACAAAGATGCGTTCAATAGTCTC	538
QY	547	TAAAGTTTTTGTGAGTGCCTCACTTGGCTAAATGACAAATGATGCTGCAGGTT	606
Db	539	TAAAGTTTTTGTGAGTGCCTCACTTGGCTAAATGACAAATGATGCTGCAGGTT	598
QY	607	GCTATTTCACTTCAATGAGCTGAAATGTTCCAGACCTCTTCCATGGAAGCTAAATT	666
Db	599	GCTATTTCACTTCAATGAGCTGAAATGTTCCAGACCTCTTCCATGGAAGCTAAATT	658
QY	667	ATTGAGACCAAGAAAGCCCTGAATGAAATTCACAAATTAATTCATGCGACTTCTCTG	726
Db	659	ATTGAGACCAAGAAAGCCCTGAATGAAATTCACAAATTAATTCATGCGACTTCTCTG	718
QY	727	TGGAAGACCTTGTGAAGAAATTGGTGTGATTTAGTGAATGTTGCTATCTGGGTGGCA	786
Db	719	TGGAAGACCTTGTGAAGAAATTGGTGTGATTTAGTGAATGTTGCTATCTGGGTGGCA	778
QY	787	CTGTGTGATTAACCAAAAGAGATGCTTACTGTGATGGAATTCAGTTCTCGCATCA	846
Db	779	CTGTGTGATTAACCAAAAGAGATGCTTACTGTGATGGAATTCAGTTCTCGCATCA	838
QY	847	TTATTTGAAGACTACCAAAATTAATGCTTAAATTTTCATTTGCTACCTCTTTTATTA	906
Db	839	TTATTTGAAGACTACCAAAATTAATGCTTAAATTTTCATTTGCTACCTCTTTTATTA	898
QY	907	TGCTTTGGAATGTTCACTTAAGAATTTTAATAAGTTATGTAATACATCGAATGA	966
Db	899	TGCTTTGGAATGTTCACTTAAGAATTTTAATAAGTTATGTAATACATCGAATGA	958
QY	967	AAAGCAAGCTAAATATGTTTACAGACCAAGTAGTGAATTCACACTGTTTAAATCTAG	1026
Db	959	AAAGCAAGCTAAATATGTTTACAGACCAAGTAGTGAATTCACACTGTTTAAATCTAG	1018
QY	1027	CATTATTCATTTTGCTTCATCAAAAAGTGTTCATATTTTTTTTAGTGTGTAATA	1086
Db	1019	CATTATTCATTTTGCTTCATCAAAAAGTGTTCATATTTTTTTTAGTGTGTAATA	1078
QY	1087	CTTTCTTATGTCACATCTCTCAACCTATATAATTGGAATATGTTGGTCTTTTGT	1146
Db	1079	CTTTCTTATGTCACATCTCTCAACCTATATAATTGGAATATGTTGGTCTTTTGT	1138
QY	1207	TAAATGTTAAGATTTTTTTTATATCTGTAAATTAATAATTAATTTCCAAAC	1257
Db	1199	TAAATGTTAAGATTTTTTTTATATCTGTAAATTAATAATTAATTTCCAAAC	1249

QY	967	AAAGCAAGCTAAATATGTTTACGACCAAGTGTGATTTCAAGCTGTTTAAATCTAG	1026
Db	959	AAAGCAAGCTAAATATGTTTACGACCAAGTGTGATTTCAAGCTGTTTAAATCTAG	1018
QY	1027	CATTATTCATTTTGCTTCATCAAAAGTGTTCATATATTTTATAGTGTAGATA	1086
Db	1019	CATTATTCATTTTGCTTCATCAAAAGTGTTCATATATTTTATAGTGTAGATA	1078
QY	1087	CTTCTTCATGTGCACTCTCTCAACTATAATTGGAAATGTGTGCTTTTGT	1146
Db	1079	CTTCTTCATGTGCACTCTCTCAACTATAATTGTGTGTGCTTTTGT	1138
QY	1147	TTTTCTCTAGTATAGCATTTTAAAAAATAATAAAAGTACCAATCTTTGTACATTTG	1206
Db	1139	TTTTCTCTAGTATAGCATTTTAAAAAATAATAAAAGTACCAATCTTTGTACATTTG	1198
QY	1207	TAAATGTAAAGATTTTTTTATATCTGTATAAATAAATAATTTTCCAACTA	1257
Db	1199	TAAATGTAAAGATTTTTTTATATCTGTATAAATAAATAATTTTCCAACTA	1249



Qy	547	TAGAGTTTTGTTCACTGGCTCACTTGGCTTAAATGAGAAATGATGCTGTCAAGGTT	608
Db	515	TAAAGATTTTGTTCAGTGGCTCACTTGGCTTAAATGAGAAATGATGCTGTCAAGGTT	574
Qy	607	GGATTTTCACATTCATGAGCTGATGTTTACAGACCTCTTCCCATGAGACTTAATTT	666
Db	575	GGATTTTCACATTCATGAGCTGATGTTTACAGACCTCTTCCCATGAGACTTAATTT	634
Qy	667	ATTTGACCAAGGAGCCCTGAATGAATTCACAATTATATTCATGCACTTCTTCTG	726
Db	635	ATTTGACCAAGGAGCCCTGAATGAATTCACAATTATATTCATGCACTTCTTCTG	694
Qy	727	TGAGAGACTTTGTGAAGAAATTGGTCTGATTAATGATGATGTTGCTATCTGGTGGCA	786
Db	695	TGAGAGACTTTGTGAAGAAATTGGTCTGATTAATGATGATGTTGCTATCTGGTGGCA	754
Qy	787	CTTGTTCAAGTTAACCCAAAAGAGATGCTTTCATCTGATGGAATTCAGTTTCTGGCATCA	846
Db	755	CTTGTTCAAGTTAACCCAAAAGAGATGCTTTCATCTGATGGAATTCAGTTTCTGGCATCA	814
Qy	847	TTATTGAAGACTACCAAAATAA	869
Db	815	TTATTGAAGACTACCAAAATAA	837

```

RESULT 6
US-09-834-759-510
Sequence 510, Application US/09834759
Patent No. 6680197
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C9
CURRENT APPLICATION NUMBER: US/09/834,759
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 547
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 510
LENGTH: 732
TYPE: DNA
ORGANISM: Homo sapiens
US-09-834-759-510

```

Query Match	58.2%	Score 732;	DB 4;	Length 732;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 732;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	138	ATGCGACCCGAGGGCCCCCGCGCGCTCCCGGAGCGGCTCCGCGCGCTCTGCTGCTCTG	137
Db	1	ATGCGACCCGAGGACCCCGCGCGCTCCCGGAGCGGCTCCGCGCGCTCTGCTGCTCTG	60
Qy	198	CTGCTGAGCTGCGCGCGCGCGCTCTGAGCGCTCTTGAGATCCCGAAGGGAGCAAAAGGCG	257
Db	~ 61	CTGCTGAGCTGCGCGCGCGCGCGCTCTGAGCGCTCTTGAGATCCCGAAGGGAGCAAAAGGCG	120
Qy	258	CAGCTCCGCGAGAGGAGGTGATGACCTGTATTAATGAAATGTGCTTCAAGGGCCAGCA	317
Db	121	CAGCTCCGCGAGAGGAGGTGATGACCTGTATTAATGAAATGTGCTTCAAGGGCCAGCA	180
Qy	318	GGAGTGCCTGTGCGAAGCGGAGCGCTGGGGCGCAATGTATTCGGGGTAAACCTGGGATC	377
Db	181	GGAGTGCCTGTGCGAAGCGGAGCGCTGGGGCGCAATGTATTCGGGGTAAACCTGGGATC	240
Qy	378	CCAGGTGCGGATGATTCAAAGAGAAAGGGGAGATGTGAGGAAAGCTTTGAGGAG	437

Db	241	CCAGGTGGGATGAGATTCAAAAGGAGAAAAAGGGGGAAAGTCTGAGGGAAAGCTTTGAGAG	300
Oy	438	TCCTGACACCCCACTACAGCAGATGTTCAATGAGTTCATTGAATTATGGCATAGATCTT	487
Db	301	TCCTGGACACCAACTACAGCAGATGTTCAATGAGTTCATTGAATTATGGCATAGATCTT	360
Oy	498	GGGAAATATGCGAGATGACATTTTCAAAAGATGCGTCAATATAGTCTTAAGAGTTTG	557
Db	361	GGGAAATATGCGAGATGACATTTTCAAAAGATGCGTCAATATAGTCTTAAGAGTTTG	420
Oy	558	TTCAATGGCTCACTTGGCTAAATATGCAGAAATGCAATGCTGTCAAGCGTTGGATTACAA	617
Db	421	TTCAATGGCTCACTTGGCTAAATATGCAGAAATGCAATGCTGTCAAGCGTTGGATTACAA	480
Oy	618	TTCAATGGAGCTGAATATGTTCAAGACCTCTCCCAATGAGCTATATTTATTTGAGACCA	677
Db	481	TTCAATGGAGCTGAATATGTTCAAGACCTCTCTCCCAATGAGCTATATTTATTTGAGACCA	540
Oy	678	GGAAGCCTGGAATGATTCACAAATTAATAATTCATGCGACTTCTTCTGTGGAGGACTT	737
Db	541	GGAAGCCTGGAATGATTCACAAATTAATAATTCATGCGACTTCTTCTGTGGAGGACTT	600
Oy	738	TGTGAAGGAATTTGGTCTGGATTACTGATATGTGCTATCTGGGTATGGACATGTGTCAT	797
Db	601	TGTGAAGGAATTTGGTCTGGATTACTGATATGTGCTATCTGGGTATGGACATGTGTCAT	660
Oy	798	TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGCATCATATTAATGAAGAA	857
Db	661	TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGCATCATATTAATGAAGAA	720
Oy	858	CTACCAAAATAA 869	
Db	721	CTACCAAAATAA 732	

```

RESULT 7
: Sequence 511, Application US/09834759
: Patent No. 6680197
: GENERAL INFORMATION:
: APPLICANT: Jiang, Yugu
: APPLICANT: Dillon, David C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Xu, Jiaqiang
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
: FILE REFERENCE: 210121.470C9
: CURRENT APPLICATION NUMBER: US/09/834,759
: CURRENT FILING DATE: 2001-04-13
: NUMBER OF SEQ ID NOS: 547
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 511
: LENGTH: 729
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-834-759-511

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Query Match 58.0%; Score 729; DB 4; Length 729;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	138	ATGCGACCCCAAGGGCCCCCGCGCGCTCCCCGAGAGGGAGCTCGCGGCGCTCTGCTGCTCTG	127
Db	1	ATGCGACCCCAAGGGCCCCCGCGCGCTCCCCGAGAGGGAGCTCTGCTGCTCTG	60
Oy	198	CTGCTGAGCTGCGCGCGCGCTCTGAGCGCTCTGTAGATCCCAAGGGGAAACAAAGGCG	257
Db	61	CTGCTGAGCTGCGCGCGCGCTCTGAGCGCTCTGTAGATCCCAAGGGGAAAGCAAAAGGCG	120
Oy	258	CAGCTCCGCGAGAGGAGGTGTGTGACCTGTATATATGAGATGTGCTTACAAAGGCGCAGCA	317

Db 121 CAGCTCCGAGAGGAGGAGGTGGACCTGTATTAATGAAATGCTTACAGGCGCAGCA 180  
QY 318 GGAGTCCCTGTGTGAGACGGAGACCCCTGGGCCAATGTATTCGGGTATACCTGGGATC 377  
Db 181 GGAGTCCCTGTGTGAGACGGAGACCCCTGGGCCAATGTATTCGGGTATACCTGGGATC 240  
QY 378 CCAAGTCCGGATGATTCAAAGAGAAAAGGGGAATGTCTGAGGGAACCTTTGAGAG 437  
Db 241 CCAAGTCCGGATGATTCAAAGAGAAAAGGGGAATGTCTGAGGGAACCTTTGAGAG 300  
QY 438 TCCTGGACACCCCACTACAGAGCTGTCTATGAGTTGATTAATGATGATCTT 497  
Db 301 TCTTGACACCCCACTACAGAGCTGTCTATGAGTTGATTAATGATGATCTT 360  
QY 498 GGGAAATTCGGAGGTGATCATTACAAAGATGCTTCAATAGTGTCTAAGATTTG 557  
Db 361 GGGAAATTCGGAGGTGATCATTACAAAGATGCTTCAATAGTGTCTAAGATTTG 420  
QY 558 TTCAGTGGCTCACTTGGCTAAATGCAAGATGCTGTGAGGCTGTGATTTGACA 617  
Db 421 TTCAGTGGCTCACTTGGCTAAATGCAAGATGCTGTGAGGCTGTGATTTGACA 480  
QY 618 TTCATGAGCTGATGATTCAGGACCTTCCCATGAGCTATTAATTTGACCA 677  
Db 481 TTCATGAGCTGATGATTCAGGACCTTCCCATGAGCTATTAATTTGACCA 540  
QY 678 GGAAGCCTGAAATGAAATTCACAAATTAATTCATGACCTCTCTGAGAGACTT 737  
Db 541 GGAAGCCTGAAATGAAATTCACAAATTAATTCATGACCTCTCTGAGAGACTT 600  
QY 738 TGTGAAGAAATGTGCTGATTAAGATGTTGCTATCTGGTGGCACTTGTTCAGT 797  
Db 601 TGTGAAGAAATGTGCTGATTAAGATGTTGCTATCTGGTGGCACTTGTTCAGT 660  
QY 798 TACCCAAAAGAGATGCTTCTACTGATGAAATTCAGTTCTCGCATCTTATTGAGAA 857  
Db 661 TACCCAAAAGAGATGCTTCTACTGATGAAATTCAGTTCTCGCATCTTATTGAGAA 720  
QY 858 CTACCAAAA 866  
Db 721 CTACCAAAA 729

RESULT 8  
US-09-205-258-125  
Sequence 125, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007p1  
CURRENT APPLICATION NUMBER: US/09/205,258  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 125  
LENGTH: 1288  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (1286)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-205-258-125



Query Match	52.7%	Score 662	DB 4	Length 1288
Best Local Similarity	99.5%	Pred. No. 0		
Matches 1182	Conservative	0	Mismatches	2
			Indels	4
			Gaps	3
Qy	67	CAGACGCTGACCAACGCTTCCTCTCCCTGGATCTCTCCGGCTCCAGCTCCGCGCTCCGCGC	126	
Db	59	CAGAGCGTGAACCAAGCTTCCTCTCTCGGATCTCTCCGGCTCCAGCTCCGCGCTCCGCGC	118	
Qy	127	AGCCGGGAGCCATGCGACCCCAAGGGGCCCGCGCTCCCGCAGCGGCTCCGCGGCTCC	186	
Db	119	AGCCGGGAGCCATGCGACCCCAAGGGGCCCGCGCTCCCGCAGCGGCTCCGCGGCTCC	178	
Qy	187	TGCTGCTCTCTGCTGTCAGCTGCGCGCGCGCTGCGAGGCGCTCTGAGATCCCAAGGGGA	246	
Db	179	TGCTGCTCTCTGCTGTCAGCTGCGCGCGCGCTGCGAGGCGCTCTGAGATCCCAAGGGGA	238	
Qy	247	AGCAAAAGCGCAGCTCCGGCAGAGAGAGTGTGTGACCTGTATTAATGTAATGTCTTAC	306	
Db	239	AGCAAAAGCGCAGCTCCGGCAGAGAGAGTGTGTGACCTGTATTAATGTAATGTCTTAC	296	
Qy	307	AAGGCGCAGCAGAGAGTGCCTGTGTCAGACGAGAGGCCCTTGGGGCCAAATGTATTCGGGTA	366	
Db	297	AAGGCGCAGCAGAGAGTGCCTGTGTCAGACGAGAGGCCCTTGGGGCCAAATGTGCGGTA	356	
Qy	367	CACCTGGGATCCCAAGTGGGATGGAATTCAAAGAGAAAAGGGGAAATGTCTGAGGGAAA	426	
Db	357	CACCTGGGATCCCAAGTGGGATGGAATTCAAAGAGAAAAGGGGAAATGTCTGAGGGAAA	416	
Qy	427	GCTTGAAGAGTCTGTCAGACCCCACTCAAGCAGTGTTCATGGAGTTCATTTGAATTTAG	486	
Db	417	GCTTGAAGAGTCTGTCAGACCCCACTCAAGCAGTGTTCATGGAGTTCATTTGAATTTAG	476	
Qy	487	GCATGATCTTGGGAAAATTCGGAGTGTACATTTACAAAGATGGTTCAAATATGTCTC	546	
Db	477	GCATGATCTTGGGAAAATTCGGAGTGTACATTTACAAAGATGGTTCAAATATGTCTC	536	
Qy	547	TAAAGTTTTGTTCACTGAGCTCACTTCCGCTTAAATTCAGAAATGCATGCTGTACGCTT	606	
Db	537	TAAAGTTTTGTTCACTGAGCTCACTTCCGCTTAAATTCAGAAATGCATGCTGTACGCTT	596	
Qy	607	GGATTTTCACTCAATGAGAGTGAATGTTCAGAGCCTCTCCCATGAAAGCTAATAATT	666	
Db	597	GGATTTTCACTCAATGAGAGTGAATGTTCAGAGCCTCTCTCCCATGAAAGCTAATAATT	656	
Qy	667	ATTGGAACCAAGAAAGCCCTGAAATGATTCACAATTAATTAATTCATGCACTTCTCTG	726	
Db	657	ATTGGAACCAAGAAAGCCCTGAAATGATTCACAATTAATTAATTCATGCACTTCTCTG	716	
Qy	727	TGGAAGACTTGTGAGAGAAATGTGTGTCGATTAGTGAATGTTCATCTGGATTGCA	786	
Db	717	TGGAAGACTTGTGAGAGAAATGTGTGTCGATTAGTGAATGTTCATCTGGATTGCA	776	
Qy	787	CTGTGTCGATTAACCAAAAGAGATGTCTTCACTGATGGAATTCAGTTCTCGCATCA	846	
Db	777	CTGTGTCGATTAACCAAAAGAGATGTCTTCACTGATGGAATTCAGTTCTCGCATCA	836	
Qy	847	TTAATGAAGACTACCAAAATTAATGCTTAAATTTCAATTTGCTACCTCTTTTTTTATTA	906	
Db	837	TTAATGAAGACTACCAAAATTAATGCTTAAATTTCAATTTGCTACCTCTTTTTTTATTA	896	
Qy	907	TGCTTGAATGTCTCACTTAATGACATTTTAAATAAGTTTANGATATACCTGAATGA	966	
Db	897	TGCTTGAATGTCTCACTTAATGACATTTTAAATAAGTTTANGATATACCTGAATGA	956	
Qy	967	AAAGAAAGCTAAATATGTTTACACCAAAAGTGTGATTTTCACTGTTTTTAAATCTAG	1028	
Db	957	AAAGAAAGCTAAATATGTTTACACCAAAAGTGTGATTTTCACTGTTTTTAAATCTAG	1018	
Qy	1027	CATTATTCATTTTCTTCAATCAAAAGTGTTCATATTTTTTTTTTTAGTGGTTGAAATA	1088	
Db	1016	CATTATTCATTTTCTTCAATCAAAAGTGTTCATATTTTTTTTTTTAGTGGTTGAAATA	1078	
Qy	1087	CTTCTTCATATGTCATCTCTCAACCTAATAATT-GGAATATGTGTGTGCTTTTGT	1148	

Db	Query	Match	Score	DB	Length	Mismatches	Indels	Gaps
Db	1076	CTTCTTCATAGTACATCTCTCAACCTATTAATTGGAAATATGTGTGTCTTTTGT	1135					
Qy	1146	TTTTTCTCTTATAGTACATTTTAAAAAAATATAAAAGTACCAATCTTTGTACATTT	1205					
Db	1136	TTTTTCTCTTATAGTACATTTTAAAAAAATATAAAAGTACCAATCTTTGTACATTT	1195					
Qy	1206	GTAATATGTAAGATTTTTTTTATATCTGTAAATAAAAATTTATTTCC	1253					
Db	1196	GTAATATGTAAGATTTTTTTTATATCTGTAAATAAAAATTTATTTCC	1243					

RESULT 9

US-09-222-575-63/c

Sequence 63, Application US/09222575

Patent No. 6387697

GENERAL INFORMATION:

APPLICANT: Yudiu, Jiang

APPLICANT: Dillon, Devin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer

TITLE OF INVENTION: and Methods for Their Use

FILE REFERENCE: 210121.470

CURRENT APPLICATION NUMBER: US/09/222.575

CURRENT FILING DATE: 1998-12-28

NUMBER OF SEQ ID NOS: 174

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 63

LENGTH: 683

TYPE: DNA

ORGANISM: Human

US-09-222-575-63

Query Match

Best Local Similarity 99.6%; Pred. No. 3.8e-253;

Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db	Query	Match	Score	DB	Length	Mismatches	Indels	Gaps
Qy	516	ACATTTTCAAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGCCTCACTTCGG	575					
Db	683	ACATTTTCAAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGCCTCACTTCGG	624					
Qy	576	CTAAATGCAAAATGCAATGCTGTCAGCGTTGTATTTTCACTTCAATGAGCTGAATGT	635					
Db	623	CTAAATGCAAAATGCAATGCTGTCAGCGTTGTATTTTCACTTCAATGAGCTGAATGT	564					
Qy	636	TCAGAGCCTCTCCCATGAGCTATATTTATTTTGGACCAAGAAAGCCCTGAATGAT	695					
Db	563	TCAGAGCCTCTCCCATGAGCTATATTTATTTTGGACCAAGAAAGCCCTGAATGAT	504					
Qy	696	TCACCAATTAATATTCATGCACTCTCTGTGGAAGACCTTGTGAAGAAATTTGGTGT	755					
Db	503	TCACCAATTAATATTCATGCACTCTCTGTGGAAGACCTTGTGAAGAAATTTGGTGT	444					
Qy	756	GGATTAGTGAATGTTGCTATCTGAGTTGGCACTTGTTCAGATTACCAAAAGAGATGCT	815					
Db	443	GGATTAGTGAATGTTGCTATCTGAGTTGGCACTTGTTCAGATTACCAAAAGAGATGCT	384					
Qy	816	TCCTACTGATGGAATTCAGTTTCTTCGATCATATTTGAAGAACTACCAAAATTAATGCTT	875					
Db	383	TCCTACTGATGGAATTCAGTTTCTTCGATCATATTTGAAGAACTACCAAAATTAATGCTT	324					
Qy	876	TAAATTTTCAATTTGCTACCTCTTTTATTTTATTTATTTGCTTGAATGTTCACTTAAATGACAT	935					
Db	323	TAAATTTTCAATTTGCTACCTCTTTTATTTTATTTATTTGCTTGAATGTTCACTTAAATGACAT	264					
Qy	936	TTTAAATTAAGTTTATGTAATACATCTGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCA	995					
Db	263	TTTAAATTAAGTTTATGTAATACATCTGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCA	204					
Qy	996	AAGTGTATTTTCAACACTGTTTTTAAATATAGCATTTATCTTTGCTTCATCAAAAGTG	1055					
Db	203	AAGTGTATTTTCAACACTGTTTTTAAATATAGCATTTATCTTTGCTTCATCAAAAGTG	144					

Query Match 42.2%; Score 530; DB 4; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.8e-253;  
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1056 GTTTCATATATTTTGTAGTGGTAGAATACCTTCTTCATGACATCTCTCAACCT 1115  
DB 143 GTTTCATATATTTTGTAGTGGTAGAATACCTTCTTCATGACATCTCTCAACCT 84

QY 1116 ATAAATTTGGAAATATGTGTGTCTTTTGTCTTCTTAGATAGATTTTAAAAA 1175  
DB 83 ATAAATTTGGAAATATGTGTGTCTTTTGTCTTCTTAGATAGATTTTAAAAA 24

QY 1176 ATATAAAGCTACCAATCTTGT 1198  
DB 23 ATATAAAGCTACCAATCTTGT 1

RESULT 10  
US-09-389-681-63/c  
; Sequence 63, Application US/09389681A  
; Patent No. 6518237  
; GENERAL INFORMATION:  
; APPLICANT: Yugui, Jiang  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; FILE REFERENCE: 210121.47003  
; CURRENT APPLICATION NUMBER: US/09/389,681A  
; CURRENT FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 63  
; LENGTH: 683  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-389-681-63

QY 516 ACATTACAAAGATGCGTCAATATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 575  
DB 683 ACATTACAAAGATGCGTCAATATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 624

QY 576 CTAATAATGCAAAATGATGATGCTGTCAGCGTTGGATTTTCAATTCATGAGCTGAATGT 635  
DB 623 CTAATAATGCAAAATGATGATGCTGTCAGCGTTGGATTTTCAATTCATGAGCTGAATGT 564

QY 636 TCAGAACCTCTCCCATTTGAAGCTATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 695  
DB 563 TCAGAACCTCTCCCATTTGAAGCTATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 504

QY 696 TCAACAATTAATATTCATGCACTTCTGTGGAAGACCTTGGAGGAATTTGATGT 755  
DB 503 TCAACAATTAATATTCATGCACTTCTGTGGAAGACCTTGGAGGAATTTGATGT 444

QY 756 CGATTAGTGATGTGCTATCTGGGTGGCACTTGTTCAGATTACCAAAAGAGATGCT 815  
DB 443 CGATTAGTGATGTGCTATCTGGGTGGCACTTGTTCAGATTACCAAAAGAGATGCT 384

QY 816 TCTACTGATGGAATTCAGTTTCTGCAATCATTTTGAAGAACTACCAAAATTAATGCTT 875  
DB 383 TCTACTGATGGAATTCAGTTTCTGCAATCATTTTGAAGAACTACCAAAATTAATGCTT 324

QY 876 TAAATTTCAATTTGCTACTCTTTTATTAATGCTTGAATGTTCACTTAATGACAT 935  
DB 323 TAAATTTCAATTTGCTACTCTTTTATTAATGCTTGAATGTTCACTTAATGACAT 264

QY 936 TTTAAATAGTTTATGTATCATCTGAATGAAGCAAAAGCTAAATATGTTTACAGACA 995  
DB 263 TTTAAATAGTTTATGTATCATCTGAATGAAGCAAAAGCTAAATATGTTTACAGACA 204

QY 996 AAGTGTGATTCACACGCTGTTTAAATCTAGCATTAATCTTTGCTTCATCAAAAGTG 1055

DB 203 AAGTGTGATTCACACGCTGTTTAAATCTAGCATTAATCTTTGCTTCATCAAAAGTG 144

QY 1056 GTTTCATATATTTTGTAGTGGTAGAATACCTTCTTCATGACATCTCTCAACCT 1115  
DB 143 GTTTCATATATTTTGTAGTGGTAGAATACCTTCTTCATGACATCTCTCAACCT 84

QY 1116 ATAAATTTGGAAATATGTGTGTCTTTTGTCTTCTTAGATAGATTTTAAAAA 1175  
DB 83 ATAAATTTGGAAATATGTGTGTCTTTTGTCTTCTTAGATAGATTTTAAAAA 24

QY 1176 ATATAAAGCTACCAATCTTGT 1198  
DB 23 ATATAAAGCTACCAATCTTGT 1

RESULT 11  
US-09-620-405B-63/c  
; Sequence 63, Application US/09620405B  
; Patent No. 6528054  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugui  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.47008  
; CURRENT APPLICATION NUMBER: US/09/620,405B  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 495  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 63  
; LENGTH: 683  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-620-405B-63

Query Match 42.2%; Score 530; DB 4; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.8e-253;  
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 516 ACATTACAAAGATGCGTCAATATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 575  
DB 683 ACATTACAAAGATGCGTCAATATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 624

QY 576 CTAATAATGCAAAATGATGATGCTGTCAGCGTTGGATTTTCAATTCATGAGCTGAATGT 635  
DB 623 CTAATAATGCAAAATGATGATGCTGTCAGCGTTGGATTTTCAATTCATGAGCTGAATGT 564

QY 636 TCAGAACCTCTCCCATTTGAAGCTATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 695  
DB 563 TCAGAACCTCTCCCATTTGAAGCTATTAATTTTGGACCAAGAAAGCCCTGAATGAAT 504

QY 696 TCAACAATTAATATTCATGCACTTCTGTGGAAGACCTTGGAGGAATTTGATGT 755  
DB 503 TCAACAATTAATATTCATGCACTTCTGTGGAAGACCTTGGAGGAATTTGATGT 444

QY 756 CGATTAGTGATGTGCTATCTGGGTGGCACTTGTTCAGATTACCAAAAGAGATGCT 815  
DB 443 CGATTAGTGATGTGCTATCTGGGTGGCACTTGTTCAGATTACCAAAAGAGATGCT 384

QY 816 TCTACTGATGGAATTCAGTTTCTGCAATCATTTTGAAGAACTACCAAAATTAATGCTT 875  
DB 383 TCTACTGATGGAATTCAGTTTCTGCAATCATTTTGAAGAACTACCAAAATTAATGCTT 324

QY 876 TAAATTTCAATTTGCTACTCTTTTATTAATGCTTGAATGTTCACTTAATGACAT 935  
DB 323 TAAATTTCAATTTGCTACTCTTTTATTAATGCTTGAATGTTCACTTAATGACAT 264

QY 936 TTTAAATAGTTTATGTATCATCTGAATGAAGCAAAAGCTAAATATGTTTACAGACA 995

Db 263 TTTAAATAGTTATGTATACATCTGAAGAAAAGCAAGCTAAATATGTTTACAGACCA 204  
Qy 996 AAGTGTGATTTTACACCTGTTTAAATCTAGCATTTTCTGTTCAATCAAAAGTG 1055  
Db 203 AAGTGTGATTTTACACCTGTTTAAATCTAGCATTTTCTGTTCAATCAAAAGTG 144  
Qy 1056 GTTTCATATTTTTTTTGTAGTGGTGAATPACTTTCTGCACTGCTCAACCT 1115  
Db 143 GTTTCATATTTTTTTTGTAGTGGTGAATPACTTTCTGCACTGCTCAACCT 84  
Qy 1116 ATAAATTTGGAATATTTGTGGTCTTTGTTTCTCTAGTATAGCAATTTTAAAAA 1175  
Db 83 ATAAATTTGGAATATTTGTGGTCTTTGTTTCTCTAGTATAGCAATTTTAAAAA 24  
Qy 1176 ATATAAAGCTACCAATCTTTGT 1198  
Db 23 ATATAAAGCTACCAATCTTTGT 1

## RESULT 12

US-09-339-338-63/c  
; Sequence 63, Application US/09339338A  
; Patent No. 6573368  
; GENERAL INFORMATION:  
; APPLICANT: Yuguu, Jiang  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C2  
; CURRENT APPLICATION NUMBER: US/09/339,338A  
; NUMBER OF SEQ ID NOS: 315  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 63  
; LENGTH: 683  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-339-338-63

Query Match 42.2%; Score 530; DB 4; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.8e-253;  
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 516 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 575  
Db 683 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624  
Qy 576 CTAAATTCGCAAGATGCAATGCTGTGACGCTTGTGATTTTTCATTCATGAGCTGAATGT 635  
Db 623 CTAAATTCGCAAGATGCAATGCTGTGACGCTTGTGATTTTTCATTCATGAGCTGAATGT 564  
Qy 636 TCAGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 695  
Db 563 TCAGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 504  
Qy 696 TCAACAATTAATATTCATGCACTTCTCTGTGAAAGACTTTGTGAAGAAATGTGCT 755  
Db 503 TCAACAATTAATATTCATGCACTTCTCTGTGAAAGACTTTGTGAAGAAATGTGCT 444  
Qy 756 GGATTAGTGAATTTGCTATCTGGGTTGCACTTGTTCAGATTAACCAAAAGAGATGCT 815  
Db 443 GGATTAGTGAATTTGCTATCTGGGTTGCACTTGTTCAGATTAACCAAAAGAGATGCT 384  
Qy 816 TCTACTGATGGAATTCAGTTTCTGCGATCATTTATGAAGAACTACCAAAATTAATGCTT 875  
Db 383 TCTACTGATGGAATTCAGTTTCTGCGATCATTTATGAAGAACTACCAAAATTAATGCTT 324  
Qy 876 TAAATTTGATTTGCTATCTTTTATTTATTTATGCTTTGAATGCTTCACTTAATGACAT 935  
Db 323 TAAATTTGATTTGCTATCTTTTATTTATTTATGCTTTGAATGCTTCACTTAATGACAT 264

Qy 936 TTTAAATAGTTTANGTATACATCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 995  
Db 263 TTTAAATAGTTTANGTATACATCTGAATGAAGAAAGCTAAATATGTTTACAGACCA 204  
Qy 996 AAGTGTGATTTTACACCTGTTTAAATCTAGCATTTTCTGTTCAATCAAAAGTG 1055  
Db 203 AAGTGTGATTTTACACCTGTTTAAATCTAGCATTTTCTGTTCAATCAAAAGTG 144  
Qy 1056 GTTTCATATTTTTTTTGTAGTGGTGAATPACTTTCTGCACTGCTCAACCT 1115  
Db 143 GTTTCATATTTTTTTTGTAGTGGTGAATPACTTTCTGCACTGCTCAACCT 84  
Qy 1116 ATAAATTTGGAATATTTGTGGTCTTTGTTTCTCTAGTATAGCAATTTTAAAAA 1175  
Db 83 ATAAATTTGGAATATTTGTGGTCTTTGTTTCTCTAGTATAGCAATTTTAAAAA 24  
Qy 1176 ATATAAAGCTACCAATCTTTGT 1198  
Db 23 ATATAAAGCTACCAATCTTTGT 1

## RESULT 13

US-09-433-826B-63/c  
; Sequence 63, Application US/09433826B  
; Patent No. 6579973  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuguu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C4  
; CURRENT APPLICATION NUMBER: US/09/433,826B  
; NUMBER OF SEQ ID NOS: 474  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 63  
; LENGTH: 683  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-433-826B-63

Query Match 42.2%; Score 530; DB 4; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.8e-253;  
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 516 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 575  
Db 683 ACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624  
Qy 576 CTAAATTCGCAAGATGCAATGCTGTGACGCTTGTGATTTTTCATTCATGAGCTGAATGT 635  
Db 623 CTAAATTCGCAAGATGCAATGCTGTGACGCTTGTGATTTTTCATTCATGAGCTGAATGT 564  
Qy 636 TCAGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 695  
Db 563 TCAGACCTCTTCCCATTTGAAGCTATATTTTGGACCAAGAAAGCCCTGAATGAAT 504  
Qy 696 TCAACAATTAATATTCATGCACTTCTCTGTGAAAGACTTTGTGAAGAAATGTGCT 755  
Db 503 TCAACAATTAATATTCATGCACTTCTCTGTGAAAGACTTTGTGAAGAAATGTGCT 444  
Qy 756 GGATTAGTGAATTTGCTATCTGGGTTGCACTTGTTCAGATTAACCAAAAGAGATGCT 815  
Db 443 GGATTAGTGAATTTGCTATCTGGGTTGCACTTGTTCAGATTAACCAAAAGAGATGCT 384  
Qy 816 TCTACTGATGGAATTCAGTTTCTGCGATCATTTATGAAGAACTACCAAAATTAATGCTT 875  
Db 383 TCTACTGATGGAATTCAGTTTCTGCGATCATTTATGAAGAACTACCAAAATTAATGCTT 324

QY 876 TAAATTCATTTGCTACCTCTTTTATATATGCTGGAAGTTCACCTTAATGACAT 935  
DB 323 TAAATTCATTTGCTACCTCTTTTATATATGCTGGAAGTTCACCTTAATGACAT 264  
QY 936 TTTAAATAGTTATGTTATCATCTGATGAAAAGCAAGCTAAATATGTTTACAGACA 995  
DB 263 TTTAAATAGTTATGTTATCATCTGATGAAAAGCAAGCTAAATATGTTTACAGACA 204  
QY 996 AAGTGCATTTTCACCTGTTTTTAAATCTAGCATTTATCTTGTGCTCAATCAAAAGT 1055  
DB 203 AAGTGCATTTTCACCTGTTTTTAAATCTAGCATTTATCTTGTGCTCAATCAAAAGT 144  
QY 1056 GTTTCATATTTTTTTTAAAGTTAGTTAGTAAGTAATCTTCTTCATAGTCAATCTCAACCT 1115  
DB 143 GTTTCATATTTTTTTTAAAGTTAGTTAGTAAGTAATCTTCTTCATAGTCAATCTCAACCT 84  
QY 1116 ATAAATTTGGAATTTGTTGCTGCTTTTGTGTTTCTTCTAGTATAGCATTTTAAAAA 1175  
DB 83 ATAAATTTGGAATTTGTTGCTGCTTTTGTGTTTCTTCTAGTATAGCATTTTAAAAA 24  
QY 1176 ATATAAAGCTACCAATCTTTGT 1198  
DB 23 ATATAAAGCTACCAATCTTTGT 1

RESULT 14  
US-09-604-287A-63/c  
Sequence 63, Application US/09604287A  
Patent No. 6586572  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugu  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.470C7  
CURRENT APPLICATION NUMBER: US/09/604,287A  
CURRENT FILING DATE: 2000-06-22  
NUMBER OF SEQ ID NOS: 489  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 63  
LENGTH: 683  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-604-287A-63

Query Match 42.2%; Score 530; DB 4; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.8e-253;  
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 516 ACATTACAAAGATGCGTTCAATATGCTCTAAGATTTTGTGAGTGGCTCACTTGG 575  
DB 683 ACATTACAAAGATGCGTTCAATATGCTCTAAGATTTTGTGAGTGGCTCACTTGG 624  
QY 576 CTAATAATGCAAAATGATGCTGTCAGCGTTGTATTTTCACTCAATGAGTGAATGT 635  
DB 623 CTAATAATGCAAAATGATGCTGTCAGCGTTGTATTTTCACTCAATGAGTGAATGT 564  
QY 636 TCAGAGCTCTTCCCATTTGAGCTATTAATTTTGTGACCAAGAACCTTGAATGAT 695  
DB 563 TCAGAGCTCTTCCCATTTGAGCTATTAATTTTGTGACCAAGAACCTTGAATGAT 504  
QY 696 TCAACAATTAATATTCATGCACTTCTGTGGAAGACCTTGTGAAGAAATGATGCT 755  
DB 503 TCAACAATTAATATTCATGCACTTCTGTGGAAGACCTTGTGAAGAAATGATGCT 444  
QY 756 GGATTAAGTGAATGTTGCTATCTGAGTGGCACTTGTGATTAACCAAAAGAGATGCT 815  
DB 443 GGATTAAGTGAATGTTGCTATCTGAGTGGCACTTGTGATTAACCAAAAGAGATGCT 384

QY 816 TCTACGATGGAATTCAGTTTCTGCGATCATTAATGAAGACTACCAAAATTAATGCTT 875  
DB 383 TCTACGATGGAATTCAGTTTCTGCGATCATTAATGAAGACTACCAAAATTAATGCTT 324  
QY 876 TAAATTCATTTGCTACCTCTTTTATATATGCTGGAAGTTCACCTTAATGACAT 935  
DB 323 TAAATTCATTTGCTACCTCTTTTATATATGCTGGAAGTTCACCTTAATGACAT 264  
QY 936 TTTAAATAGTTATGTTATCATCTGATGAAAAGCAAGCTAAATATGTTTACAGACA 995  
DB 263 TTTAAATAGTTATGTTATCATCTGATGAAAAGCAAGCTAAATATGTTTACAGACA 204  
QY 996 AAGTGCATTTTCACCTGTTTTTAAATCTAGCATTTATCTTGTGCTCAATCAAAAGT 1055  
DB 203 AAGTGCATTTTCACCTGTTTTTAAATCTAGCATTTATCTTGTGCTCAATCAAAAGT 144  
QY 1056 GTTTCATATTTTTTTTAAAGTTAGTTAGTAAGTAATCTTCTTCATAGTCAATCTCAACCT 1115  
DB 143 GTTTCATATTTTTTTTAAAGTTAGTTAGTAAGTAATCTTCTTCATAGTCAATCTCAACCT 84  
QY 1116 ATAAATTTGGAATTTGTTGCTGCTTTTGTGTTTCTTCTAGTATAGCATTTTAAAAA 1175  
DB 83 ATAAATTTGGAATTTGTTGCTGCTTTTGTGTTTCTTCTAGTATAGCATTTTAAAAA 24  
QY 1176 ATATAAAGCTACCAATCTTTGT 1198  
DB 23 ATATAAAGCTACCAATCTTTGT 1

RESULT 15  
US-09-285-480-63/c  
Sequence 63, Application US/09285480  
Patent No. 6590076  
GENERAL INFORMATION:  
APPLICANT: Yugu, Jiang  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
FILE REFERENCE: 210121.470C1  
CURRENT APPLICATION NUMBER: US/09/285,480  
CURRENT FILING DATE: 1999-04-02  
NUMBER OF SEQ ID NOS: 181  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 63  
LENGTH: 683  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-285-480-63

Query Match 42.2%; Score 530; DB 4; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.8e-253;  
Matches 680; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 516 ACATTACAAAGATGCGTTCAATATGCTCTAAGATTTTGTGAGTGGCTCACTTGG 575  
DB 683 ACATTACAAAGATGCGTTCAATATGCTCTAAGATTTTGTGAGTGGCTCACTTGG 624  
QY 576 CTAATAATGCAAAATGATGCTGTCAGCGTTGTATTTTCACTCAATGAGTGAATGT 635  
DB 623 CTAATAATGCAAAATGATGCTGTCAGCGTTGTATTTTCACTCAATGAGTGAATGT 564  
QY 636 TCAGAGCTCTTCCCATTTGAGCTATTAATTTTGTGACCAAGAACCTTGAATGAT 695  
DB 563 TCAGAGCTCTTCCCATTTGAGCTATTAATTTTGTGACCAAGAACCTTGAATGAT 504  
QY 696 TCAACAATTAATATTCATGCACTTCTGTGGAAGACCTTGTGAAGAAATGATGCT 755  
DB 503 TCAACAATTAATATTCATGCACTTCTGTGGAAGACCTTGTGAAGAAATGATGCT 444  
QY 756 GGATTAAGTGAATGTTGCTATCTGAGTGGCACTTGTGATTAACCAAAAGAGATGCT 815

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Db      443 GGATTAGTGGATGTTGCTATCTGGGTTGGVACTTGTTCAGATTACCCAAAAGGAGATGCT 384
Qy      816 TCTACTGAGTGGAAATTCAGTTTCTGGCATCATATTGAAGAATCTACCAAAATTAATGCTT 875
Db      383 TCTACTGAGTGGAAATTCAGTTTCTGGCATCATATTGAAGAATCTACCAAAATTAATGCTT 324
Qy      876 TAATTTTCATTTTGCTACCTCTTTTATTATATGCTTGGATGTTCACTTAATGACAT 935
Db      323 TAATTTTCATTTTGCTACCTCTTTTATTATATGCTTGGATGTTCACTTAATGACAT 264
Qy      936 TTTAAATTAAGTTTATGTATACATCTGAATGAAAAGCAAGCTAAATATGTTTACAGACCA 995
Db      263 TTTAAATTAAGTTTATGTATACATCTGAATGAAAAGCAAGCTAAATATGTTTACAGACCA 204
Qy      996 AAGTGGATTTTCACAGTGTTTTAAATCTAGCATTAATTCATTTTGCTTCATCAATAAGTG 1055
Db      203 AAGTGGATTTTCACAGTGTTTTAAATCTAGCATTAATTCATTTTGCTTCATCAATAAGTG 144
Qy      1056 GTTTCATATATTTTTTTTAAAGTTAGTGAATACTTCTCATAGTCAATTCCTCAACCT 1115
Db      143 GTTTCATATATTTTTTTTAAAGTTAGTGAATACTTCTCATAGTCAATTCCTCAACCT 84
Qy      1116 ATAAATTTGGAATATGTGTGTCTTTTCTTTTCTTTAGTATAGCAATTTTAAAAA 1175
Db      83 ATAAATTTGGAATATGTGTGTCTTTTCTTTTCTTTAGTATAGCAATTTTAAAAA 24
Qy      1176 ATATAAAGCTACCAATCTTTGT 1198
Db      23 ATATAAAGCTACCAATCTTTGT 1
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Search completed: December 25, 2004, 05:11:59  
Job time : 129 secs

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Db	181	GCTCTGCTGCTCTGCTCTGCTGAGTGCCTGGGCGCTGAGGCGCTCGAATCCCA	240
QY	241	AGGGGAAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGTGA	300
Db	241	AGGGGAAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGTGA	300
QY	301	GCCTTAACAGGGCCAGACAGAGTCTGCTGTGAACGGGAGCTTGTATGGAATGT	360
Db	301	GCCTTAACAGGGCCAGACAGAGTCTGCTGTGAACGGGAGCTTGTATGGAATGT	360
QY	361	CGGGTACACCTGGGATCCCAAGTCTGGATGATTTCAAGAGAGAAAGGGGAATGTCTGA	420
Db	361	CGGGTACACCTGGGATCCCAAGTCTGGATGATTTCAAGAGAGAAAGGGGAATGTCTGA	420
QY	421	GGGAAAGCTTTGAGAGTCTTGACACCACTACACAGAGTGTCAATGAGTTCAATGA	480
Db	421	GGGAAAGCTTTGAGAGTCTTGACACCACTACACAGAGTGTCAATGAGTTCAATGA	480
QY	481	ATTATGCGATAGATCTTGGGAAATGTCGGAGTGCATTATTAAGAAATGCGTCAAAAT	540
Db	481	ATTATGCGATAGATCTTGGGAAATGTCGGAGTGTACATTATTAAGAAATGCGTCAAAAT	540
QY	541	GTGCTTAAGAGTTTGTTCAGTGTCACTTCGGCTAAATGACAGAAATGATGCTGTTC	600
Db	541	GTGCTCTAAGAGTTTGTTCAGTGTCACTTCGGCTAAATGACAGAAATGATGCTGTTC	600
QY	601	AGCGTGGATATTCACATTCAGAGAGCTGAATGTTCAAGACCTCTTCCCAATGAGCTA	660
Db	601	AGCGTGGATATTCACATTCAGAGAGCTGAATGTTCAAGACCTCTTCCCAATGAGCTA	660
QY	661	TAAATTAATTTGACCAAGAGAGCCCTGAATGAAATTCACATTAATTAATTCATCGCACT	720
Db	661	TAAATTAATTTGACCAAGAGAGCCCTGAATGAAATTCACATTAATTAATTCATCGCACT	720
QY	721	CTTCTGTGGAAGACCTTGTGAAAGAAATGTGTCTGGATTAAGATGTGTCTATCTGGG	780
Db	721	CTTCTGTGGAAGACCTTGTGAAAGAAATGTGTCTGGATTAAGATGTGTCTATCTGGG	780
QY	781	TTGGACATGTTCAAGATTCACCCAAAGAGAGATGCTCTACCTGGATGGAATTCAGTTCTTC	840
Db	781	TTGGACATGTTCAAGATTCACCCAAAGAGAGATGCTCTACCTGGATGGAATTCAGTTCTTC	840
QY	841	GCATCAATTAATGAGAGACTACCAAAATTAATGCTTAAATTTTCATTGTGTA	900
Db	841	GCATCAATTAATGAGAGACTACCAAAATTAATGCTTAAATTTTCATTGTGTA	900
QY	901	TTATTAATGCTTGGAGATGTTCACTTAATGACATTTTAATTAAGTTATGTAATACATCT	960
Db	901	TTATTAATGCTTGGAGATGTTCACTTAATGACATTTTAATTAAGTTATGTAATACATCT	960
QY	961	GAAATGAAAGCAAAAGCTAAATATGTTTACAGACAAAGTGTGATTTCAACATGTTTAA	1020
Db	961	GAAATGAAAGCAAAAGCTAAATATGTTTACAGACAAAGTGTGATTTCAACATGTTTAA	1020
QY	1021	AATGAGCAATTAATCAATTTTGTCTTCAATCAAAAGTGTTCATTAATTTTAAATGTT	1080
Db	1021	AATGAGCAATTAATCAATTTTGTCTTCAATCAAAAGTGTTCATTAATTTTAAATGTT	1080
QY	1081	AGAAATACCTTCTTCAATGACATCTCTCAACCTTAATTTGAAATATGTGTGTGCT	1140
Db	1081	AGAAATACCTTCTTCAATGACATCTCTCAACCTTAATTTGAAATATGTGTGTGCT	1140
QY	1141	TTTGTCTTAAAGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	1200
Db	1141	TTTGTCTTAAAGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	1200
QY	1201	AATTTGTAAGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	1257
Db	1201	AATTTGTAAGTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	1257

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LOCUS	AX376298				
DEFINITION	Sequence 365 from Patent WO0168848.				
ACCESSION	AX376298				
VERSION	AX376298.1	GI:19170540			
KEYWORDS					
SOURCE	Homio sapiens (human)				
ORGANISM	Homio sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and Zhang, Z.				
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
JOURNAL	Patent: WO 0168848-A 365 20-SEP-2001;				
FEATURES	Genentech, Inc. (US)				
source	Location/Qualifiers				
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	/db_xref="taxon:9606"				
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Query Match	100.0%; Score 1257; DB 6; Length 1257;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 1257;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 GGAGGAGGCGCGCGGCTGAAAAGCGCATTTATGACCTTCGCGGCTTCGGAGCGCG 60				
Db	1 GGAGGAGGCGCGCGGCTGAAAAGCGCATTTATGACCTTCGCGGCTTCGGAGCGCG 60				
QY	61 CGGAGCCAGACGCTGACCAACGCTTCCTCCCGGCTTCCTCCCGGCTTCAGCTCCGCGCTG 120				
Db	61 CGGAGCCAGACGCTGACCAACGCTTCCTCCCGGCTTCCTCCCGGCTTCAGCTCCGCGCTG 120				
QY	121 CCGGCGACCCGGAGGACATGCGACCCCGGCGGCTTCCTCCCGGCTTCAGCTCCGCGCTG 180				
Db	121 CCGGCGACCCGGAGGACATGCGACCCCGGCGGCTTCCTCCCGGCTTCAGCTCCGCGCTG 180				
QY	181 GCCTCTGCTGCTCTGCTGCTGCTGCAAGTCCCGGCGGCTTCGAGGCTTCGAGATCCCA 240				
Db	181 GCCTCTGCTGCTCTGCTGCTGCTGCAAGTCCCGGCGGCTTCGAGGCTTCGAGATCCCA 240				
QY	241 AGGGAGAACAAAGGCGGACGCTCCGGGAGAGGAGGTGTGACCTGTATTAATGGAATG 300				
Db	241 AGGGAGAACAAAGGCGGACGCTCCGGGAGAGGAGGTGTGACCTGTATTAATGGAATG 300				
QY	301 GCTTACAAAGGCGCAGCAGAGAGTGCCTGATGAGACGAGACCCCTGGGGCCAATGTTATTC 360				
Db	301 GCTTACAAAGGCGCAGCAGAGAGTGCCTGATGAGACGAGACCCCTGGGGCCAATGTTATTC 360				
QY	361 CGGCTGACCTTCGGATCCAGGCTGGGATGGATCAAAAGAGAAAAGGGGGAATGCTGAG 420				
Db	361 CGGCTGACCTTCGGATCCAGGCTGGGATGGATCAAAAGAGAAAAGGGGGAATGCTGAG 420				
QY	421 GGGAAAGCTTTGAGAGAGCTTGAGACCCCAACCTAACAAGCAGTGTTCATGGAATTCATGA 480				
Db	421 GGGAAAGCTTTGAGAGAGCTTGAGACCCCAACCTAACAAGCAGTGTTCATGGAATTCATGA 480				
QY	481 ATTATGCGATGATCTTGGGAAAATTGCGGAGGTGATCATTTACAAAGATGCGTTCAAAAT 540				
Db	481 ATTATGCGATGATCTTGGGAAAATTGCGGAGGTGATCATTTACAAAGATGCGTTCAAAAT 540				
QY	541 GTGCTCTAAGAGTTTGTTCAGTGCGCTCACTTCGGCTAAATGACAGAAATGCAATGCTGTC 600				
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QY	601 AGCGTGGATATTCACATTCATATGAGAGCTGAATGTTCCAGACCTCTTCCATTTGAAGCTA 660				
Db	601 AGCGTGGATATTCACATTCATATGAGAGCTGAATGTTCCAGACCTCTTCCATTTGAAGCTA 660				





QY 1021 ATCTAGCATTTATTCATTTGGCTTCATCAAAAGGTTTCAATATTTTTTTAGTGGT 1080  
DB 1021 ATCTAGCATTTATTCATTTTGGCTTCATCAAAAGGTTTCAATATTTTTTTAGTGGT 1080  
QY 1081 AGAATCTTTCTTCATNGTCAATCTTCTCAACCTAATTTGGAAATTTGTGTGCT 1140  
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QY 1141 TTTGTTTTTCTCTGTATAGCATTTTTTAAAAAATATAAGCTACCAATCTTGTAC 1200  
DB 1141 TTTGTTTTTCTCTGTATAGCATTTTTTAAAAAATATAAGCTACCAATCTTGTAC 1200  
QY 1201 AATTGTAAATGTTAAGAAATTTTTTTATATCTGTAAATATAAATTTTCCAA 1257  
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RESULT 4  
AX459648 1257 bp DNA linear PAT 08-JUL-2002  
LOCUS Sequence 2 from Patent WO0216602.  
DEFINITION AX459648  
ACCESSION AX459648  
VERSION AX459648.1 GI:21725519  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Polakis, P.,  
TITLE Williams, P.M., Wood, W.I., Wu, T.D. and Zhang, Z.  
JOURNAL Compositions and methods for the diagnosis and treatment of tumor  
PATENT: WO 0216602-A 2 28-FEB-2002;  
FEATURES  
LOCATION/Qualifiers  
source 1.1257  
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/db\_xref="taxon:9606"

ORIGIN  
Query Match 100.0%; Score 1257; DB 6; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGTTGAAAGCGCATTTGATGACCGTGGCGGCGGCGGCGG 60  
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QY 61 CGAGACGACGCTGACCACTTCTCTCTCGGTCTCTCGGCTCCAGCTCCGCGCTG 120  
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QY 121 CCCGCGAGCGGAGGACGATGCGACCCGAGGCGCGCGCGCTCCGCGAGCGGCTCCG 180  
DB 121 CCCGCGAGCGGAGGACGATGCGACCCGAGGCGCGCGCGCTCCGCGAGCGGCTCCG 180  
QY 181 GCTTCCTGCTGCTCTGCTGCTGACGTGCGCGCGCTCCGAGCGCTCTGAGATCCCA 240  
DB 181 GCTTCCTGCTGCTCTGCTGCTGACGTGCGCGCGCTCCGAGCGCTCTGAGATCCCA 240  
QY 241 AGGGGAAACAAAGGCGGAGCTCCGCGAGAGGAGGTGTGGAACCTGTATAATGAAATG 300  
DB 241 AGGGGAAACAAAGGCGGAGCTCCGCGAGAGGAGGTGTGGAACCTGTATAATGAAATG 300  
QY 301 GCTTACAAGGCGCAGCAGAGTGTGCTGAGCGAGGAGCGCTGCGGCGCAATGTTATTC 360  
DB 301 GCTTACAAGGCGCAGCAGAGTGTGCTGAGCGAGGAGCGCTGCGGCGCAATGTTATTC 360  
QY 361 CGGGTACCTCTGGAGTCCAGGTCCGAGTGTGATTCAAAGAGAGGAGGAGGAGTCTGA 420  
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DB 541 GTGCTCTAAGATTTTGTTCAGTGGCTCACTTGGCTTAAATGAGAAATGATGCTGTC 600  
QY 601 AACGTTGATTTTCACTTCAATGAGAGTGTGAGGAAATTTGAGATGTTGCTATCGGG 780  
DB 601 AACGTTGATTTTCACTTCAATGAGAGTGTGAGGAAATTTGAGATGTTGCTATCGGG 780  
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RESULT 5  
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LOCUS Sequence 245 from Patent WO020690.  
DEFINITION AX491138  
ACCESSION AX491138  
VERSION AX491138.1 GI:22323906  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
TITLE Godowski, P.J., Gurney, A.L., Hillan, K.J., Masters, S.A., Pan, J.,  
JOURNAL Patent, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.

TITLE and Ye, W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0200690-A 245 03-JAN-2002;  
Genentech, Inc. (US)

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source location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CCGGAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 180  
DB 121 CCGGAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 180  
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DB 181 GCCTCTGCTGCT 240  
QY 241 AGGAG 300  
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DB 361 CGGAG 420  
QY 421 GGGAG 480  
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QY 1201 AATTTGATTAATGTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1257  
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RESULT 6  
AX697362 1257 bp DNA linear PAT 02-APR-2003  
LOCUS Sequence 430 from Patent WO0078961.  
DEFINITION AX697362  
ACCESSION AX697362.1 GI:29498494  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,  
Baton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,  
Godowski, P.J., Gueney, A.L., Smith, V., Tunas, D., Wood, W.I.,  
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Melanbe, C.K.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0078961-A 430 28-DEC-2000;  
Genentech Inc. (US)  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CGAGAGCGAGCGCTGACGACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
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QY 181 GCCTCTGCTGCT 240

[illegible]

LOCUS AV358914 1257 bp mRNA linear pri 03-OCT-2003  
DEFINITION Homo sapiens clone DNA76393 CTRCL1 (UNQ762) mRNA, complete cds.  
ACCESSION AY358914  
VERSION AY358914.1 GI:371782945  
KEYWORDS FLI CDNA.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1257)  
Clark,H.F., Garney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Denel,B.,  
Held,J., Batom,D., Foster,J., Grimaldi,C., Gu,O., Hase,P.E.,  
Heldens,S., Nhang,A., Kim,H.S., Kilmowski,L., Jin,Y., Johnson,S.,  
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
Schonfeld,J., Sehnagiri,S., Simmons,L., Singh,J., Smith,V.,  
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wiandt,D., Woode,K.,  
Xie,M.H., Yanaura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
Goddard,A., Wood,W.I. and Goddard,P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
PUBMED 12975309  
2 (bases 1 to 1257)  
REFERENCE Clark,H.F.  
AUTHORS Direct Submission  
TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES	
Source	Location/Qualifiers
gene	1..1257
CDS	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="DNA76393" 1..1257 /locus_tag="UNQ762" 138..869 /locus_tag="UNQ762" /note="PRO1550" /codon_start=1 /product="CTHRC1" /protein_id="AA089273.1" /db_xref="GI:37182946" /translation="MRRCPGASAPORTRLILLIQLPAPASASETPKQKQALQ RKYNDLYNGMCTLGSPAGVPPGRDSSPAANIIPGIPGIPGIDGKIACTIKRNSALRVPSGLDKRCNNACCRWFT TNNYQQGWSLNTGIDLGKIACTIKRNSALRVPSGLDKRCNNACCRWFT ENGACSGSPLEITAIITYLDGSPENNSTINIRTSVGLCEGIGAGIVVAIVMGTC SDYPGADSGTWNVSVKIIIIIEELPK"

Query Match	100.0%;	Score 1257;	DB 9;	Length 1257;
Best Local Similarity	100.0%;	Prod. No. 0;		
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QY	1	GGAGAGAGCGCGCGGTGAAAGCGCATTGATGACAGCTCGCGGCGGCGCTCGAGACCGG	60	
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QY	61	CGAGACGAGAGCGCTGACCAAGTTCTCTCTCGGTCTCTTCGGCTTCAGCTCCGGCGTG	120	
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QY	121	CGCGGACGCGGAGGAGCATGGAGCCGACGAGGCGCCGCGCGCTCCCGGAGGCGCTCCGGG	180	
Db	121	CGCGGACGCGGAGGAGCATGGAGCCGACGAGGCGCCGCGCGCTCCCGGAGGCGCTCCGGG	180	
QY	181	GCGTCTCTCTCTCTCTCTGCTGCTGACGTGCGCGCGCGTGCAGGCGCTCTGAGATCCCA	240	
Db	181	GCGTCTCTCTCTCTCTCTGCTGCTGACGTGCGCGCGCGCTGAGAGCTCTGAGATCCCA	240	
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Qy      361 CGGGTACACCTGGGATCCGAGGTCCGGATGATTCGAAAGAGAGAGAGGGGGAATGTCTGA 420
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Qy      421 GGGAAAGCTTTTGAAGAGTCTGTGACACCAACTACAGCAGTGTTCATGAGATTCTGA 480
Db      421 GGGAAAGCTTTTGAAGAGTCTGTGACACCAACTACAGCAGTGTTCATGAGATTCTGA 480
Qy      481 ATTATGGCAATAGTCTTTGGGAAAATTGGGAGTGTCAATTTAAGAGTCCGTCAAAATA 540
Db      481 ATTATGGCAATAGTCTTTGGGAAAATTGGGAGTGTCAATTTAAGAGTCCGTCAAAATA 540
Qy      541 GTGCTCTAAGAGTTTGTTCAGTGTGCTCACTTGGCTAAATGTCAGAAATGTCATGCTGTC 600
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Db      721 CTTCTGTGAGAGACTTTGTGAGAGAAATGGTGTGATGAGATGTTGCTATCTGGG 780
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Db      781 TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACTGTGAGAAATTCAGTTTCTC 840
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Db      1021 ATCTAGCATTTATCATTTTGTCTCAATCAAAAGTGTTCATATTTTGTGTTT 1080
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Db      1081 AGAATACCTTCTCATAGTCACTGCTCAACCTAATTAATTTGAAATATGTTGTGCTC 1140
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DEFINITION AX829144
ACCESSION AX829144.1 GI:39838921
VERSION

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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Mack,D.H., Glah,K.C. and Afar,D.
TITLE Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer
JOURNAL Patent: WO 02059377-A 37 01-AUG-2002;
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 Generation and initial analysis of more than 15,000 full-length  
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 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-SEP-2001) National Institutes of Health, Mammalian

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 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 On Aug 19, 2003 this sequence version replaced gi:15559789.  
 Contact: MGC help desk  
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 Akher, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
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VERSION	BD269636.1
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SOURCE	Homo sapiens (human)
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. Tang,T.Y., Lal,P., Baughn,M.R., Yue,H., Young,J.A., Lu,D.A.M. and Azimzal,Y.
AUTHORS	Human secretory proteins Patent: JP 2002537805-A 5 12-NOV-2002; JNCYTE PHARMACEUTICALS INC
TITLE	OS Homo sapiens (human) PN JP 2002537805-A/5
JOURNAL	PD 12-NOV-2002 PF 03-MAR-2000 JP 2000602763 PR 05-MAR-1999 US 60/123117 PI TOM Y TANG,PREETI LAL,MARIAH R BAUGHN,HENRY YUE,JANICE AU PI YOUNG.
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AUTHORS Lindner,V. and Friesel,R.E.  
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Db 906 AAGTTATGATATACATCTGAATGAAGAAAGCAAGCTTAATGTTTACAGACCAAGTGTG 965  
| | | | |  
QY 1003 ATTTCACCTGTTTAAATCTAGCATTAATTCATTTGCTTCAATCAAAAGTGTTCAA 1062  
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Db 966 ATTTCACCTGTTTAAATCTAGCATTAATTCATTTGCTTCAATCAAAAGTGTTCAA 1025  
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QY 1063 TATTTTATGTTGTTAGTAATCTTTCTTCAATGACATCTCTCAACCTTAATTT 1122  
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| | | | |  
QY 1123 GGAATATGTTGTTGTTGTTTCTTCTTGAATGATTAATGATTAATTAATTAATTA 1182  
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QY 1183 AGCTAACCAATCTTTGTAATTTGTAATGTAAGAAATTTTATATCTGTTAAATTA 1242  
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QY 1243 AAATTAATTCACACA 1257  
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LOCUS Homo sapiens collagen triple helix repeat-containing protein 1  
DEFINITION (CTHRC1) mRNA, complete cds.  
ACCESSION AY136825  
VERSION AY136825.1 GI:25989620  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1221)  
AUTHORS Lehnert,W., Moore,D.P., Harmon,K.J., Mancini,M.L. and Lindner,V.  
TITLE Expression of the novel collagen triple helix repeat-containing  
gene (Cthrc1) suggests functions in multiple organ systems  
JOURNAL Unpublished  
AUTHORS Lindner,V.  
REFERENCE Direct Submission  
TITLE Submitted (29-JUL-2002) Center for Molecular Medicine, Maine  
JOURNAL Medical Center Research Institute, 81 Research Drive, Scarborough,  
ME 04074, USA  
FEATURES Location/Qualifiers





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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 25, 2004, 05:33:57 ; Search time 94 Seconds

(without alignments)  
1837.465 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MRPOGPASPGRLRGILLLL.....GDASNGMNSVSRNIIIEELPK 243

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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Database :

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3: /cgn2\_6/prodata/1/ina/6A COMB.seq: \*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1301	100.0	729	4	US-09-834-759-511 Sequence 511, App
2	1301	100.0	732	4	US-09-834-759-510 Sequence 510, App
3	1301	100.0	837	4	US-09-834-759-512 Sequence 512, App
4	1301	100.0	837	4	US-09-834-759-513 Sequence 513, App
5	1294	99.5	1220	4	US-09-692-081-3 Sequence 3, Appl
6	1291	99.2	1342	4	US-09-489-847-89 Sequence 89, Appl
7	1266	97.3	1286	4	US-09-489-847-124 Sequence 124, App
8	1258.5	96.7	1288	4	US-09-205-258-125 Sequence 125, App
9	1216	93.5	1192	4	US-09-692-081-1 Sequence 1, Appl
10	1211	93.1	734	4	US-09-692-081-9 Sequence 9, Appl
11	734	56.4	403	4	US-09-692-081-6 Sequence 6, Appl
12	626	48.1	683	3	US-09-222-575-63 Sequence 63, Appl

13	626	48.1	683	4	US-09-389-681-63 Sequence 63, Appl
14	626	48.1	683	4	US-09-620-405B-63 Sequence 63, Appl
15	626	48.1	683	4	US-09-339-338-63 Sequence 63, Appl
16	626	48.1	683	4	US-09-433-828B-63 Sequence 63, Appl
17	626	48.1	683	4	US-09-604-287A-63 Sequence 63, Appl
18	626	48.1	683	4	US-09-285-480-63 Sequence 63, Appl
19	626	48.1	683	4	US-09-834-759-63 Sequence 63, Appl
20	626	48.1	683	4	US-09-590-751A-63 Sequence 63, Appl
21	129.5	10.0	3170	4	US-09-169-768-1 Sequence 1, Appl
22	129.5	10.0	3171	4	US-09-169-768-15 Sequence 15, Appl
23	129.5	10.0	3181	1	US-08-655-086-1 Sequence 1, Appl
24	129.5	10.0	3349	4	US-09-169-768-13 Sequence 13, Appl
25	129.5	10.0	3531	4	US-09-169-768-7 Sequence 7, Appl
26	129.5	10.0	3541	4	US-09-169-768-9 Sequence 9, Appl
27	129.5	10.0	4167	4	US-09-169-768-12 Sequence 12, Appl
28	129.5	10.0	4409	4	US-09-331-347C-22 Sequence 22, Appl
29	120.5	9.3	1196	1	US-08-167-939A-5 Sequence 5, Appl
30	120.5	9.3	1196	1	US-08-567-538A-5 Sequence 5, Appl
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32	120	9.2	2543	3	US-09-073-663-11 Sequence 11, Appl
33	120	9.2	20966	4	US-09-776-976-7 Sequence 7, Appl
34	120	9.2	20966	4	US-09-909-547-7 Sequence 7, Appl
35	120	9.2	20966	4	US-09-569-852B-1 Sequence 1, Appl
36	118.5	9.1	1981	4	US-09-620-312D-870 Sequence 870, App
37	118.5	9.1	2823	4	US-09-919-497-7 Sequence 7, Appl
38	118.5	9.1	3171	4	US-09-169-768-19 Sequence 19, Appl
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41	115.5	8.9	6674	4	US-09-620-312D-110 Sequence 110, App
42	115.5	8.8	695	4	US-09-338-933-212 Sequence 212, App
43	115	8.8	695	4	US-09-215-681-212 Sequence 212, App
44	115	8.8	695	4	US-09-216-002A-212 Sequence 212, App
45	115	8.8	695	4	US-09-667-857-212 Sequence 20, Appl
46	115	8.8	1881	3	US-09-029-348-20 Sequence 1, Appl
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48	113	8.7	4707	3	US-09-458-791-1 Sequence 1, Appl
49	113	8.7	4707	3	US-09-459-066-1 Sequence 1, Appl
50	113	8.7	4707	4	US-09-814-912A-80 Sequence 80, Appl
51	113	8.7	9164	4	US-09-569-852B-4 Sequence 4, Appl
52	113	8.6	1313	2	US-08-463-911-6 Sequence 6, Appl
53	112.5	8.6	445	4	US-09-569-852B-5 Sequence 5, Appl
54	112.5	8.6	445	4	US-09-513-999C-129 Sequence 129, App
55	112	8.6	709	4	US-09-398-522-115 Sequence 115, App
56	112	8.6	1297	4	US-09-800-728-80 Sequence 80, Appl
57	112	8.5	4359	4	US-09-484-970B-4 Sequence 4, Appl
58	111	8.5	18609	3	US-08-943-731-1 Sequence 1, Appl
59	111	8.5	4517	3	US-09-140-804-9 Sequence 9, Appl
60	110.5	8.5	4517	4	US-09-686-838B-9 Sequence 9, Appl
61	110.5	8.5	4517	4	US-09-776-976-5 Sequence 5, Appl
62	110.5	8.5	4517	4	US-09-909-547-5 Sequence 5, Appl
63	110.5	8.5	1299	4	US-09-976-594-814 Sequence 814, App
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65	110	8.5	6158	4	US-09-919-497-6 Sequence 6, Appl
66	110	8.5	6158	4	US-09-620-312D-1061 Sequence 1061, App
67	110	8.4	3389	4	US-09-297-269-39 Sequence 39, Appl
68	109	8.3	1576	2	US-08-463-911-1 Sequence 1, Appl
69	108.5	8.3	1276	4	US-09-776-976-3 Sequence 3, Appl
70	108	8.3	1276	4	US-09-909-547-3 Sequence 3, Appl
71	108	8.3	1276	4	US-09-795-061-3 Sequence 3, Appl
72	108	8.3	6200	4	US-09-800-728-44 Sequence 44, Appl
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74	108	8.2	2487	4	US-09-620-312D-160 Sequence 160, App
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76	107.5	8.3	1149	4	US-09-800-728-47 Sequence 47, Appl
77	107.5	8.3	1149	4	US-09-800-728-47 Sequence 47, Appl
78	106.5	8.2	1050	4	US-09-620-312D-160 Sequence 160, App
79	106.5	8.2	1588	6	US-09-800-729-46 Patent No. 5510466-1
80	106.5	8.2	1807	6	US-09-404-879A-213 Patent No. 5510466
81	105.5	8.1	804	4	US-09-338-933-213 Sequence 213, App
82	105.5	8.1	804	4	US-09-215-681-213 Sequence 213, App
83	105.5	8.1	804	4	US-09-216-002A-213 Sequence 213, App
84	105.5	8.1	804	4	US-09-667-857-213 Sequence 213, App
85	105.5	8.1	804	4	US-09-667-857-213 Sequence 213, App

86 105.5 8.1 1134 3 US-09-342-681C-15 Sequence 15, App1  
87 105.5 8.1 1338 4 US-09-336-536-1 Sequence 1, App1  
88 105.5 8.1 1347 3 US-09-140-804-1 Sequence 1, App1  
89 105.5 8.1 1347 4 US-09-686-838B-1 Sequence 1, App1  
90 105.5 8.1 1377 4 US-09-866-028-41 Sequence 41, App1  
91 105.5 8.1 1377 4 US-10-140-002-361 Sequence 361, App1  
92 105.5 8.1 1377 4 US-09-944-457-41 Sequence 41, App1  
93 105.5 8.1 1661 3 US-09-342-681C-3 Sequence 3, App1  
94 105 8.1 1868 1 US-08-392-367B-1 Sequence 1, App1  
95 105 8.1 1868 3 US-08-893-467A-1 Sequence 1, App1  
96 105 8.1 2230 4 US-09-620-312D-282 Sequence 282, App1  
97 105 8.1 3120 4 US-09-169-768-29 Sequence 29, App1  
98 104.5 8.0 1152 4 US-09-776-976-1 Sequence 1, App1  
99 104.5 8.0 1152 4 US-09-909-547-1 Sequence 1, App1  
100 104 8.0 444 4 US-09-397-787-161 Sequence 161, App1

ALIGNMENTS

RESULT 1  
US-09-834-759-511  
Sequence 511, Application US/09834759  
Patent No. 6680197  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugui  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.470C9  
CURRENT FILING DATE: 2001-04-13  
NUMBER OF SEQ ID NOS: 547  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 511  
LENGTH: 729  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-834-759-511

Alignment Scores:  
Pred. No.: 1.07e-128 Length: 729  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-063-734-122 (1-243) x US-09-834-759-511 (1-729)

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QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInIleProGlyGlyLeuGInyAla 40  
Db 61 CTGCTGCGAGCTGCGCCGCGCGCTCGAGCGCTCTGAGATCCCGAAGGGAGAGAAAGCG 120  
QY 41 GInLeuArgGInaArgGInaValaValaLeuLeuLeuLeuLeuLeuLeuLeuLeu 60  
Db 121 CAGCTCGCGAG 180  
QY 61 G1yValProG1yAArgSPG1ySerProG1yAlaIaSerValIleProG1yThProG1yIle 80  
Db 181 GAGATGCTGCTGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 240  
QY 81 ProG1yAArgSPG1yPheLeuG1yG1yLeuG1yG1yLeuLeuLeuLeuLeuLeuLeu 100  
Db 241 CCAAGTCGCGAGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

QY 101 SerTrpThrProAsnTrpGlnCysSerTrpSerSerLeuAsnTrpGlyIleAspLeu 120  
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QY 121 G1yValIleAlaG1yCysThrPheThrIleMetArgSerAnsSerAlaLeuArgValLeu 140  
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QY 141 PheSerG1ySerLeuArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160  
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QY 161 PheAsnG1yAlaG1yCysSerG1yProLeuProIleGlnAlaIleIleTrpLeuAspGln 180  
Db 481 TTCATGAGAGCTGATGATGTTACAGACCTCTCCATTAAGCTAATTAATTTTGGACCAA 540  
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QY 201 CysG1yG1yIleG1yAlaG1yLeuValaAspValaAlaIleTrpValG1yThCysSerAsp 220  
Db 601 TGTGAAGGAATGGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
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Db 661 TACCCAAAG 720  
QY 241 LeuProLys 243  
Db 721 CTACCAAAA 729

RESULT 2  
US-09-834-759-510  
Sequence 510, Application US/09834759  
Patent No. 6680197  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugui  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.470C9  
CURRENT FILING DATE: 2001-04-13  
NUMBER OF SEQ ID NOS: 547  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 510  
LENGTH: 732  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-834-759-510

Alignment Scores:  
Pred. No.: 1.08e-128 Length: 732  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-063-734-122 (1-243) x US-09-834-759-510 (1-732)

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QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInIleProGlyGlyLeuGInyAla 40

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Db      61 CTGCTGACAGCTCCCGCCGCTCGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGGCG
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Qy      61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db      181 GGAGTGCCTGCTCGAGACCGGAGCCCTGGGCCAATGTTATTCGGGATCACCTGGGATC 240
Qy      81 ProGlyArgAspGlyPheLeysGlyGlyGlyCysLeuArgGlyLeuSerPheGlyGlu 100
Db      241 CCAGGTCCGGATGATTAACAAGAGAAAGGGGAAATGTCTGAGGGAAGCTTTGAGAG 300
Qy      101 SerTPHrProAsnTyrlsGlnCysSerTPSerSerLeuAsnTyrlIleAspLeu 120
Db      301 TCCTGGACCCCACTACAGACAGTGTTCATGAGATTCATTAATATGCAATAGATCTT 360
Qy      121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValIle 140
Db      361 GGAAAAATTCGGAGTGTACATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTG 420
Qy      141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTPHrTPHrPheThr 160
Db      421 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGCAATGCTGTCAGCGTTGATTTTCA 480
Qy      161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlAspGln 180
Db      481 TTCATATGGAGTGAATGTTGAGAGCTCTCCATTAAGCAATATTAATTTATTTGAGCAA 540
Qy      181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
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Qy      201 CysGluGlyIleGlyValaGlyLeuValaAspValaIleTPValaGlyThrCysSerAsp 220
Db      601 TGTGAAGGAATGTGCTGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTGTCAGAT 660
Qy      221 TyPProLysGlyAspAlaSerThrGlyTPAsnSerValSerArgIleIleIleGluGlu 240
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Qy      241 LeuProLys 243
Db      721 CTACCAAAA 729

RESULT 3
US-09-834-759-512
; Sequence 512, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Heppler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS OF METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121, 470C9
; CURRENT APPLICATION NUMBER: US/09/834, 759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 512
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-512
Alignment Scores:

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Pred. No.: 1,32e-128 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4

US-10-063-734-122 (1-243) x US-09-834-759-512 (1-837)

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Qy      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnLysAla 40
Db      166 CTGCTGACAGCTCCCGCCGCTCGAGCCCTCTGAGATCCCAAGGGAAGCAAAAGGCG 225
Qy      41 GlnLeuArgGlnArgGlnValValAspLeuTyraenGlyMetCysLeuGlnGlyProAla 60
Db      226 CAGTCCCGCAGAGGAGGTGTGACCTGTATTAAGAAATGTCTTAACAAGGCCAGCA 285
Qy      61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
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Qy      81 ProGlyArgAspGlyPheLeysGlyGlyGlyCysLeuArgGlyLeuSerPheGlyGlu 100
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Qy      101 SerTPHrProAsnTyrlsGlnCysSerTPSerSerLeuAsnTyrlIleAspLeu 120
Db      406 TCCTGGACCCCACTACAGACAGTGTTCATGAGATTCATTAATATGCAATAGATCTT 465
Qy      121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValIle 140
Db      466 GGAAAAATTCGGAGTGTACATTTCAACAAGATGCGTTCAAAATAGTCTCTAAGAGTTTG 525
Qy      141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTPHrTPHrPheThr 160
Db      526 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGCAATGCTGTCAGCGTTGATTTTCA 585
Qy      161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlAspGln 180
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Qy      181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db      646 GGAAAGCTTGAATGATTTCAACAATTAATTAATTCAGCACTTCTCTGAGAGGACTT 705
Qy      201 CysGluGlyIleGlyValaGlyLeuValaAspValaIleTPValaGlyThrCysSerAsp 220
Db      706 TGTGAAGGAATGTGCTGATTAAGTGAATGTTGCTATCTGGGTTGGCACTTGTCAGAT 765
Qy      221 TyPProLysGlyAspAlaSerThrGlyTPAsnSerValSerArgIleIleIleGluGlu 240
Db      766 TACCCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCGCAATTAATTTGAAGA 825
Qy      241 LeuProLys 243
Db      826 CTACCAAAA 834

RESULT 4
US-09-834-759-513
; Sequence 513, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Heppler, William T.
; APPLICANT: Henderson, Robert A.

```





Db	701	TGTGAAGAAATTGTCGTGATTAGTGATGTTGCTACTCTGGTTGGCATCTGTTCAGAT	760
Qy	221	TYRPROLYGGLYASPAALASERTHRGLYTRPANSERVALSERAGLLELLEGLUGLU	240
Db	761	TACCCCAAGAGATGCTTCTACTGATGGAATTGACGTTCTCCGATCATATTATGAAGAA	820
Qy	241	LEUPROLYS 243	
Db	821	CTACCAAAA 829	
RESULT 6			
US-09-489-847-89			
Sequence 89, Application US/09489847			
Patent No. 6476195			
GENERAL INFORMATION:			
APPLICANT: Rosen et al			
TITLE OF INVENTION: 98 Human Secreted Proteins			
FILE REFERENCE: P2031P1			
CURRENT APPLICATION NUMBER: US/09/489,847			
EARLIER FILING DATE: 2000-01-24			
EARLIER APPLICATION NUMBER: PCT/US99/17130			
EARLIER FILING DATE: 1999-07-29			
EARLIER APPLICATION NUMBER: 60/094,657			
EARLIER FILING DATE: 1998-07-30			
EARLIER APPLICATION NUMBER: 60/095,486			
EARLIER FILING DATE: 1998-08-05			
EARLIER APPLICATION NUMBER: 60/096,319			
EARLIER FILING DATE: 1998-08-12			
EARLIER APPLICATION NUMBER: 60/095,454			
EARLIER FILING DATE: 1998-08-06			
EARLIER APPLICATION NUMBER: 60/095,455			
EARLIER FILING DATE: 1998-08-06			
NUMBER OF SEQ ID NOS: 376			
SOFTWARE: PatentIn Ver. 2.0			
: SEO ID NO 89			
: LENGTH: 1342			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
US-09-489-847-89			
Alignment Scores:			
Pred. No.: 3,086-127			
Score: 1281.00			
Percent Similarity: 99.59%			
Best Local Similarity: 99.18%			
Query Match: 99.23%			
DB: 4			
Gaps: 0			
US-10-063-734-122 (1-243) x US-09-489-847-89 (1-1342)			
Qy	1	MetArpProGInGnIyProAlaIaIaSeRProGInArGLeuArGILyLeuLeuLeuLeu 20	
Db	141	ATGCGACCCCAAGGCGCCGCCCTCTCCCGACGGCGCTCCGGGCTCTGCTGCTCTG 200	
Qy	21	LeuLeuGlnLeuProAlaProSeSerAlaSeRGLuILleProLYGILyVGLInLYeAla 40	
Db	201	CTGCTCACTGCCCCGCCCTGCGAGCGCTCTGAGATCCCAAGGGGGAACAAAGCG 260	
Qy	41	GlnLeuArGILaRgILuAlaValaIaIaPleuArYzAeNgILyMetCySLeuGInGILyProAla 60	
Db	261	CAGCTCCGGGACAGGGAGGTGTGTGACCTGTATATGGAATGTCTTACCAAGGGCCAGCA 320	
Qy	61	GILyAlaProGILyARgAPGLySeRProGILyAlaAenValILleProGILyTRProGILyILle 80	
Db	321	GAGATCCTCGTGTGAGACCGGAGCCCTGGGGCCCAATGGCAATTCGGGGTACACCTGGGATC 380	
Qy	81	ProGILyARgAPGLyPheLYsGILyGILyGILyGILyGILyGILyGILyGILyGILyGILy 100	
Db	381	CCAGGTCCGGGATGGAATTCAAAGAAAGAAAGGGGGAATGTGAGAGGAAAGCTTGAAGAG 440	
Qy	101	SeTRpTRThProAenArYrLYsGILyCySeRTTPSeSerILeAenArYrGILyILleAPLeu 120	
Db	441	TCCCTGAGACCCCAATCAAGACAGAGGTGTTCATGTGAGATTCAATGAATTTATGGATAGATCTT 500	

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Qy      122  GLYVSLLEALGLUCYETHPhethrIryMeArGserAnsSerAlaLeuAryAlleu 140
Db      501  GGGAAATATTCGAGAGTACATTTCACAAAGATGCTTCAAAATAGCTCTTAAGATTTTG 560
Qy      141  PheSerGIySerLeuAryLeuLySeCyArGAsmAlaCyScglInArtpIryPheThr 160
Db      561  TTCAGTGGCTCACTTCGGCTAAATAGCAAAATGCAATGATGCTGTAGCGCTTGATTTTACA 620
Qy      161  PheAsnGLYAlaGLUCySeSerGIyProLeuProIleGLuAlaIleIeYrLeuAspGln 180
Db      621  TTCAAATGAGAGCTGAATGTCACGAGACCTCTTCCATTAACTAAATATTTTGGACCA 680
Qy      181  GlySerProGLuMetAsnSerThrIleAsnIleIsarqTrhSerSerValGIuGLyLeu 200
Db      681  GGAAGCCCTGAATGAAATTCACAACTTAATATTCATGCGACTTCTTCTGGAAGACTT 740
Qy      201  CySGluGLYIleGLYAlaGLYLeuValAspValAlaIleTrpValGIyTrhCySerAsp 220
Db      741  TGTGAAGGAATGTGGTGTGATTAATGATGTTCCTATCTGGGTGACATTTGTTCAGAT 800
Qy      221  TyrTrpGLyGLYAspAlaSerThrGLYrTrpAsnSerValSerAglIleIleIleGluGln 240
Db      801  TACCCAAAAGGAGATGCTTCTTACGTGAGATTCAGATTCTTCGCATCATTAATGAAGA 860
Qy      241  LeuProLySe 243
Db      861  CTRCMAAA 869

RESULT 7
US-09-489-847-124
; Sequence 124, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 124
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1284)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-124

Alignment Scores:
Pred. No.:      1,29e-124      Length:      1286
Score:          1266.00      Matches:      241
Percent Similarity: 99.18%      Conservative: 0
Best Local Similarity: 97.31%      Mismatches:  2
Query Match:      4          Indels:      1
                        Gaps:      0

US-10-063-734-122 (1-243) x US-09-489-847-124 (1-1286)

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QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20  
Db 131 ATCGACCCCAAGGGCCCCCGCCCTCCCGCAGGGCTCCGGCCCTCCGCTCTG 190  
QY 21 LeuLeuGlnLeuProAlaIaProSerSerAlaSerGlnIleProGlyGlyGlnAla 40  
Db 191 CTGCTCAGCTGCGCCCGCGCGCTGAGCGCTGAGATCCCAAGGGGAAAGGGCG 250  
QY 41 GlnLeuArgGlnArgGlnValValaIaPheLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60  
Db 251 CA-CTCCGGCAGGGAGGAGTGGAGCTGCTATATATGATGATGCTTACAGGGCCAGCA 309  
QY 61 GlyValProGlyValArgAspGlySerProGlyValaAsnValIleProGlyTyrProGlyIle 80  
Db 310 GGAGTCCCTGCTGAGAGCGGAGCCCTGGGGCCAAATGCCATTCCGGTACACCTGGGATC 369  
QY 81 ProGlyValArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
Db 370 CCGAGTGGAGTGAATTCAAAGAGAAAGAGGAGAAATGCTGAGGGAAAGCTTTGAGGAG 429  
QY 101 SerTyrThrProAsnTyrIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
Db 430 TCTGGACACCCCAACTACAGAGCTGCTCATGAGATTCATTGATTAATGACATAGATCT 489  
QY 121 GlyValIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValIleu 140  
Db 490 GGGAAATTCGAGAGTGAATTCATTACAAAGATGCTTCAAAATGCTCTCTAAGAGTTTG 549  
QY 141 PheSerGlySerLeuArgLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160  
Db 550 TTCAGTGGCTCACTTGGCTTAATATCAAGAAATGCAATGCTGAGGGTGGATTTTCAACA 609  
QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180  
Db 610 TTCATGAGAGTGAATTCAGAGCTCTTCCATTGAAGCTATATTTTGGACCA 669  
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlyGlyLeu 200  
Db 670 GGAAGCCCTGAATGATTCACAAATTAATTAATTCATCGCATCTTCTGAGAGACTT 729  
QY 201 CysGlnGlyIleGlyValaGlyLeuValaIaIleTyrValGlyThrCysSerArg 220  
Db 720 TGTGAAGGATTCGCTGCTGATTAAGGATGTTGCTATCTGGGTTGGCCTGTTCAAGT 789  
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGln 240  
Db 790 TACCAAAAGAGATGCTTCTACTGATGATGATTCAGTTTCTCGCATCTATTGAGAGA 849  
QY 241 LeuProGly 243  
Db 850 CTACCAAAA 858

RESULT 8  
US-09-205-258-125  
Sequence 125, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 125  
LENGTH: 1288

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1286)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-125

Alignment Scores:
Pred. No.: 8,09e-124 Length: 1288
Score: 1258.50 Matches: 240
Percent Similarity: 99.18% Conservative: 1
Best Local Similarity: 98.77% Mismatches: 2
Query Match: 96.73% Indels: 1
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-205-258-125 (1-1288)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20
Db |||||
21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlu11eProLySgLySgLySgAla 40
Db |||||
41 GlnLeuArgGlnArgGluValValAlaPLeuTyArgGlyMeCySLeuGlnGlyProAla 60
Db |||||
61 GlyValProGlyValArgAspGlySerProGlyValAsnVal11eProGlyThrProGly11e 80
Db |||||
81 ProGlyValArgAspGlyPheLySgLySgLySgLySgLySgLySgLySgLySgLySgLySg 100
Db |||||
101 SerThrThrProAsnTyLySgGlnCySerThrSerSerLeuAsnTyLy11eAspLeu 120
Db |||||
121 GlyLySg11eAlaGlnCySerThrPheThrLySgMetArgSerSerSerAlaLeuArgVal11e 140
Db |||||
141 PheSerGlySerLeuArgLeuLySgCyArgAsnAlaCySgLySg11eArgTyLyPheThr 160
Db |||||
161 PheArgGlyValAlaGlnCySgSerGlyProLeuPro11eGluAla11e11eTyLyLeuAspGln 180
Db |||||
181 GlySerProGlnMetSerSerThr11eAsn11eHisArgThrSerSerVal11eGluLyLeu 200
Db |||||
201 CySgGlnGly11eGlyValAlaGlyLeuValAspValAla11eThrValGlyThrCySgSerAsp 220
Db |||||
221 TyrProLySgLyValAspAlaSerThrGlyTTPAsnSerValSerArg11e11e11eGluGln 240
Db |||||
788 TACCCAAAGAGAGATCTTCTACTGATGGAATTCAAGTTTCGATCTTCGATCATTTATGAAGAA 847
QY 241 LeuProLyS 243
Db |||||
848 CTACCAAAA 856

RESULT 9
US-09-692-081-1
; Sequence 1, Application US/09692081
```

```

; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: FRIESEL, Robert F.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; FILE REFERENCE: 36-13 Lindner et al. (200036.0013)
; CURRENT APPLICATION NUMBER: US/09/692,081
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-692-081-1

Alignment Scores:
Pred. No.: 2.31e-119 Length: 1192
Score: 1216.00 Matches: 231
Percent Similarity: 95.51% Conservative: 3
Best Local Similarity: 94.29% Mismatches: 9
Query Match: 93.47% Indels: 2
DB: 4 Gaps: 1

US-10-063-734-122 (1-243) x US-09-692-081-1 (1-1192)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGly-----LeuLeuLeu 18
Db |||||
97 ATGCACCCCAAGGCGCCGCCCTCCACAGCTGCTGCTGCTCTTCTTGTGTCTA 156
QY 19 LeuLeuLeuGlnLeuProAlaProSerSerAlaSerGlu11eProLySgLySgGln 38
Db |||||
157 CTGCTCTTCTGAGCTGTCCGCGCCCTCCAGCGCTCTGAGAAATCCCAAGGTAAAGCAA 216
QY 39 LySgAlaGlnLeuArgGlnArgGluValValAlaPLeuTyArgGlyMeCySLeuGlnGly 58
Db |||||
217 AAAGCGTGATCCGGAGAGGGAAGTGTAAGACTGTATATGCGATGCGCTACAAAGA 276
QY 59 ProAlaGlyVal11eProGlyValArgAspGlySerProGlyValAsnVal11eProGlyThrPro 78
Db |||||
277 CCAGGAGGATCTGCTGTGCGATGGAGCCCTGGGGCCAAATGGCAATTCCTGCGACACCG 336
QY 79 Gly11eProGlyValArgAspGlyPheLySgLySgLySgLySgLySgLySgLySgLySgLySg 98
Db |||||
337 GGAATCCAGTCCGGATGATTCAAAGAGAGAAAGGAGATGCTTAAGGAAAGCTTT 396
QY 99 GlnGlnSerThrProAsnTyLySgGlnCySerThrSerSerLeuAsnTyLy11e 118
Db |||||
397 GAGGAATCCTGGAGCCCAAACTACAAGAGTGTTCAATGAGTTCACTTATTATGCAATA 456
QY 119 AspLeuGlyLySg11eAlaGlnCySerThrPheThrLySgMetArgSerSerSerAlaLeuArg 138
Db |||||
457 GATCTTGGGAAATATGGGAAATGATCATTCACAAAGATCGATCCAAAGCGCTCTTCA 516
QY 139 Val11ePheSerGlySerLeuArgLeuLySgCyArgAsnAlaCySgLySg11eArgTyLyPhe 158
Db |||||
517 GTTCTGTAGTGCTGCTGCTGCTCAATAGAGAAATGCTTGCTGCAAGCTGTGAT 576
QY 159 PheThrPheAsnGlyValAlaGlnCySgSerGlyProLeuPro11eGluAla11e11eTyLyLeu 178
Db |||||
577 TTTAACCTTTAATGAGACTGAATGTTCAAGACTCTTCCATTTGAAGCTATCATCTATCTG 636
QY 179 AspGlnGlySerProGlnMetSerSerThr11eAsn11eHisArgThrSerSerVal11eGlu 198
Db |||||
637 GACCAAGAGAGCCCTGAGTTAAATCAATTAATTCATCGTACTTCTCCCGGGA 696
QY 199 GlyLeuCySgGlnGly11eGlyValAlaGlyLeuValAspValAla11eThrValGlyThrCyS 218
Db |||||
697 GGACTGTGAAGGAGTGTGCTGAGCTGTGAGAGTGAGCACTTGGGTGGCACTGTG 756
QY 219 SerAspTyProLySgLyValAspAlaSerThrGlyTTPAsnSerValSerArg11e11e11e 238
Db |||||
757 TCAGATTACCCCAAGAGAGAGCGTTCTACTGGGTGAATTTGTGTGCCGATCATCATTT 816
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DB 42 ACCTGTCAGATTACCCCAAGAGACGGTCTACTGCGG 1
RESULT 12
US-09-222-575-63/C
; Sequence 63, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-63
Alignment Scores:
Pred. No.: 3,586-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 3 Gaps: 0
US-10-063-734-122 (1-243) x US-09-222-575-63 (1-683)
QY 127 ThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
DB 683 ACATTTCACAAAGATGCGTTCAATAGTCTCAAGAGTTTGTTCAGTGGCTCATTCCG 624
QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTyrPheThrPheAsnGlyAlaGluCys 166
DB 623 CTAAATGACAGAAATGATGCTGTCAGCGTGGTATTCACATTCAATGAGAGCTGAATGT 564
QY 167 SerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTCCCACTGAAAGCTATTAATTATTTGACCAAGAGAGCCCTGAATGAAT 504
QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuGlyIleGlyAla 206
DB 503 TCACAAATTAATATTCATGCACTTCTCTGTGGAAGACTTTGTGAAGAAATGGTGTCT 444
QY 207 GlyLeuValAspValAlaIleTyrValGlyThrCysSerAspTyrProLysGlyAspAla 226
DB 443 GGATGATGATGATGCTCTATCTGGGTGGVACTTGTTCAGATTACCCAAAGAGATGCT 384
QY 227 SerThrGlyTyrAsnSerValSerArgIleIleIleGluGluLeuProLys 243
DB 383 TCTACTGATGAGAAATCAGTTCTCGATCATTAATGAAGAACTACCAAAA 333
RESULT 13
US-09-389-681-63/C
; Sequence 63, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.47003
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
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; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-63
Alignment Scores:
Pred. No.: 3,586-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 4 Gaps: 0
US-10-063-734-122 (1-243) x US-09-389-681-63 (1-683)
QY 127 ThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146
DB 683 ACATTTCACAAAGATGCGTTCAATAGTCTCAAGAGTTTGTTCAGTGGCTCATTCCG 624
QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTyrPheThrPheAsnGlyAlaGluCys 166
DB 623 CTAAATGACAGAAATGATGCTGTCAGCGTGGTATTCACATTCAATGAGAGCTGAATGT 564
QY 167 SerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGlySerProGluMetAsn 186
DB 563 TCAGGACCTCTCCCACTGAAAGCTATTAATTATTTGACCAAGAGAGCCCTGAATGAAT 504
QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuGlyIleGlyAla 206
DB 503 TCACAAATTAATATTCATGCACTTCTCTGTGGAAGACTTTGTGAAGAAATGGTGTCT 444
QY 207 GlyLeuValAspValAlaIleTyrValGlyThrCysSerAspTyrProLysGlyAspAla 226
DB 443 GGATGATGATGATGCTCTATCTGGGTGGVACTTGTTCAGATTACCCAAAGAGATGCT 384
QY 227 SerThrGlyTyrAsnSerValSerArgIleIleIleGluGluLeuProLys 243
DB 383 TCTACTGATGAGAAATCAGTTCTCGATCATTAATGAAGAACTACCAAAA 333
RESULT 14
US-09-620-405B-63/C
; Sequence 63, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.47008
; CURRENT APPLICATION NUMBER: US/09/620,405B
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-620-405B-63
Alignment Scores:
Pred. No.: 3,586-57 Length: 683
Score: 626.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.12% Indels: 0
DB: 4 Gaps: 0
```

US-10-063-734-122 (1-243) x US-09-620-405B-63 (1-683)

QY 127 ThrPheThrIlySMeArGSeArSArSArSAlaLeuArGValleuPheSeGlySerLeuArg 146  
DB 683 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 624

QY 147 LeuIySCyArGArSArSAlaCySCySGlnArgTrpTyrrPheThrPheAnsGlyAlaGluCyS 166  
DB 623 CTAAATATGCAAGAAATGATGCTGTCAAGCGTTGGATTTCACATTCATGAGAGCTGAATGT 564

QY 167 SerGlyProLeuProlIegIuaIleIleTyrrLeuAspGlnGlySerProGluMetAsn 186  
DB 563 TCAGGACCTCTTCCCATTTGAAGCTATTAATTATTATTTGACCAAGAAAGCCCTGAATGAAT 504

QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuProlGlyIleGlyAla 206  
DB 503 TCACACATTATATATTCATGCACTTCTTCTGTGAAAGAGACTTGTGAAGAAATGGTGTCT 444

QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCySerAspTyrrProIySGlyAspAla 226  
DB 443 GGATTAGTGGATGTTGCTATCTGTGGTGGYACTTGTTCAGATTACCCAAAGAGATGTCT 384

QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProlGly 243  
DB 383 TCTACTGGATGGAAATTCAGTTTCTCGATCATTAATTGAAGAACTACCAAAA 333

RESULT 15  
US-09-339-338-63/c  
; Sequence 63, Application US/09339338A  
; Patent No. 6573368  
; GENERAL INFORMATION:  
; APPLICANT: Yungui, Jiang  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C2  
; CURRENT APPLICATION NUMBER: US/09/339,338A  
; NUMBER OF SEQ ID NOS: 315  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 63  
; LENGTH: 683  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-339-338-63

Alignment Scores:  
Pred. No.: 3,586-57 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-339-338-63 (1-683)

QY 127 ThrPheThrIlySMeArGSeArSArSArSAlaLeuArGValleuPheSeGlySerLeuArg 146  
DB 683 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 624

QY 147 LeuIySCyArGArSArSAlaCySCySGlnArgTrpTyrrPheThrPheAnsGlyAlaGluCyS 166  
DB 623 CTAAATATGCAAGAAATGATGCTGTCAAGCGTTGGATTTCACATTCATGAGAGCTGAATGT 564

QY 167 SerGlyProLeuProlIegIuaIleIleTyrrLeuAspGlnGlySerProGluMetAsn 186  
DB 563 TCAGGACCTCTTCCCATTTGAAGCTATTAATTATTATTATTGACCAAGAAAGCCCTGAATGAAT 504

QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuProlGlyIleGlyAla 206  
DB 503 TCACACATTATATATTCATGCACTTCTTCTGTGAAAGAGACTTGTGAAGAAATGGTGTCT 444

DB 503 TCACACATTATATATTCATGCACTTCTTCTGTGAAAGAGACTTGTGAAGAAATGGTGTCT 444

QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCySerAspTyrrProIySGlyAspAla 226  
DB 443 GGATTAGTGGATGTTGCTATCTGTGGTGGYACTTGTTCAGATTACCCAAAGAGATGTCT 384

QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProlGly 243  
DB 383 TCTACTGGATGGAAATTCAGTTTCTCGATCATTAATTGAAGAACTACCAAAA 333

RESULT 16  
US-09-433-826B-63/c  
; Sequence 63, Application US/09433826B  
; Patent No. 6579973  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C4  
; CURRENT APPLICATION NUMBER: US/09/433,826B  
; NUMBER OF SEQ ID NOS: 474  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 63  
; LENGTH: 683  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-433-826B-63

Alignment Scores:  
Pred. No.: 3,586-57 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-433-826B-63 (1-683)

QY 127 ThrPheThrIlySMeArGSeArSArSArSAlaLeuArGValleuPheSeGlySerLeuArg 146  
DB 683 ACATTTCACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 624

QY 147 LeuIySCyArGArSArSAlaCySCySGlnArgTrpTyrrPheThrPheAnsGlyAlaGluCyS 166  
DB 623 CTAAATATGCAAGAAATGATGCTGTCAAGCGTTGGATTTCACATTCATGAGAGCTGAATGT 564

QY 167 SerGlyProLeuProlIegIuaIleIleTyrrLeuAspGlnGlySerProGluMetAsn 186  
DB 563 TCAGGACCTCTTCCCATTTGAAGCTATTAATTATTATTATTGACCAAGAAAGCCCTGAATGAAT 504

QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuProlGlyIleGlyAla 206  
DB 503 TCACACATTATATATTCATGCACTTCTTCTGTGAAAGAGACTTGTGAAGAAATGGTGTCT 444

QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCySerAspTyrrProIySGlyAspAla 226  
DB 443 GGATTAGTGGATGTTGCTATCTGTGGTGGYACTTGTTCAGATTACCCAAAGAGATGTCT 384

QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProlGly 243  
DB 383 TCTACTGGATGGAAATTCAGTTTCTCGATCATTAATTGAAGAACTACCAAAA 333

RESULT 17  
US-09-604-287A-63/c  
; Sequence 63, Application US/09604287A  
; Patent No. 6585572  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu

APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jianshun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.470C7  
CURRENT APPLICATION NUMBER: US/09/604,287A  
CURRENT FILING DATE: 2000-06-22  
NUMBER OF SEQ ID NOS: 489  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 63  
LENGTH: 683  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-604-287A-63

Alignment Scores:  
Pred. No.: 3,58e-57 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-604-287A-63 (1-683)

QY 127 ThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146  
DB 683 ACATTACAAAGATGGCTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTPYrPheThrPheAsnGlyAlaGluCys 166  
DB 623 CTAAATGCGAAGATGCTGCTCAGCGTGTGATTTTCACATTCATGAGCTGATGT 564

QY 167 SerGlyProLeuProIleGluAlaIleLeuYrLeuAspGlnGlySerProGluMetAsn 186  
DB 563 TCAGGACCTCTTCCATTGAACTATTAATTTATTTGACCAAGAGCCCTGAATGAAAT 504

QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGlnGlyIleGlyAla 206  
DB 503 TCAACATTAATATTCATGCACTTCTCTGTGGAAGACTTTGTGAAGAAATGGTGT 444

QY 207 GlyLeuValAspValAlaIleTPValGlyThrCysSerAspTYrProLysGlyAspAla 226  
DB 443 GGATTAGTGATGCTGCTATCTGGGTGGYACTTGTTCAGATTACCAAAAGAGATGCT 384

QY 227 SerThrGlyTPAsnSerValSerArgIleIleIleGluGluLeuProLys 243  
DB 383 TCTACTGATGGAATTCAGTTTCTCGATCATTAATGAGAACTACCAAAA 333

RESULT 18  
US-09-285-480-63/C  
Sequence 63, Application US/09285480  
Patent No. 659076  
GENERAL INFORMATION:  
APPLICANT: Yuqi, Jiang  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jianshun  
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
FILE REFERENCE: 210121.470C1  
CURRENT APPLICATION NUMBER: US/09/285,480  
CURRENT FILING DATE: 1999-04-02  
NUMBER OF SEQ ID NOS: 181  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 63  
LENGTH: 683  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-285-480-63

Alignment Scores:  
Pred. No.: 3,58e-57 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-285-480-63 (1-683)

QY 127 ThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146  
DB 683 ACATTACAAAGATGGCTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTPYrPheThrPheAsnGlyAlaGluCys 166  
DB 623 CTAAATGCGAAGATGCTGCTCAGCGTGTGATTTTCACATTCATGAGCTGATGT 564

QY 167 SerGlyProLeuProIleGluAlaIleLeuYrLeuAspGlnGlySerProGluMetAsn 186  
DB 563 TCAGGACCTCTTCCATTGAACTATTAATTTATTTGACCAAGAGCCCTGAATGAAAT 504

QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGlnGlyIleGlyAla 206  
DB 503 TCAACATTAATATTCATGCACTTCTCTGTGGAAGACTTTGTGAAGAAATGGTGT 444

QY 207 GlyLeuValAspValAlaIleTPValGlyThrCysSerAspTYrProLysGlyAspAla 226  
DB 443 GGATTAGTGATGCTGCTATCTGGGTGGYACTTGTTCAGATTACCAAAAGAGATGCT 384

QY 227 SerThrGlyTPAsnSerValSerArgIleIleIleGluGluLeuProLys 243  
DB 383 TCTACTGATGGAATTCAGTTTCTCGATCATTAATGAGAACTACCAAAA 333

RESULT 19  
US-09-834-759-63/C  
Sequence 63, Application US/09834759  
Patent No. 6680197  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yuqi  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jianshun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.470C9  
CURRENT APPLICATION NUMBER: US/09/834,759  
CURRENT FILING DATE: 2001-04-13  
NUMBER OF SEQ ID NOS: 547  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 63  
LENGTH: 683  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-834-759-63

Alignment Scores:  
Pred. No.: 3,58e-57 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: 4 Gaps: 0

US-10-063-734-122 (1-243) x US-09-834-759-63 (1-683)

QY 127 ThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146  
DB 683 ACATTACAAAGATGGCTTCAATATGCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624

QY 147 LeuLYsCyAaRgSaNa1aCySgInARgTYrPheThrPheAaNg1yAlaGluCyS 166  
DB 623 CTAAATGAGAAATGATGCTCTCAAGCGTGGATTTTCATTCATGAGAGCTGAATGT 564  
QY 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAaPngInGlySerProGluMetAa 186  
DB 563 TCAGGACCTCTTCCCATTTGAAGCTATATTTATTTGACCAAGAAAGCCCTGAATGAAT 504  
QY 187 SerThrIleAaNIleHisArgThrSerSerValGluGlyLeuGlyGluGlyIleGlyAla 206  
DB 503 TCACACATTAATATTCATGCGACTTCTCTGAGAAAGAACTTGTGAAGAAATGGTGTCT 444  
QY 207 GlyLeuValAspValAlaIleTyPValGlyTyhCySeraSPtyrProLySGlyAspAla 226  
DB 443 GGATTAAGTGAATGTTGCTATCTGCTGGTGGACTGTTCAGATTAACCAAGAAAGATGCT 384  
QY 227 SerThrGlyTyTPAaSerValSerArgIleIleIleGluGluLeuProLyS 243  
DB 383 TCTACTGAGTGAATTCAGTTTCTCGATCATATTAAGAACTACCAAAA 333  
RESULT 20  
US-09-590-751A-63/c  
Sequence 63, Application US/09590751A  
Patent No. 6756477  
GENERAL INFORMATION:  
APPLICANT: Yugu, JIANG  
APPLICANT: Dillon, David C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, JIANGCHUN  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.470C6  
CURRENT APPLICATION NUMBER: US/09/590,751A  
CURRENT FILING DATE: 2000-06-08  
NUMBER OF SEQ ID NOS: 479  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 63  
LENGTH: 683  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-590-751A-63  
Alignment Scores:  
Pred. No.: 3,586-57 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
Gaps: 0  
US-10-063-734-122 (1-243) x US-09-590-751A-63 (1-683)  
QY 127 ThrPheThrLYsMetArgSerAaSerAlaLeuArgValIleuPheSerGlySerLeuArg 146  
DB 683 ACATTTCAGAAAGATGCGTTCATTAATGCTCTTAAGAGTTTGTTCAGTGGCTCACTTGG 624  
QY 147 LeuLYsCyAaRgSaNa1aCySgInARgTYrPheThrPheAaNg1yAlaGluCyS 166  
DB 623 CTAAATGAGAAATGATGCTCTCAAGCGTGGATTTTCATTCATGAGAGCTGAATGT 564  
QY 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAaPngInGlySerProGluMetAa 186  
DB 563 TCAGGACCTCTTCCCATTTGAAGCTATATTTATTTGACCAAGAAAGCCCTGAATGAAT 504  
QY 187 SerThrIleAaNIleHisArgThrSerSerValGluGlyLeuGlyGluGlyIleGlyAla 206  
DB 503 TCACACATTAATATTCATGCGACTTCTCTGAGAAAGAACTTGTGAAGAAATGGTGTCT 444  
QY 207 GlyLeuValAspValAlaIleTyPValGlyTyhCySeraSPtyrProLySGlyAspAla 226  
DB 443 GGATTAAGTGAATGTTGCTATCTGCTGGTGGACTGTTCAGATTAACCAAGAAAGATGCT 384

QY 227 SerThrGlyTyTPAaSerValSerArgIleIleIleGluGluLeuProLyS 243  
DB 383 TCTACTGAGTGAATTCAGTTTCTCGATCATATTAAGAACTACCAAAA 333  
RESULT 21  
US-09-169-768-1  
Sequence 1, Application US/09169768  
Patent No. 6492508  
GENERAL INFORMATION:  
APPLICANT: GRUSKIN, ELLIOT A.  
APPLICANT: BUECHTER, DOUGLAS  
APPLICANT: BROKAW, JANE  
APPLICANT: ZHANG, GUANGHUI  
APPLICANT: PHOLELA, DAVID  
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DILMORTH & BARRESE  
STREET: 333 EARLE OVINGTON BOULEVARD  
CITY: UNIONDALE  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 11553  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/169,768  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: STEEN, JEFFREY S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 228-8484  
TELEFAX: (516) 228-8516  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3170 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-169-768-1  
Alignment Scores:  
Pred. No.: 0,00159 Length: 3170  
Score: 129.50 Matches: 43  
Percent Similarity: 49.56% Conservative: 13  
Best Local Similarity: 38.05% Mismatches: 36  
Query Match: 9.95% Indels: 23  
Gaps: 4  
US-10-063-734-122 (1-243) x US-09-169-768-1 (1-3170)  
QY 3 ProGlnGlyProAlaIleSerProGlnArgLeuArgGlyLeu-LeuLeuLeuLeuLeu 22  
DB 523 CCCACCGGCCCCGCTGCT 570  
QY 22 uGlnLeuProAlaIleSerSerAlaSerGluIleProLySGlyLySAlaGlnLe 42  
DB 571 AAGGTGAAGCTG-----GTCCCAAGGAGCCCGAGAGCTCTGAAGCT 612  
QY 42 uArgGlnArgGluValValAspLeu-----TyrAaNgIyMetCySLeuGlnGlyProAl 60  
DB 613 CCCAGGGGTGGTGTGTAGCTGGCCCCCTGGCCCTGGCTGGTGTGCTCTGAGCTGCT 671  
QY 60 agIyValPProGlyArAspGlySerProGlyAlaAaValIleProGlyTyhProGlyI 80  
DB 672 TGAACACCTCGTGTGCTGATGACAGCTGTGTCTTAAGGTGCCAATGGTGTCTCTGAT 731







Qy 22 uGlnLeuProAlaProSerSerAlaSerGluLeuProLysGlyLysGlnLysAlaGlnLeu 42  
Db 590 AAGGGTGAAGCTG-----GTCCCAAGGGCCCGGAGGCTCTGAAGT 631  
Qy 42 uArgGlnArgGluValValAspLeu-----TyrAsnGlyMetCysLeuGlnGlyProAl 60  
Db 632 CCCAGGGTGTGCTGATGACAGCCCTGAGCCCTGAGCTGTGCTCT-GGCCCTGC 690  
Qy 60 aGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyTl 80  
Db 691 TGAAGACCTGTGCTGATGACAGCCCTGCTAAAGTGCCTCAATGCTGCTCTGAT 750  
Qy 80 eProGlyArgAspGlyPheLysGlyGlnLysGlyGlnCysLeuArgGluSerPheGluGl 100  
Db 751 TCTGTGTGCTCTGCTGCTTCCCTGCTCCGAGGC-----CC 786  
Qy 100 uSerThrProAsnThrLysGlnCysSerTrpSer 112  
Db 787 CTC-TGAGCCCAAGGCGCCGCGGCTCTGTGCTC 822  
RESULT 26  
US-09-169-768-9  
Sequence 9, Application US/09169768  
GENERAL INFORMATION:  
PATENT No. 6492508  
APPLICANT: GRUSKIN, ELLIOT A.  
APPLICANT: BUECHTER, DOUGLAS  
APPLICANT: BROKAW, JANE  
APPLICANT: ZHANG, GUANGHUI  
APPLICANT: PAOLELLA, DAVID  
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DILMORTH & BARRESE  
STREET: 333 EARLE OVINGTON BOULEVARD  
CITY: UNIONDALE  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 11553  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/169,768  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: STEEN, JEFFREY S.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 228-8484  
TELEFAX: (516) 228-8516  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3541 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-169-768-9  
Alignment Scores:  
Pred. No.: 0.00188 Length: 3541  
Score: 129.50 Matches: 43  
Percent Similarity: 49.56% Conservative: 13  
Best Local Similarity: 38.05% Mismatches: 36  
Query Match: 9.95% Indels: 23  
DB: 4 Gaps: 4  
Qy 3 ProGlnGlyProAlaIaSerProGlnArgLeuArgGlyLeu-LeuLeuLeuLeuLeuLeu 22

Db 542 CCCACGGGCGCCGCTGCTCTCT-----GGCTTCCCTGTGCTGTGCTGTGCT 589  
Qy 22 uGlnLeuProAlaProSerSerAlaSerGluLeuProLysGlyLysGlnLysAlaGlnLeu 42  
Db 590 AAGGGTGAAGCTG-----GTCCCAAGGGCCCGGAGGCTCTGAAGT 631  
Qy 42 uArgGlnArgGluValValAspLeu-----TyrAsnGlyMetCysLeuGlnGlyProAl 60  
Db 632 CCCAGGGTGTGCTGATGACAGCCCTGAGCCCTGAGCTGTGCTCT-GGCCCTGC 690  
Qy 60 aGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyTl 80  
Db 691 TGAAGACCTGTGCTGATGACAGCCCTGCTAAAGTGCCTCAATGCTGCTCTGAT 750  
Qy 80 eProGlyArgAspGlyPheLysGlyGlnLysGlyGlnCysLeuArgGluSerPheGluGl 100  
Db 751 TCTGTGTGCTCTGCTGCTTCCCTGCTCCGAGGC-----CC 786  
Qy 100 uSerThrProAsnThrLysGlnCysSerTrpSer 112  
Db 787 CTC-TGAGCCCAAGGCGCCGCGGCTCTGTGCTC 822

RESULT 27  
US-09-169-768-12  
Sequence 12, Application US/09169768  
GENERAL INFORMATION:  
PATENT No. 6492508  
APPLICANT: GRUSKIN, ELLIOT A.  
APPLICANT: BUECHTER, DOUGLAS  
APPLICANT: BROKAW, JANE  
APPLICANT: ZHANG, GUANGHUI  
APPLICANT: PAOLELLA, DAVID  
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DILMORTH & BARRESE  
STREET: 333 EARLE OVINGTON BOULEVARD  
CITY: UNIONDALE  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 11553  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/169,768  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: STEEN, JEFFREY S.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 228-8484  
TELEFAX: (516) 228-8516  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4167 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-169-768-12  
Alignment Scores:  
Pred. No.: 0.0024 Length: 4167  
Score: 129.50 Matches: 43  
Percent Similarity: 49.56% Conservative: 13  
Best Local Similarity: 38.05% Mismatches: 36  
Query Match: 9.95% Indels: 23  
DB: 4 Gaps: 4





QY 226 aserthnglytTpanserValserArgillellelgluInleuPro 242  
DB 601 GAGCTCCGGGTGACCTCGTGAAGGACACACAGTTTGC 649  
RESULT 31  
US-08-555-669-11  
Sequence 11, Application US/08555669  
Patent No. 5773248  
GENERAL INFORMATION:  
APPLICANT: Brewton, Richard G.  
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/555,669  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,1227  
REFERENCE/DOCKET NUMBER: 8389-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2543 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 47..2098  
US-08-555-669-11  
Alignment Scores:  
Pred. No.: 0.0116 Length: 2543  
Score: 120.00 Matches: 43  
Percent Similarity: 38.40% Conservative: 5  
Best Local Similarity: 34.40% Mismatches: 33  
Query Match: 9.22% Indels: 45  
DB: 1 Gaps: 5  
US-10-063-734-122 (1-243) x US-08-555-669-11 (1-2543)  
QY 6 ProAlaIaSerProGln---ArgleuArgGly----- 15  
DB 11 CCCGCCCGGAGCGGAGCTCGCTCAGCCATGCGCGGCGCGCGCGCGCGCG 70  
QY 16 -----leuLeuLeuLeuLeuLeuLeuProAlaProSerSerAlaSerGluLe 33  
DB 71 CCGCTCTGCTCTGCTCTCTCTCTCGGCGAGCTTGTGGCGCGCGCGGCGGAGAGATG 130  
QY 34 ProlysglyLysGlnLysAlaGlnleuArgGlnArgGlnValAlaPleuTyraGly 53  
DB 131 GGA----- 133  
QY 54 MetCysleuGlnGlyProAlaGlyValProGlyArgAepGlySerProGlyAlaAsnVal 73

DB 134 -----CTCCCGGGCCCCCGGGCCCCCAGGGGCGCTGGAAAGCCCGGCGAGACGC 187  
QY 74 11e-----ProGlyThrProGlyTyleProGlyArgAepGlyPheLys 87  
DB 188 ATTGACGAGAGAGACTGTCTCTCCAGGTCTGCTGCTCCCGGAGACCAAGGGGGCCCA 247  
QY 88 GlnGlyLysGlyGlnCysLeuArgGluSerPheGlnGluSerTTPThrProAntyTyls 107  
DB 248 GGAAGGCC-GGGGAAACAGAGGA-----GGCTGGCTCGCGGAGACTGCC 291  
QY 108 glnCysSerTpsr 112  
DB 292 GGGTGTGATGTCT 306  
RESULT 32  
US-09-073-663-11  
Sequence 11, Application US/09073663  
Patent No. 6127523  
GENERAL INFORMATION:  
APPLICANT: Brewton, Richard G.  
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McGregor & Adler, LLP  
STREET: 8011 Candle Lane  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh OS 8.1  
SOFTWARE: Microsoft Word for Macintosh  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,663  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benjamin Aaron Adler, Ph.D., J.D.  
REGISTRATION NUMBER: 35,423  
REFERENCE/DOCKET NUMBER: D5913D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 777-2321  
TELEFAX: (713) 777-6908  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2543 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 47..2098  
US-09-073-663-11  
Alignment Scores:  
Pred. No.: 0.0116 Length: 2543  
Score: 120.00 Matches: 43  
Percent Similarity: 38.40% Conservative: 5  
Best Local Similarity: 34.40% Mismatches: 33  
Query Match: 9.22% Indels: 45  
DB: 3 Gaps: 5  
US-10-063-734-122 (1-243) x US-09-073-663-11 (1-2543)  
QY 6 ProAlaIaSerProGln---ArgleuArgGly----- 15  
DB 11 CCCGCCCGGAGCGGAGCTCGCTCAGCCATGCGCGGCGCGCGCGCGCGCG 70  
QY 16 -----leuLeuLeuLeuLeuLeuLeuProAlaProSerSerAlaSerGluLe 33



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OTHER INFORMATION: 9-27-261.mis
NAME/KEY: primer bind
LOCATION: 3788..3806
OTHER INFORMATION: 9-27-261.mis complement
NAME/KEY: primer bind
LOCATION: 11099..11117
OTHER INFORMATION: 99-14387-129.mis
NAME/KEY: primer bind
LOCATION: 11119..11137
OTHER INFORMATION: 99-14387-129.mis complement
NAME/KEY: primer bind
LOCATION: 15101..15119
OTHER INFORMATION: 9-12-48.mis
NAME/KEY: primer bind
LOCATION: 15121..15139
OTHER INFORMATION: 9-12-48.mis complement
NAME/KEY: primer bind
LOCATION: 15177..15195
OTHER INFORMATION: 9-12-124.mis
NAME/KEY: primer bind
LOCATION: 15197..15215
OTHER INFORMATION: 9-12-124.mis complement
NAME/KEY: primer bind
LOCATION: 15408..15426
OTHER INFORMATION: 9-12-355.mis
NAME/KEY: primer bind
LOCATION: 15428..15446
OTHER INFORMATION: 9-12-355.mis complement
NAME/KEY: primer bind
LOCATION: 15481..15499
OTHER INFORMATION: 9-12-428.mis
NAME/KEY: primer bind
LOCATION: 15501..15519
OTHER INFORMATION: 9-12-428.mis complement
NAME/KEY: primer bind
LOCATION: 15844..15862
OTHER INFORMATION: 99-14405-105.mis
NAME/KEY: primer bind
LOCATION: 15864..15882
OTHER INFORMATION: 99-14405-105.mis complement
NAME/KEY: primer bind
LOCATION: 17151..17169
OTHER INFORMATION: 9-16-189.mis
NAME/KEY: primer bind
LOCATION: 17171..17189
OTHER INFORMATION: 9-16-189.mis complement
US-09-776-976-7

Alignment Scores:
Pred. No.: 0.279      Length: 20966
Score: 120.00      Matches: 61
Percent Similarity: 39.41%      Conservative: 19
Best Local Similarity: 30.05%      Mismatches: 66
Query Match: 9.22%      Indels: 59
DB: 4      Gaps: 11

US-10-063-734-122 (1-243) x US-09-776-976-7 (1-20966)
QY 13 LeuArgGlyLeuLeuLeu-----LeuLeuLeuGlnLeuPro----- 25
Db 15146 CTCAGATGCTGTGCTGGAGCTGTCTACTGCTATTAGCTCCCGKATGACGAG 15205
QY 26 -----AlaProSerSerLaserGlnLleProLysGlyLysGlnLysAla 40
Db 15206 GAAACCAAGACTCAAGGCGCCGAGTCTGCTCCCTGCCCAAG----- 15250
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyrAnGlyMetCysLeuGlnGlyProAla 60
Db 15251 -----GGGCGCTGCACAGGTTGGATGCG 15274
QY 61 GlnValProGlyValArgAspGlySerProGlyAlaAsnValLleProGlyThrProGlyLle 80
Db 15275 GGCATCCACAGGCGAT-----CCGGGCGCATTAAT-----GGGCGCCCAAGCGCGT 15316
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QY 81 ProGlyValArgAspGlyPheLysGlyGlnLysGlyLeuArgGlnSerPheGlnGlu 100
Db 15317 GATGGCAAGAGATGGACCCCTGGTGAGAGAGGTAGAA-AGGAGATCCAGGTAAAGATGT 15375
QY 101 SerTPThrProAsnTyrLysGlnCysSerTPSerSerLeuAsnTyr----- 116
Db 15376 TTCTGG-----CTCTTTTATCAAGACTCTCTACCTGATATTAACTATTAAAGKATTTC 15432
QY 117 -----GlyLleAspLeuGlyLysLleAlaGlnCysThrPheThrLysMetArg 132
Db 15433 ATTATTAACTAAAGGCGCTGACACAGGAGAAA-CCAAAGCTTTTATTATGTT----- 15482
QY 133 SerAnSerAlaLeuArgValLeuPheSerGlySerLeuArgLeuLysCysValArgAsnAla 152
Db 15483 AACCATTAAGCAACTGATGATATTGGGGTGGCTTCCACAGATGAGTGTAGA---TGG 15539
QY 153 CysCysGlnArgTyrPheThrPheAsnGlyValaGlnCysSerGlyProLeuProIle 172
Db 15540 TGCCCTTAATACCAAGACTTGGGCTTTCGTCGATCTGACCTCTTTCCATCCCTTTTC 15599
QY 173 GluAlaIleIleTyrLeuAspGlnGlySerProGlnLysAsnSerThrIleAsnIleHis 192
Db 15600 CCATCT-----TCACCC-----TCATCCCATTCACGATACAT 15632
QY 193 ArgThrSer 195
Db 15633 TCATATTCT 15641

RESULT 34
US-09-909-547-7
Sequence 7, Application US/09903547
Patent No. 6579852
GENERAL INFORMATION:
APPLICANT: Fruebis, Joachim
APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Binaim, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76 Use, CIP
CURRENT FILING DATE: US/09/909,547
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/776,976
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/176,228
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
SEQ ID NO 7
LENGTH: 20966
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..4811
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
LOCATION: 4812..4851
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 15144..15365
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 16277..20559
OTHER INFORMATION: exon 3
NAME/KEY: misc feature
LOCATION: 20560..20966
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OTHER INFORMATION: 3' regulatory region  
NAME/KEY: allele  
LOCATION: 3787  
OTHER INFORMATION: 9-27-261 : polymorphic base G or C  
NAME/KEY: allele  
LOCATION: 11118  
OTHER INFORMATION: 99-14387-129 : polymorphic base A or C  
NAME/KEY: allele  
LOCATION: 15120  
OTHER INFORMATION: 9-12-48 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 15196  
OTHER INFORMATION: 9-12-124 : polymorphic base G or T  
NAME/KEY: allele  
LOCATION: 15427  
OTHER INFORMATION: 9-12-355 : polymorphic base G or T  
NAME/KEY: allele  
LOCATION: 15500  
OTHER INFORMATION: 9-12-428 : polymorphic base A or G  
NAME/KEY: allele  
LOCATION: 15863  
OTHER INFORMATION: 99-14405-105 : polymorphic base A or G  
NAME/KEY: allele  
LOCATION: 17170  
OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A  
NAME/KEY: primer bind  
LOCATION: 3528..3545  
OTHER INFORMATION: 9-27.pu  
NAME/KEY: primer bind  
LOCATION: 3928..3946  
OTHER INFORMATION: 9-27.rp complement  
NAME/KEY: primer bind  
LOCATION: 10990..11008  
OTHER INFORMATION: 99-14387.pu  
NAME/KEY: primer bind  
LOCATION: 11423..11442  
OTHER INFORMATION: 99-14387.rp complement  
NAME/KEY: primer bind  
LOCATION: 15073..15092  
OTHER INFORMATION: 9-12.pu  
NAME/KEY: primer bind  
LOCATION: 15503..15520  
OTHER INFORMATION: 9-12.rp complement  
NAME/KEY: primer bind  
LOCATION: 15759..15776  
OTHER INFORMATION: 99-14405.pu  
NAME/KEY: primer bind  
LOCATION: 16191..16211  
OTHER INFORMATION: 99-14405.rp complement  
NAME/KEY: primer bind  
LOCATION: 16982..17001  
OTHER INFORMATION: 9-16.pu  
NAME/KEY: primer bind  
LOCATION: 17384..17402  
OTHER INFORMATION: 9-16.rp complement  
NAME/KEY: misc binding  
LOCATION: 3775..3799  
OTHER INFORMATION: 9-27-261.probe  
NAME/KEY: misc binding  
LOCATION: 15184..15208  
OTHER INFORMATION: 9-12-124.probe  
NAME/KEY: misc binding  
LOCATION: 15415..15439  
OTHER INFORMATION: 9-12-355.probe  
NAME/KEY: misc binding  
LOCATION: 15488..15512  
OTHER INFORMATION: 9-12-428.probe

NAME/KEY: misc binding  
LOCATION: 15851..15875  
OTHER INFORMATION: 99-14405-105.probe  
NAME/KEY: misc binding  
LOCATION: 17158..17182  
OTHER INFORMATION: 9-16-189.probe  
NAME/KEY: primer bind  
LOCATION: 3768..3786  
OTHER INFORMATION: 9-27-261.mis  
NAME/KEY: primer bind  
LOCATION: 3788..3806  
OTHER INFORMATION: 9-27-261.mis complement  
NAME/KEY: primer bind  
LOCATION: 11099..11117  
OTHER INFORMATION: 99-14387-129.mis  
NAME/KEY: primer bind  
LOCATION: 11119..11137  
OTHER INFORMATION: 9-12-428.mis complement  
NAME/KEY: primer bind  
LOCATION: 15101..15119  
OTHER INFORMATION: 9-12-48.mis  
NAME/KEY: primer bind  
LOCATION: 15121..15139  
OTHER INFORMATION: 9-12-48.mis complement  
NAME/KEY: primer bind  
LOCATION: 15177..15195  
OTHER INFORMATION: 9-12-124.mis  
NAME/KEY: primer bind  
LOCATION: 15197..15215  
OTHER INFORMATION: 9-12-124.mis complement  
NAME/KEY: primer bind  
LOCATION: 15408..15426  
OTHER INFORMATION: 9-12-355.mis  
NAME/KEY: primer bind  
LOCATION: 15428..15446  
OTHER INFORMATION: 9-12-355.mis complement  
NAME/KEY: primer bind  
LOCATION: 15481..15499  
OTHER INFORMATION: 9-12-428.mis  
NAME/KEY: primer bind  
LOCATION: 15501..15519  
OTHER INFORMATION: 9-12-428.mis complement  
NAME/KEY: primer bind  
LOCATION: 15844..15862  
OTHER INFORMATION: 99-14405-105.mis  
NAME/KEY: primer bind  
LOCATION: 15864..15882  
OTHER INFORMATION: 99-14405-105.mis complement  
NAME/KEY: primer bind  
LOCATION: 17151..17169  
OTHER INFORMATION: 9-16-189.mis  
NAME/KEY: primer bind  
LOCATION: 17171..17189  
OTHER INFORMATION: 9-16-189.mis complement  
US-09-909-547-7  
Alignment Scores:  
Pred. No.: 0.279  
Score: 120.00  
Percent Similarity: 39.41%  
Best Local Similarity: 30.05%  
Query Match: 9.22%  
DB: 4  
Gaps: 11  
US-10-063-734-122 (1-243) x US-09-909-547-7 (1-20966)  
Qy 13 leuATGgGlyleuLeu-----leuLeuLeuGlnLeuPro----- 25  
Db 15146 CTCAGATGCTGTGCTGGAGCTGTCTACTGCTATTAGCTTCCCGCATGACCAAG 15205  
Qy 26 -----AlaProSerSerAlaSerGluIleProLySGlyLysGlnYsAla 40  
Db 15206 GAAACGACGATCAAGGCGCGAGTCTTCCCTGCCCAAG----- 15250

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Qy 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 15251 -----GGGGCCCTGCACAGGTTGGATGGCC 15274
Qy 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 15275 GGCATCCCGAGGCGAT-----CCGGGCCATATAT-----GGGGCCCGACGGCCCGT 15316
Qy 81 ProGlyArgAspGlyPheLeuGlyGlyGluCysLeuArgGlySerPheGluGlu 100
Db 15317 GATGGCAGAGATGGACCCCTGGTGGAGAGGTGAGAA-AGGAGATCCAGGTAAAGATGT 15375
Qy 101 SerThrProAsnTyrIleGlyGlyCysSerThrSerLeuAsnTyr----- 116
Db 15376 TTCTGG---CCTCTTTCATCAGACGACCTCTACATGATATTAACATATGAAGKATTC 15432
Qy 117 -----GlyLeuPheGlyGlyIleAlaGluCysThrPheThrIlyMetArg 132
Db 15433 ATTATTAATAAGGCTTACACACAGGAGAA-GCAAACTTTTATATTT----- 15482
Qy 133 SerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArgLeuIlyCysArgAsnAla 152
Db 15483 AACCATAGCAACCTGATGATTTGGGTTGCTTCCAGAGATGAGTGA---TGG 15539
Qy 153 CysCysGlnArgTyrPheThrPheAsnGlyAlaGluCysSerGlyProLeuProIle 172
Db 15540 TGCCCTTAACCAAGACTTGGCTTGCATCTGCATCTGCAGACCTCTTCCATCCCTTTC 15599
Qy 173 GluAlaIleIleTyrLeuAspGlnGlySerProGlyMetAsnSerThrIleAsnIleHis 192
Db 15600 CCATCT-----TACCC-----TCATCCTATATCCAGTACAT 15632
Qy 193 ArgThrSer 195
Db 15633 TCATATCT 15641

RESULT 35
US-09-569-852B-1
Sequence 1, Application US/09569852B
Patent No. 6582909
GENERAL INFORMATION:
APPLICANT: Bouquelere, Lydie
APPLICANT: Demison, Blake
APPLICANT: Yen-Pocin, Frances
TITLE OF INVENTION: APM1 Biallelic Markers and Uses Thereof
FILE REFERENCE: GEN-T113XC2
CURRENT APPLICATION NUMBER: US/09/569, 852B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: PCT/IB99/01858
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 09/434, 848
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: US 60/119, 593
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: US 60/107, 113
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 20966
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(4811)
OTHER INFORMATION: 5' regulatory region
NAME/KEY: primer bind
LOCATION: (14683)..(14701)
OTHER INFORMATION: 17-34-860.mis
NAME/KEY: primer bind
LOCATION: (14703)..(14721)

OTHER INFORMATION: 17-34-860.mis complement
NAME/KEY: primer bind
LOCATION: (14728)..(14756)
OTHER INFORMATION: 17-34-915.mis
NAME/KEY: primer bind
LOCATION: (14758)..(14776)
OTHER INFORMATION: 17-34-915.mis complement
NAME/KEY: primer bind
LOCATION: (14796)..(14814)
OTHER INFORMATION: 17-35-71.mis
NAME/KEY: primer bind
LOCATION: (14816)..(14834)
OTHER INFORMATION: 17-35-71.mis complement
NAME/KEY: primer bind
LOCATION: (15031)..(15049)
OTHER INFORMATION: 17-35-306.mis
NAME/KEY: primer bind
LOCATION: (15051)..(15069)
OTHER INFORMATION: 17-35-306.mis complement
NAME/KEY: primer bind
LOCATION: (15101)..(15119)
OTHER INFORMATION: 9-12-48.mis
NAME/KEY: primer bind
LOCATION: (15121)..(15139)
OTHER INFORMATION: 9-12-48.mis complement
NAME/KEY: primer bind
LOCATION: (15177)..(15195)
OTHER INFORMATION: 9-12-124.mis
NAME/KEY: primer bind
LOCATION: (15197)..(15215)
OTHER INFORMATION: 9-12-124.mis complement
NAME/KEY: primer bind
LOCATION: (15408)..(15426)
OTHER INFORMATION: 9-12-355.mis
NAME/KEY: primer bind
LOCATION: (15428)..(15446)
OTHER INFORMATION: 9-12-355.mis complement
NAME/KEY: primer bind
LOCATION: (15481)..(15499)
OTHER INFORMATION: 9-12-428.mis
NAME/KEY: primer bind
LOCATION: (15501)..(15519)
OTHER INFORMATION: 9-12-428.mis complement
NAME/KEY: primer bind
LOCATION: (15661)..(15679)
OTHER INFORMATION: 17-36-47.mis
NAME/KEY: primer bind
LOCATION: (15681)..(15699)
OTHER INFORMATION: 17-36-47.mis complement
NAME/KEY: primer bind
LOCATION: (15771)..(15789)
OTHER INFORMATION: 17-36-120.mis
NAME/KEY: primer bind
LOCATION: (15791)..(15809)
OTHER INFORMATION: 17-36-120.mis complement
NAME/KEY: primer bind
LOCATION: (15844)..(15862)
OTHER INFORMATION: 99-14405-105.mis
NAME/KEY: primer bind
LOCATION: (15864)..(15882)
OTHER INFORMATION: 99-14405-105.mis complement
NAME/KEY: primer bind
LOCATION: (17151)..(17169)
OTHER INFORMATION: 9-16-189.mis
NAME/KEY: primer bind
LOCATION: (17171)..(17189)
OTHER INFORMATION: 9-16-189.mis complement
NAME/KEY: primer bind
LOCATION: (17810)..(17828)
OTHER INFORMATION: 17-37-629.mis
NAME/KEY: primer bind
LOCATION: (17830)..(17848)
OTHER INFORMATION: 17-37-629.mis complement
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NAME/KEY: primer_bind
LOCATION: (17992)..(18010)
OTHER INFORMATION: 17-37-811.mis
NAME/KEY: primer_bind
LOCATION: (18012)..(18030)
OTHER INFORMATION: 17-37-811.mis complement
NAME/KEY: primer_bind
LOCATION: (18470)..(18488)
OTHER INFORMATION: 17-38-349.mis
NAME/KEY: primer_bind
LOCATION: (18490)..(18508)
OTHER INFORMATION: 17-38-349.mis complement
NAME/KEY: primer_bind
LOCATION: (926)..(944)
OTHER INFORMATION: 17-30-216.mis
NAME/KEY: primer_bind
LOCATION: (946)..(964)
OTHER INFORMATION: 17-30-216.mis complement
NAME/KEY: primer_bind
LOCATION: (3719)..(3737)
OTHER INFORMATION: 9-27-211.mis
NAME/KEY: primer_bind
LOCATION: (3739)..(3757)
OTHER INFORMATION: 9-27-211.mis complement
NAME/KEY: primer_bind
LOCATION: (3754)..(3772)
OTHER INFORMATION: 9-27-246.mis
NAME/KEY: primer_bind
LOCATION: (3774)..(3792)
OTHER INFORMATION: 9-27-246.mis complement
NAME/KEY: primer_bind
LOCATION: (3768)..(3786)
OTHER INFORMATION: 9-27-261.mis
NAME/KEY: primer_bind
LOCATION: (3788)..(3806)
OTHER INFORMATION: 9-27-261.mis complement
NAME/KEY: primer_bind
LOCATION: (5076)..(5094)
OTHER INFORMATION: 17-31-298.mis
NAME/KEY: primer_bind
LOCATION: (5096)..(5114)
OTHER INFORMATION: 17-31-298.mis complement
NAME/KEY: primer_bind
LOCATION: (5191)..(5209)
OTHER INFORMATION: 17-31-413.mis
NAME/KEY: primer_bind
LOCATION: (5211)..(5229)
OTHER INFORMATION: 17-31-413.mis complement
NAME/KEY: primer_bind
LOCATION: (5364)..(5382)
OTHER INFORMATION: 17-31-413.mis complement
NAME/KEY: primer_bind
LOCATION: (10618)..(10636)
OTHER INFORMATION: 17-32-24.mis
NAME/KEY: primer_bind
LOCATION: (10638)..(10656)
OTHER INFORMATION: 17-32-24.mis complement
NAME/KEY: primer_bind
LOCATION: (11020)..(11038)
OTHER INFORMATION: 99-14387-50.mis
NAME/KEY: primer_bind
LOCATION: (11040)..(11058)
OTHER INFORMATION: 99-14387-50.mis complement
NAME/KEY: primer_bind
LOCATION: (11099)..(11117)
OTHER INFORMATION: 99-14387-129.mis
NAME/KEY: primer_bind
LOCATION: (11119)..(11137)
OTHER INFORMATION: 99-14387-129.mis complement
NAME/KEY: primer_bind
LOCATION: (11169)..(11187)
OTHER INFORMATION: 99-14387-199.mis
NAME/KEY: primer_bind
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LOCATION: (11189)..(11207)
OTHER INFORMATION: 99-14387-199.mis complement
NAME/KEY: primer_bind
LOCATION: (13954)..(13972)
OTHER INFORMATION: 17-33-TGAGACT.mis
NAME/KEY: primer_bind
LOCATION: (13974)..(13992)
OTHER INFORMATION: 17-33-TGAGACT.mis complement
NAME/KEY: exon
LOCATION: (4812)..(4851)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (15144)..(15365)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (16277)..(20559)
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (20560)..(20966)
OTHER INFORMATION: 3' regulatory region
```

```
Alignment Scores:
Pred. No.: 0.279 Length: 20966
Score: 120.00 Matches: 61
Percent Similarity: 39.41% Conservative: 19
Best Local Similarity: 30.05% Mismatches: 66
Query Match: 9.22% Indels: 59
DB: 4 Gaps: 11
```

US-10-063-734-122 (1-243) x US-09-569-852B-1 (1-20966)

```
QY 13 LeuArgGlyLeuLeu-----LeuLeuLeuGlnLeuPro----- 25
Db 15146 CTCAGAGTCTGTGTGGAGCTGTTCTACGTCTATTAGCTCTGCCGKATGACCG 15205
QY 26 -----AlaProSerSerAlaSerGluLeProLySGlySGlnysAla 40
Db 15206 GAAACCAAGCATCAAGGCGCCGAGTCCGCTCCCGCCAG----- 15250
QY 41 GlnLeuArgGlnArgGlnValAlaPheLeuTyraGlnMetCysLeuGlnGlyProAla 60
Db 15251 -----GGGCGCTGCACAGTTGATGAGCG 15274
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 15275 GGCATCCAGGCGAT-----CCGGCCATPAT-----GGGCCCCAGGCCGT 15316
QY 81 ProGlyArgAspGlyPheLySGlyGlnLySGlyGlnCysLeuArgGlnSerPheGlnGlu 100
Db 15317 GATGCGAGAGATGCGACCCCTGCTGAGAGGATGAGAA-AGAGATCCAGATAGATGT 15375
QY 101 SerTyrThrProAsnTyrlsGlnCysSerTyrPheSerSerLeuAsnTy----- 116
Db 15376 TTCCTG---CCTCTTCATCAGACCTCTCAGATGATATAACTATGAAGCATTC 15432
QY 117 -----GlyLeaPheGlnGlyValIleAlaGlnCysThrPheThrMetArg 132
Db 15433 ATTATTAACTAAGGCTAGACAGGAGAAA-GCAAAGCTTTTATATT----- 15482
QY 133 SerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArgLeuGlnCysArgAsnAla 152
Db 15483 AACCATACAGCAACCTGATGTGTTGGTGTGCTCTCCAAAGATGACGTAGA---TGG 15539
QY 153 CysCysGlnArgTyrPheThrPheAsnGlyAlaGlnCysSerGlyProLeuPhe 172
Db 15540 TGCCTATATACCAAGACTTGGCTTGTGCTGATGACAGCTCTTTTCCATCCCTTTC 15599
QY 173 GlnAlaIleIleTyrlsLeuAspGlnGlySerProGlnMetAsnSerThrIleAsnIleHis 192
Db 15600 CCATCT-----TCACCC-----TCATCCCTATTTCCAGATACAT 15632
QY 193 ArgThrSer 195
|||
```

```

Db          15633 TCATATTC 15641

RESULT 36
US-09-620-312D-870
/ Sequence 870, Application US/09620312D
/ Patent No. 6569662
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yunqing
/ APPLICANT: Wang, Dunrui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinghast
/ APPLICANT: Dumanac, Radoje T.
/ TITLE OF INVENTION: No. 6569662el Nucleic Acids and
/ FILE REFERENCE: Polypeptides
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ CURRENT FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1105
/ SOFTWARE: pc FL_genes Version 1.0
/ SEQ ID NO 870
/ LENGTH: 1981
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (413) .. (1165)
US-09-620-312D-870

Alignment Scores:
Pred. No.: 0.0115 Length: 1981
Score: 118.50 Matches: 36
Percent Similarity: 40.18% Conservative: 9
Best Local Similarity: 32.14% Mismatches: 24
Query Match: 9.11% Indels: 44
DB: 4 Gaps: 4

US-10-063-734-122 (1-243) x US-09-620-312D-870 (1-1981)
QY 20 LeuLeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyLeuGlnLys 39
Db 686 ATCTTCACCAAGATTCCTCCACGACCTCTCATCATCCGCG----- 72
QY 40 AlAGlIneuArgGlnArgGluValValaIleAspLeuTyraGngLysMetCysLeuGlnGlyPro 59
Db 725 -----ACTGTCCAAGGGCGCT 739
QY 60 AlAGlYValProGlyIArgAspGlySerProGlyAla----- 71
Db 740 CCTGGGGAGCTCGGAGGCGCAGGCTCACTGGAGGCCCTCGTGAACAAGAACCCCGAGGC 799
QY 72 -----AsnVal-----IleProGlyThrProGlyIleProGlyIArgAsp 84
Db 800 ACAACGAGGCTTCCCGGAATGCGAGGCGTGCACGAGGAGCCCGAGGAGAACGAGTCTAACT 859
QY 85 GlyPheIysGlyGlyIuIysGlyGlyGluCysLeuArgGluSerPheGlnGluGlnSerTrrThrPro 104
Db 860 GGTATCAAGAGAGAAAAGGAATTC-AGGCGT-----TGGAAACCA 900

```

[illegible]

STREET: 333 EARLE OVINGTON BOULEVARD  
CITY: UNIONDALE  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 11553  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/169,768  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: STEEN, JEFFREY S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 228-8484  
TELEFAX: (516) 228-8516  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3171 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-169-768-19

Alignment Scores:  
Pred. No.: 0.0233 Length: 3171  
Score: 118.50 Matches: 33  
Percent Similarity: 38.46% Conservative: 23  
Best Local Similarity: 36.26% Mismatches: 23  
Query Match: 9.11% Indels: 33  
DB: Gaps: 4

US-10-063-734-122 (1-243) x US-09-169-768-19 (1-3171)  
QY 3 ProGlnGlyProAlaAlaSer-----ProGlnArgLeuArgGlyLeuLeuLeuLeu 20  
DB 586 CCGAGAGGCGCGCGGAGCGAGGCTCCAGAGCGGCTCGTGT----- 630  
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnVala 40  
DB 631 -----GAACCGGCGCGCGCGGCGG-----CCGCGCGGT----- 657  
QY 41 GlnLeuArgGlnArgGlnValaValaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60  
DB 658 -----GCGGCGGCGCGCGGCGG-----GCGGCGGCGCGGCGGT 672  
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValleProGlyThrProGlyIle 80  
DB 673 GGTACCGCTGCGCGGAGCGGTGAGCGAGTCCAGAAAGTCCCAAGCGCGCGCGGTATT 732  
QY 81 ProGlyArgAspGlyPheLeuGlyGlnValaValaGly 91  
DB 733 GCAGGTGACCGGCGCTTCCCGGATGCCCGCGCG 765

RESULT 39  
US-08-494-168-1  
Sequence 1, Application US/08494168  
Patent No. 5731192  
GENERAL INFORMATION:  
APPLICANT: Reeders, Stephen T.  
APPLICANT: Zhou, Jing  
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method  
TITLE OF INVENTION: of Detecting Collagen Deficiency  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA

ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/494,168  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,465  
FILING DATE: 27-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 40397/104/BAER  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5102 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(2..82, 86..97, 101..4399, 4403..4420, 4424  
US-08-494-168-1  
LOCATION: ..4465, 4469..4876, 4880..5101)

Alignment Scores:  
Pred. No.: 0.061 Length: 5102  
Score: 117.50 Matches: 42  
Percent Similarity: 44.26% Conservative: 12  
Best Local Similarity: 34.43% Mismatches: 27  
Query Match: 9.03% Indels: 42  
DB: Gaps: 8

US-10-063-734-122 (1-243) x US-08-494-168-1 (1-5102)  
QY 4 GlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeuLeuGln 23  
DB 1679 CAGGCGCCAGCAGGCGCTCA-----GGCTTAGTGGCGCTCTG----- 1717  
QY 24 LeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnValaGlnLeuArg 43  
DB 1718 -----GGTCTTTCAGA-----CCCAAGGAAG-----AAG 1744  
QY 44 GlnArgGlnValaValaAspLeuTyrAsnGlyMet----- 54  
DB 1745 GGGGAACCAATTCTGATCAATCCAAAGATGCCAGAGATCGGGGTGATTCTGCTCC 1804  
QY 55 ---CysLeuGlnGlyProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnVal 73  
DB 1805 CAGGCGCTTCCGTGTATAGAGAACCAAGAGAGAGATACAGT----- 1855  
QY 74 IleProGlyThrProGlyIlePro-----GlyArgAspGlyPheLeuGlyGlnValaGly 91  
DB 1856 TTACACAGTCTGCGAGGCTTCCGGGTATGTGACAGGCTTCCCAAGTGAAGAGGG 1915  
QY 92 GlnCysLeuArgGlnSerPheGlnGlnSerTyrProAsnTyrGlnCysSerTyr 111  
DB 1916 TT-----ACCTGACTTCTGTGTAAGAAAGGCATCTCG 1950  
QY 112 SerSer 113  
DB 1951 TCCACC 1956  
RESULT 40  
US-09-227-357-51

```
; Sequence 51, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661

; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (485)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (493)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (486)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (496)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (587)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (633)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1330)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-227-357-51

Alignment Scores:
Pred. No.: 0.0131 Length: 1333
Score: 115.50 Matches: 31
Percent Similarity: 53.73% Conservative: 5
Best Local Similarity: 46.27% Mismatches: 22
Query Match: 8.88% Indels: 9
DB: 3 Gaps: 3

US-10-063-734-122 (1-243) x US-09-227-357-51 (1-1333)
QY 30 AlaSerGluIleProLySGlyLySGlnLyAlaGlnLeuArgGlnArgGluValValaIasp 49
DB 146 GCCAGTGGACAAACCCCGGGGTAAAT-----CAGTTGAAGAAGAGAACTACTCCCCC 196
QY 50 LeuTyraAnglyMetCys-----LeuGlnGlyProAlaGlyValProGlyArg 65
DB 197 AGGTAT-----ATCTCAACATTCCTGCTGCTGGACCTCCAGAGGCCCTGGAGCA 250
QY 66 AspGlySerProGlyAlaAsnValIleProGlyThrProGlyTyrIleProGlyArgAspGly 85
DB 251 AATGTTCCCTCGGCCCCCATGTCGCGATCGGCGCTTCCAGAGAGATGTAGACGCGC 310
QY 86 PheLySGlyGluLySGlyGlu 92
DB 311 AGGAAAGAGAGAAAGGTGAA 331

RESULT 41
US-09-620-312D-110
; Sequence 110, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
```

```
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunding
APPLICANT: Wang, Dunru
APPLICANT: Wang, Zhilwei
APPLICANT: John Tillimhaet
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 656962621 Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 110
LENGTH: 6674
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1312)..(6330)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(6674)
OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-110
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Alignment Scores:
Pred. No.: 0.149 Length: 6674
Score: 115.50 Matches: 32
Percent Similarity: 40.22% Conservative: 5
Best Local Similarity: 34.78% Mismatches: 20
Query Match: 8.88% Indels: 35
DB: 4 Gaps: 4
```

```
US-10-063-734-122 (1-243) x US-09-620-312D-110 (1-6674)
QY 1 MetArgProGlnGlyProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 4954 ATGGGTCTCTCCGGGGCCCGGAGACAGCCG----- 4983
QY 21 LeuLeuGlnLeuPro--AlaProSerSerAlaSerGluLeuProGlyGlyGlnLeu 39
DB 4984 -----GGGTACCGGAGATCCCGAGCCCATGCCAGGAGGGGCCCAAGAGAGC----- 5031
QY 40 AlaGlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyPro 59
DB 5032 -----CGGGAACCT 5040
QY 60 AlaGlyValProGlyArgAspGlySerProGlyAlaAsnValLeuProGlyThrProGly 79
DB 5041 CAGGGGACAGCTGGCTGGCCAGAGACTTCCGGGAGCC-----ATGGGGCTCCAGGG 5091
QY 80 IleProGlyArgAspGlyPheGlyGlyGlyGlyGly 91
DB 5092 CTTCCTGGATGATGATGATTAAGGTGACAAAGGA 5127
RESULT 42
US-09-404-879A-212/C
; Sequence 212, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
```

```
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 212
LENGTH: 695
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(695)
OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-212
```

```
Alignment Scores:
Pred. No.: 0.00555 Length: 695
Score: 115.00 Matches: 39
Percent Similarity: 43.52% Conservative: 8
Best Local Similarity: 36.11% Mismatches: 47
Query Match: 8.84% Indels: 14
DB: 4 Gaps: 5
```

US-10-063-734-122 (1-243) x US-09-404-879A-212 (1-695)

```
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnLeuAlaGln 41
DB 335 TTAGACTGCCCAACCA-----GAAATTCATTGGAGAAATGTGTGCAGTT 288
QY 42 LeuArgGlnArgGlnValAlaAspLeuTyr-----AsnGlyMetCysLeuGlnGlyPro 59
DB 287 TCCCAACAGCTCCCAAGCTCTCTACTGCGCCCTCTTAAGTCAAGACCTCAAGGCCCT 228
QY 60 AlaGlyValProGlyArgAspGlySerProGlyAlaAsnValLeuProGlyThrProGly 79
DB 227 AAGGAGATCCAGGAGCCCTCTGTATCTTGGAGAAATGTGCAGCCCTGTATTCAGGA 168
QY 80 IleProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 98
DB 167 CAACCAAGGATCCCGGTCTCTCTGCGCCCTCGAGATCTGT-----GAATCATGCCCT 114
QY 99 -----GluGlnSerTyrThrProAsnTyrGlnCysSerTyrSerSerLeuAsnTyr 116
DB 113 ACTGTCTCCCAACACTATCTCTCCAGATGATGATGATGATGATGATGATGATGATGAT 63
QY 117 GlyIleAspLeuGlyLysIleAla 124
DB 62 GAGATGACATGAGAGACTCGCA 39
RESULT 43
US-09-338-933-212/C
; Sequence 212, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Mitcham, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 212
LENGTH: 695
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(695)
```





Query Match: 8.84% Indels: 14  
DB: 4 Gaps: 5  
US-10-063-734-122 (1-243) x US-09-216-003A-212 (1-695)  
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluIleProLyseGlyLysGlnLysAlaGln 41  
DB 335 TTAGACTGGCCCAACCA-----GAAATTCATTGGAGAAATGTTGTGCAGTT 288  
QY 42 LeuArgGlnArgGluValValAspLeuTyr-----AsnGlyMetCysLeuGlnGlyPro 59  
DB 287 TGGCCACAGCTCCCACTGCTCTACTCGCCCTCTTAATGTCAGAGACCTCAAGCCCC 228  
QY 60 AlaGlyValProGlyValArgAspGlySerProGlyValAsnValIleProGlyThrProGly 79  
DB 227 AAGGGAGATCCAGGCCCTCTGTAATTCCTGGAGAAATGTCAGACCTGTATTCAGGA 168  
QY 80 IleProGlyValArgAspGlyPheLysGlyGlyLysGlyLysLeuArgGlnSerPhe--- 98  
DB 167 CAACCAAGGTCCTCCCTGTTCTCTCGGCCCTCGGAAATCTGT-----GAATCATGCCCT 114  
QY 99 -----GluGlnSerTrpThrProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyr 116  
DB 113 ACTGTCCTCAGAACTATCTCCCAATGATTCATATGATGTCAAGTCT----- 63  
QY 117 GlyIleAspLeuGlyLysIleAla 124  
DB 62 GGAGTAGCAGTAGAGAGACTCGCA 39  
RESULT 46  
US-09-667-857-212/c  
; Sequence 212, Application US/09667857  
; Patent No. 669664  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Piling, Steven P.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Ranger, Gary Richard  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darick  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C5  
; CURRENT APPLICATION NUMBER: US/09/667,857  
; CURRENT FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 212  
; LENGTH: 695  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(695)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-667-857-212  
Alignment Scores:  
Pred. No.: 0.00555 Length: 695  
Score: 115.00 Matches: 39  
Percent Similarity: 43.52% Conservative: 8  
Best Local Similarity: 36.11% Mismatches: 47  
Query Match: 8.84% Indels: 14  
DB: 4 Gaps: 5  
US-10-063-734-122 (1-243) x US-09-667-857-212 (1-695)  
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluIleProLyseGlyLysGlnLysAlaGln 41  
DB 335 TTAGACTGGCCCAACCA-----GAAATTCATTGGAGAAATGTTGTGCAGTT 288

QY 42 LeuArgGlnArgGluValValAspLeuTyr-----AsnGlyMetCysLeuGlnGlyPro 59  
DB 287 TGGCCACAGCTCCCACTGCTCTACTCGCCCTCTTAATGTCAGAGACCTCAAGCCCC 228  
QY 60 AlaGlyValProGlyValArgAspGlySerProGlyValAsnValIleProGlyThrProGly 79  
DB 227 AAGGGAGATCCAGGCCCTCTGTAATTCCTGGAGAAATGTCAGACCTGTATTCAGGA 168  
QY 80 IleProGlyValArgAspGlyPheLysGlyGlyLysGlyLysLeuArgGlnSerPhe--- 98  
DB 167 CAACCAAGGTCCTCCCTGTTCTCTCGGCCCTCGGAAATCTGT-----GAATCATGCCCT 114  
QY 99 -----GluGlnSerTrpThrProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyr 116  
DB 113 ACTGTCCTCAGAACTATCTCCCAATGATTCATATGATGTCAAGTCT----- 63  
QY 117 GlyIleAspLeuGlyLysIleAla 124  
DB 62 GGAGTAGCAGTAGAGAGACTCGCA 39  
RESULT 47  
US-09-029-348-20  
; Sequence 20, Application US/09029348  
; Patent No. 6171827  
; GENERAL INFORMATION:  
; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER  
; TITLE OF INVENTION: NOVEL PROCOLLAGENS  
; FILE REFERENCE: 0087857PUS LISTING  
; CURRENT APPLICATION NUMBER: US/09/029,348  
; CURRENT FILING DATE: 1998-05-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 1881  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE  
; OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS  
US-09-029-348-20  
Alignment Scores:  
Pred. No.: 0.0249 Length: 1881  
Score: 115.00 Matches: 39  
Percent Similarity: 43.52% Conservative: 8  
Best Local Similarity: 36.11% Mismatches: 47  
Query Match: 8.84% Indels: 14  
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US-10-063-734-122 (1-243) x US-09-029-348-20 (1-1881)  
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluIleProLyseGlyLysGlnLysAlaGln 41  
DB 214 TTAGACTGGCCCAACCA-----GAAATTCATTGGAGAAATGTTGTGCAGTT 261  
QY 42 LeuArgGlnArgGluValValAspLeuTyr-----AsnGlyMetCysLeuGlnGlyPro 59  
DB 262 TGGCCACAGCTCCCACTGCTCTACTCGCCCTCTTAATGTCAGAGACCTCAAGCCCC 321  
QY 60 AlaGlyValProGlyValArgAspGlySerProGlyValAsnValIleProGlyThrProGly 79  
DB 322 AAGGGAGATCCAGGCCCTCTGTAATTCCTGGAGAAATGTCAGACCTGTATTCAGGA 381  
QY 80 IleProGlyValArgAspGlyPheLysGlyGlyLysGlyLysLeuArgGlnSerPhe--- 98  
DB 382 CAACCAAGGTCCTCCCTGTTCTCTCGGCCCTCGGAAATCTGT-----GAATCATGCCCT 435  
QY 99 -----GluGlnSerTrpThrProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyr 116  
DB 436 ACTGTCCTCAGAACTATCTCCCAATGATTCATATGATGTCAAGTCT----- 486  
QY 117 GlyIleAspLeuGlyLysIleAla 124

DB 487 GGAGTAGCAGTAGAGGACTCGCA 510  
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US-09-181-706-1  
Sequence 1, Application US/09181706  
Patent No. 6130068  
GENERAL INFORMATION:  
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,  
APPLICANT: Robert F. Dubose, Richard S. Johnson  
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janis C. Henry  
STREET: 51 University St.  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/181,706  
FILING DATE: October 28, 1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/958,598 (converted to a  
APPLICATION NUMBER: Provisional, see below)  
FILING DATE: October 28, 1997  
CLASSIFICATION:  
APPLICATION NUMBER: --to be assigned-- (USN 08/958,598  
APPLICATION NUMBER: conversion to Provisional application)  
FILING DATE: October 26, 1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2631-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)470-4189  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4707 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..4707  
US-09-181-706-1  
Alignment Scores:  
Pred. No.: 0.162 Length: 4707  
Score: 113.00 Matches: 77  
Percent Similarity: 34.54% Conservative: 84  
Best Local Similarity: 25.33% Mismatches: 88  
Query Match: 8.69% Indels: 116  
DB: 3 Gaps: 18  
US-10-063-734-122 (1-243) x US-09-181-706-1 (1-4707)  
QY 2 ArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeuLeu 21  
DB 31 CGCCCGCCCGCCCGCCCGCCCGCCCACTGCC-----CTGCTGCGCTATCTG 75

QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuAlaGln 41  
DB 76 CTGGCACTGGCGCTCCCGCGCGCGCGCGCGCGCTGTCGCGTGCAGCAAGCC 135  
QY 42 Leu-----ArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeu 56  
DB 136 ATCGAAGCAATCGCGCGCGCGCGCGCGCGCGCGCGCTGTTGTGGGAGCGGCACTGCTT- 194  
QY 57 GlnGlyProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGly 76  
DB 195 ---GGACCAAGCTGGAATA-----CAGCTGAGACACAGCTCTCGCGCT 236  
QY 77 ThrProGlyIleProGly-----ArgAspGlyPheLeuGly---GluGlyGlyGlu 92  
DB 237 GTACCGGAGCAAGCGGCGCAACTGCACAGACCGGCTCTCGTGGCGCCCGCGCGGCC 296  
QY 93 CysLeuArgGlu-SerPheGluGlu----- 100  
DB 297 CGCGCCCGGAGACAGCTTCAGCAAGCTGCTGCTCCCTACCGGAGGGGGCGCGCCCT 356  
QY 101 -----SerTrpThrProAsnTyrIleGlnCys----- 109  
DB 357 CGGGGGCTGCTGCTCACCGGCTGACCTTCGACCGGGCGCTGCGAGGTGCGGCCCT 416  
QY 110 -----SerTrpSerLeuAsnTyrGlyIleAspLeu----- 120  
DB 417 GGGCACTGAGCGCGCACTCTCGCGCAACGCGAGAGGTGTGTGTCGCCACCGCA 476  
QY 121 -GlyValIleAlaGluCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgVal 140  
DB 477 GGGCTCGACGCGCGCGCTGTGTGTACCGCGCGCGCGGACAC----- 519  
QY 140 uPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpThrPhe 160  
DB 520 -----CGCTGATAC----- 528  
QY 160 rPheAsnGlyValaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspG 180  
DB 529 -----CTGGCGGTGGCGCGCACTGCTGCTGCTCA 560  
QY 180 nGlySerProGluMetAsnSerThrIleAsn-----IleHisArgThrSer-- 195  
DB 561 G-----CCGAGACGCGCGAGCGCTGCAACCCCGCGCATCCGACCAAGACAGCGCAT 614  
QY 196 -----SerValGluGly-----Ile 200  
DB 615 CGCGCTCAAGACACGAGAGGGGCGAGCGCTGCGCACGAGAGCTGGGGCGCTCAAGCT 674  
QY 200 uCysGluGlyIleGlyVala---GlyLeuValaAspValAlaIleTyrValGlyThrCys-- 218  
DB 675 GTGCGAGGGCGCGCGCGCGCTGCACTTCGTGAGCGCTTCTCTGSAAGCGAGCATCTCA 734  
QY 219 -----SerAspTyrProGlyGlyAspAlaSerThrGlyTyrAsnSerVa 233  
DB 735 CTTCCTCACTACCTCACTCACTATACAGCGGC---GCTGCACCGCGCTGCGCCAGCAT 791  
QY 233 lSerArgIle 236  
DB 792 GGCGCGCATC 801  
RESULT 49  
US-09-458-791-1  
Sequence 1, Application US/09458791  
Patent No. 6174689  
GENERAL INFORMATION:  
APPLICANT: Spriggs, Melanie  
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
RECEPTOR DNA AND POLYPEPTIDES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janis C. Henry  
STREET: 51 University St.

CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/458,791  
FILING DATE: 10-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/958,598  
FILING DATE: 28-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 470-4189  
TELEFAX: (206) 233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4707 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..4707  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-458-791-1  
Alignment Scores:  
Pred. No.: 0.162 Length: 4707  
Score: 113.00 Matches: 77  
Percent Similarity: 34.54% Conservative: 28  
Best Local Similarity: 25.33% Mismatches: 84  
Query Match: 8.69% Indels: 116  
DB: 3 Gaps: 18  
US-10-063-734-122 (1-243) x US-09-458-791-1 (1-4707)  
QY 2 ArgProGlnGlyProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 21  
DB 31 GCGCCCCCGCGCCCGCAGCGCCATGCCCC-----CTGCTCGCTATCTG 75  
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnValaGln 41  
DB 76 CTGGCACTGGCGGCTCCCGCGCGGCGCGAGCGCGTGTGGGGGTGGAGCAAGCC 135  
QY 42 Leu-----ArgGlnArgGlnValaValaAspLeuTyraGlnGlyMetCysLeu 56  
DB 136 ATCGGAGCATTGCGCGCGAGCCGAGGAGCAGCGGTGTGTGTGCGGCGCACTGCTC 194  
QY 57 GlnGlyProAlaGlyValaProGlyArgAspGlySerProGlyValaAsnValaIleProGly 76  
DB 195 ---GAGACAGCTGAGCTA-----CAGCTGAGACAGCTCTCGCGGCT 236  
QY 77 ThrProGlyIleProGly-----ArgAspGlyPheLeuGly---GlnGlyGln 92  
DB 237 GTACCGGAGCAAGCGGCAATGCAAGAGCGGTCTGCTGCGCGCCCGCGGCGGCC 296  
QY 93 CysLeuArgGln-SerPheGlnGln----- 100  
DB 297 CCGGCGCGGAGAGCTTGCAGCAAGCTGTCTGCTGCTTACCGGAGGCGGCGCGGCT 356  
QY 101 -----SerTrpThrProAsnTyrlsGlnCys----- 109

DB 357 CCGGGGGCTGTGCTACACCGGCTGGACCTTCGACCGGGGCGCTGGAGGTGGGCCCT 416  
QY 110 -----SerTrpSerSerLeuAsnTyrlsIleAspLeu----- 120  
DB 417 GGGCAACTGACCCGCACTCCCTGGCAACCGGAGGTGTCTGTGCCACCGGCA 476  
QY 121 -GlyIleAlaGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgVal 140  
DB 477 GGGCTCGACGGCGGGGTGTGTACCGCGGCGGAGAACAC----- 519  
QY 140 uphSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpIlePhe 160  
DB 520 -----CGCTGGTAC----- 528  
QY 160 rPheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrl 180  
DB 529 -----CTGGCGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 560  
QY 180 nGlySerProGlnMetAsnSerThrIleAsn-----IleHisArgThrSer 195  
DB 561 G-----CCGAGAGCGGCGAGCGGCTGCAACCCCGCGCATCCGACGACGACG 614  
QY 196 -----SerValGlnGly-----Le 200  
DB 615 CCGGCTCAAGACAGAGGAGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCT 674  
QY 200 uCysGlnGlyIleGlyAla--GlyLeuValaAspValaIleTrpValaGlyThrCys 218  
DB 675 GTGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 734  
QY 219 -----SerAspTrpProGlySerGlyAspAlaSerThrGlyTrpAsnSer 233  
DB 735 CTTCCTTACTACCTTCACTAATAAGAGCGGC---GCTGCACCGGCTGCGGCGG 791  
QY 233 lSerArgIle 236  
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RESULT 50  
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; Sequence 1, Application US/09459066  
; Patent No. 6187909  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; TITLE OF INVENTION: VIRAL ENCODED SENAPHORIN PROTEIN  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS/Windows 95  
; SOFTWARE: Word for Windows 95, 7.0a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/459,066  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/958,598  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Henry, Janis C  
; REGISTRATION NUMBER: 34,347  
; REFERENCE/DOCKET NUMBER: 2631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 470-4189

TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4707 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..4707  
US-09-459-066-1

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Pred. No.:	0.162	Length:	4707
Score:	113.00	Matches:	77
Percent Similarity:	34.54%	Conservative:	28
Best Local Similarity:	25.33%	Mismatches:	84
Query Match:	8.69%	Indels:	116
DB:	3	Gaps:	18

US-10-063-734-122 (1-243) x US-09-459-066-1 (1-4707)

QY 2 ArgProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeuLeu 21  
DB 31 CGCCCCCGCGCGCCGCGAGCGCCACCTGCCCC-----CTGCTCGGCTATCTG 75  
QY 22 LeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLysGlnLysAlaGln 41  
DB 76 CTGGCAGCTGGCGGCTCCGCGCGGCGGCGAGCCCGGTGGCGGTGGAGCAAGCC 135  
QY 42 Leu-----ArgGlnArgGluValAlaSerLeuTyraSerGlyMetCysLeu 56  
DB 136 ATCGAGGCGATCGCGCGAGCGAGCGCGGTGTGTGGCGAGCGGAGCTGCTT- 194  
QY 57 GlnGlyProAlaGlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGly 76  
DB 195 ---GGACCAAGCTGAGCTA-----CAGCTGGAGCAAGCTCTCGCGCCT 236  
QY 77 ThrProGlyIleProGly-----ArgAspGlyPheLysGly---GluLysGlyGlu 92  
DB 237 GTACCGGAGCAAGCGGCAACTGCAAGAGCGGTCTGCTGGCGCCCCCGCGCGCC 296  
QY 93 CysLeuArgGlu-SerPheGluGlu-----100  
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QY 101 -----SerTyrProAsnTyrLysGlnCys-----109  
DB 357 CGGCGGCTGCTGCTCACCGGCTTGACCTTCAGCCGCGGCGGCTGGAGAGTGGCGCCT 416  
QY 110 -----SerTyrSerSerLeuAsnTyrGlyIleAspLeu-----120  
DB 417 GGGCAACTGAGCCCGCACTCCCTGCGCAACCGGCGGTGTCTGCGCACCGCGCA 476  
QY 121 -GlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLe 140  
DB 477 GGGCTCGACGGCGCGGTGTGTACCGCGCGCGGCGGAGCAAC-----519  
QY 140 uPheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160  
DB 520 -----CGCTGGTAC-----528  
QY 160 rPheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleTyrLeuAspGln 180  
DB 529 -----CTGGCGGTGGCGCGCACCTTACGTGCTGCTGA 560  
QY 180 nGlySerProGluMetAsnSerThrIleAsn-----IleHisArgThrSer-- 195  
DB 561 G-----CCGGAGAGCGGCGGCGCTGCAACCCCGCGGCGATCCGACCAAGACAGACGGGCAT 614

QY 196 -----SerValGlnGly-----Leu 200  
DB 615 CGCGCTCAAGAGCAACGAGGCGGCGAGCGCTGCGCACGAGAGCTGGGCGGCTCAAGCT 674  
QY 200 uCysGlnGlyIleGlyAla---GlyLeuValAspValAlaIleTyrPValGlyThrCys-- 218  
DB 675 GTGCGAGGCGCGGCGAGCGCTGCACTTGTGTGAGCGCTTCTCTGGAACGCGAGCATCTA 734  
QY 219 -----SerAspTyrProLysGlyAspAlaSerThrGlyTyrPheAsnSerVa 233  
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QY 233 lSerArgIle 236  
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Search completed: December 25, 2004, 07:50:50  
Job time : 117 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 25, 2004, 05:35:17 ; Search time 551 Seconds

(without alignments)  
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Title: US-10-063-734-122

Perfect score: 1301

Sequence: 1 MRPGPASPRLRGILLLL.....GDASTGMSVSRITIEELPK 243

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Delop 6.0 , Delext 7.0

Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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Database : Published Applications NA:\*

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18: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	729	US-09-834-759-511	Sequence 511, App
2	1301	100.0	729	US-10-007-805-511	Sequence 511, App
3	1301	100.0	729	US-10-076-622-511	Sequence 511, App
4	1301	100.0	729	US-10-124-805-511	Sequence 511, App
5	1301	100.0	732	US-09-834-759-510	Sequence 510, App
6	1301	100.0	732	US-10-007-805-510	Sequence 510, App
7	1301	100.0	732	US-10-076-622-510	Sequence 510, App
8	1301	100.0	732	US-10-060-036-4556	Sequence 4556, App
9	1301	100.0	732	US-10-124-805-510	Sequence 510, App
10	1301	100.0	837	US-09-834-759-512	Sequence 512, App
11	1301	100.0	837	US-09-834-759-513	Sequence 513, App
12	1301	100.0	837	US-10-007-805-512	Sequence 512, App
13	1301	100.0	837	US-10-007-805-513	Sequence 513, App
14	1301	100.0	837	US-10-076-622-512	Sequence 512, App
15	1301	100.0	837	US-10-076-622-513	Sequence 513, App
16	1301	100.0	837	US-10-060-036-4557	Sequence 4557, App
17	1301	100.0	837	US-10-124-805-512	Sequence 512, App
18	1301	100.0	837	US-10-124-805-513	Sequence 513, App
19	1301	100.0	1257	US-09-938-418-2	Sequence 2, Appl
20	1301	100.0	1257	US-09-946-374-430	Sequence 430, App
21	1301	100.0	1257	US-10-006-867-121	Sequence 121, App
22	1301	100.0	1257	US-10-052-586-365	Sequence 365, App
23	1301	100.0	1257	US-10-063-547-121	Sequence 121, App
24	1301	100.0	1257	US-10-063-551-121	Sequence 121, App
25	1301	100.0	1257	US-10-174-580-365	Sequence 365, App
26	1301	100.0	1257	US-10-176-758-365	Sequence 365, App
27	1301	100.0	1257	US-10-175-727-365	Sequence 365, App
28	1301	100.0	1257	US-10-063-616-121	Sequence 121, App
29	1301	100.0	1257	US-10-174-581-365	Sequence 365, App
30	1301	100.0	1257	US-10-176-483-365	Sequence 365, App
31	1301	100.0	1257	US-10-176-749-365	Sequence 365, App
32	1301	100.0	1257	US-10-176-914-365	Sequence 365, App
33	1301	100.0	1257	US-10-176-915-365	Sequence 365, App
34	1301	100.0	1257	US-10-063-569-121	Sequence 121, App
35	1301	100.0	1257	US-10-063-513-121	Sequence 121, App
36	1301	100.0	1257	US-10-063-515-121	Sequence 121, App
37	1301	100.0	1257	US-10-063-512-121	Sequence 121, App
38	1301	100.0	1257	US-10-173-706-365	Sequence 365, App
39	1301	100.0	1257	US-10-175-728-365	Sequence 365, App
40	1301	100.0	1257	US-10-175-722-365	Sequence 365, App
41	1301	100.0	1257	US-10-176-482-365	Sequence 365, App
42	1301	100.0	1257	US-10-176-757-365	Sequence 365, App
43	1301	100.0	1257	US-10-176-913-365	Sequence 365, App
44	1301	100.0	1257	US-10-180-552-365	Sequence 365, App
45	1301	100.0	1257	US-10-180-557-365	Sequence 365, App
46	1301	100.0	1257	US-10-063-502-121	Sequence 121, App
47	1301	100.0	1257	US-10-173-700-365	Sequence 365, App
48	1301	100.0	1257	US-10-174-572-365	Sequence 365, App
49	1301	100.0	1257	US-10-174-579-365	Sequence 365, App
50	1301	100.0	1257	US-10-174-582-365	Sequence 365, App
51	1301	100.0	1257	US-10-174-588-365	Sequence 365, App
52	1301	100.0	1257	US-10-175-729-365	Sequence 365, App
53	1301	100.0	1257	US-10-175-740-365	Sequence 365, App
54	1301	100.0	1257	US-10-175-743-365	Sequence 365, App
55	1301	100.0	1257	US-10-176-488-365	Sequence 365, App
56	1301	100.0	1257	US-10-176-492-365	Sequence 365, App
57	1301	100.0	1257	US-10-176-747-365	Sequence 365, App
58	1301	100.0	1257	US-10-176-747-365	Sequence 365, App
59	1301	100.0	1257	US-10-176-985-365	Sequence 365, App
60	1301	100.0	1257	US-10-176-987-365	Sequence 365, App
61	1301	100.0	1257	US-10-176-992-365	Sequence 365, App
62	1301	100.0	1257	US-10-176-993-365	Sequence 365, App
63	1301	100.0	1257	US-10-184-658-365	Sequence 365, App
64	1301	100.0	1257	US-10-176-991-365	Sequence 365, App
65	1301	100.0	1257	US-10-063-549-121	Sequence 121, App
66	1301	100.0	1257	US-10-173-685-365	Sequence 365, App
67	1301	100.0	1257	US-10-173-687-365	Sequence 365, App
68	1301	100.0	1257	US-10-173-705-365	Sequence 365, App
69	1301	100.0	1257	US-10-174-576-365	Sequence 365, App
70	1301	100.0	1257	US-10-174-585-365	Sequence 365, App

```
71 1301 100.0 1257 14 US-10-174-586-365 Sequence 365, App
72 1301 100.0 1257 14 US-10-175-747-365 Sequence 365, App
73 1301 100.0 1257 14 US-10-176-481-365 Sequence 365, App
74 1301 100.0 1257 14 US-10-176-483-365 Sequence 365, App
75 1301 100.0 1257 14 US-10-176-487-365 Sequence 365, App
76 1301 100.0 1257 14 US-10-176-493-365 Sequence 365, App
77 1301 100.0 1257 14 US-10-176-756-365 Sequence 365, App
78 1301 100.0 1257 14 US-10-176-911-365 Sequence 365, App
79 1301 100.0 1257 14 US-10-176-919-365 Sequence 365, App
80 1301 100.0 1257 14 US-10-176-925-365 Sequence 365, App
81 1301 100.0 1257 14 US-10-176-978-365 Sequence 365, App
82 1301 100.0 1257 14 US-10-179-510-365 Sequence 365, App
83 1301 100.0 1257 14 US-10-180-543-365 Sequence 365, App
84 1301 100.0 1257 14 US-10-180-544-365 Sequence 365, App
85 1301 100.0 1257 14 US-10-180-546-365 Sequence 365, App
86 1301 100.0 1257 14 US-10-180-547-365 Sequence 365, App
87 1301 100.0 1257 14 US-10-180-549-365 Sequence 365, App
88 1301 100.0 1257 14 US-10-180-555-365 Sequence 365, App
89 1301 100.0 1257 14 US-10-180-559-365 Sequence 365, App
90 1301 100.0 1257 14 US-10-181-000-365 Sequence 365, App
91 1301 100.0 1257 14 US-10-183-010-365 Sequence 365, App
92 1301 100.0 1257 14 US-10-183-012-365 Sequence 365, App
93 1301 100.0 1257 14 US-10-184-614-365 Sequence 365, App
94 1301 100.0 1257 14 US-10-184-623-365 Sequence 365, App
95 1301 100.0 1257 14 US-10-184-635-365 Sequence 365, App
96 1301 100.0 1257 14 US-10-184-637-365 Sequence 365, App
97 1301 100.0 1257 14 US-10-184-646-365 Sequence 365, App
98 1301 100.0 1257 14 US-10-184-647-365 Sequence 365, App
99 1301 100.0 1257 14 US-10-187-594-365 Sequence 365, App
100 1301 100.0 1257 14 US-10-187-594-365 Sequence 365, App
```

## ALIGNMENTS

## RESULT 1

```
US-09-834-759-511
; Sequence 511, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 511
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-511
```

## Alignment Scores:

```
Pred. No.: 1.07e-144 Length: 729
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
```

US-10-063-734-122 (1-243) x US-09-834-759-511 (1-729)

```
QY 1 MetatgProglnglyProAlaIaSerProglnglyAtgAlaLeuLeuLeuLeu 20
DB 1 ATGCGACCCCGAGGCGCGCGCTCCCGAGCGGCTCCGCGGCTCTCTGCTCTG 60
```

```
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProlyGlyValGlnIleAla 40
DB 61 CTGCTGCACTGCGCGCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGCGC 120
QY 41 GlnLeuAtgGlnArGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 121 CAGCTCCCGGCAAGAGGAGGTGTGACCTGTAATATGATATGATCTTCAAGAGGCCAGCA 180
QY 61 GlyValProGlyArGAspGlySerProGlyValAlaAsnValIleProGlyTyrProGlyIle 80
DB 181 GGAGGCGCTGTGTCGAGACGCGCTCGGCGCAATGTTATTCGGGTAACCTGGGATC 240
QY 81 ProGlyArGAspGlyPheLeuGlyGlnIleGlyValGlyCysLeuArGlyUserPheGlnGlu 100
DB 241 CAGGTCGGAGTGAATTCAAAGAGAAAGGGGGAATGTCTGAGGGAACCTTGGAGAG 300
QY 101 SerTyrProAsnTyrIleGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
DB 301 TCTTGACACCACTAACAAGCAGTTCATGAGTTCATTGATTTATGCAATGATCTT 360
QY 121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArGValIleu 140
DB 361 GGGAAATTTGGGAGTGTACATTACAAAGATGCGTTCAAAATAGTCTTAAGAGTTTG 420
QY 141 PheSerGlySerLeuArGLeuLysCysArGAsnAlaCysGlnArGTrpTyrPheThr 160
DB 421 TTCACTGCTACTCTTGGCTTAAATTCAGAAATCATGCTGTGCGCTGTGATTTCA 480
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
DB 481 TTCATGAGCTGATGTTCAGACCTCTCCCATTAAGCTAATATTATTGGACCA 540
QY 181 GlySerProGluMetLeuSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 541 GGAAGCCCTGAAGATTCACAAATTAATATTCATGCACTTCTCTGGAGAGACTT 600
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
DB 601 TGTGAAGAAATTGATGCTGATTTGATGATGATGCTTCTGATGCTGCTGCTGCTGCTGAT 660
QY 221 TyrProLysGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGlnGlu 240
DB 661 TACCCAAAGAGATGCTTACTAGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 241 LeuProLys 243
DB 721 CTACCAAAA 729
```

## RESULT 2

```
US-10-007-805-511
; Sequence 511, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 511
; LENGTH: 729
```

```

: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-007-805-511

Alignment Scores:
Pred. No.: 1,07e-144
Score: 1301.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 13 Gaps: 0

US-10-063-734-122 (1-243) x US-10-007-805-511 (1-729)

QY 1 MetArpProGInGlyProAlaAlaSerProGInaArgLeuArgGlyLeuLeuLeuLeu 20
Db 1 ATCGCAGCCCGAGGGCCCCCGCCCTCCCGCAGCGAGCTCCGGGCGCTCTCTCTCTG 60

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnLeuAla 40
Db 61 CTCTCTGAGCTGCCCGCCCGCCGCTGACAGCGCTCTGAGATCCCAAGGGAGCAAAAGCG 120

QY 41 GlnLeuArgGlnArgGlyValValAlaPheLeuTyrAlaGlyMetCysLeuGInGlyProAla 60
Db 121 CAGCTCCGCGAGGGAGGAGGTGGTGGACCTGTATATGAAATGCTTCAAGGGCCAGCA 180

QY 61 GlyValProGlyYArgApGlySerProGlyAlaAlaValIleProGlyYThrProGlyYLe 80
Db 181 GGAGTGGCTGTGAGACGGAGACCCTGGGGCCAATGTATTCCGGGTACACCTGGGATC 240

QY 81 ProGlyYArgApGlyYPhelyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 241 CCGAGTCCGGATGATTCATCAAGAGAAAGGGGAGATGCTGAGGGAGAAAGCTTTGAGAG 300

QY 101 SetTyrThrProAntTyrLeuGlnCysSerTyrPserSerLeuAntTyrGlyIleAspLeu 120
Db 301 TCTCTGACACCCCACTACAGACAGTGTTCATGAGATTCATGAAATTATGGCATAGACTT 360

QY 121 GlyValIleAlaGluCysThrPheThrIlySMeTArgSerAsnSerAlaLeuArgValLeu 140
Db 361 GGGAAATTCGGAGTGTACATTTCACAAAGATGCCGTCAATATGATGCTCTAAGAGTTTG 420

QY 141 PheSerGlySerLeuArgLeuGlyCysArgAlaAlaCysCysGlnArgTyrTyrPheThr 160
Db 421 TTCAGTGGCTCAGCTTCGGCTAAATTCAGAAATGCAAAATGATGTGCACGCTTGGTATTTACA 480

QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db 481 TTCATGTGACCTGAATGTTTCAGGACCTCTCCCATTTGAAGCTATATATTTATTTGACCA 540

QY 181 GlySerProGluLeuArgSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 541 GGAAGCCCTGAATGAAATTCACAAATTAATATTCATCGCACTTCTCTGTGAAGACTT 600

QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrPvalGlyThrCysSerAsp 220
Db 601 TGTCAGAAAGAAATTTGCTCTGATTTAGGATGTTCATCTGATGCTGGCTGGCACTTGTTCAGAT 660

QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrPpanSerValSerArgIleIleGluGln 240
Db 661 TACCCAAAGAAATGATCTTCTACTGATGAAATTCAGATTCTCGCATCATTAATGGAAGA 720

QY 241 LeuProGlyS 243
Db 721 CTACCAAAA 729

RESULT 3
US-10-076-622-511
: Sequence 511, Application US/10076622
: Publication No. US20030023036A1
: GENERAL INFORMATION:
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Sleath, Paul R.

```

		APPLICANT: Persing, David H.	
		TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	
		TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER	
		FILE REFERENCE: 210121.470C11	
		CURRENT APPLICATION NUMBER: US/10/076,622	
		CURRENT FILING DATE: 2002-02-13	
		NUMBER OF SEQ. ID NOS: 627	
		SOFTWARE: FastSeq for Windows Version 4.0	
		SEQ ID NO 511	
		LENGTH: 729	
		TYPE: DNA	
		ORGANISM: Homo sapiens	
		US-10-076-622-511	
Alignment Scores:			
Pred. No.:		1,076-144	Length: 729
Score:		1301.00	Matches: 243
Percent Similarity:		100.00%	Conservative: 0
Best Local Similarity:		100.00%	Mismatches: 0
Query Match:		100.00%	Indels: 0
DB:		14	Gaps: 0
US-10-063-734-122 (1-243) x US-10-076-622-511 (1-729)			
QY	1	MeTAArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu	20
DB	1	ATGCGAGCCCGAGGCGCCCGCCCTCCCGCAGCGCGCGCGCCCTCCGCTGCTCTG	60
QY	21	LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuLeuProGlyGlyLeuAla	40
DB	61	CTGCTGAGCTGCGCGCGCGCCCTCGAGCGCTCTGAGATCCCGAGGAGCAAAAGCG	120
QY	41	GlnLeuArgGlnArgGluValValAspLeuTyraenglyMetCysLeuGlnGlyProAla	60
DB	121	CAGCTCCGCGAGGAGGAGGTGTGACCTGTATATGAAATGTCTTACAAAGGCGCAGCA	180
QY	61	GlyValProGlyValArgAspGlySerProGlyAlaAlaenValLeuProGlyTyLe	80
DB	181	GGAATGCTGTGTGTGAGACGCGAGCGCCCTGGGCGCAATGTATATCCGAGTACCTGGAGATC	240
QY	81	ProGlyValArgAspGlyPheLeuGlyGlyGlyGlyCysLeuArgGlySerPheGluGlu	100
DB	241	CGAGGTGCGGATGTGATTTCAAAGAGAAAGAGGAGAAATCTCGAGGAGAAAGCTTTGAGGAG	300
QY	101	SetrTPThProAsnTyrlYsgInCysSerTPSerSerLeuAsnTyrglyLeaspLeu	120
DB	301	TCTCGGAGCAACCAACACAGCAAGCTTCATGAGATTCATTGAATTAAGCATAGATCTT	360
QY	121	GlyValLeuAlaGluCysThrPheThrlySmetArgSerAsnSerAlaLeuArgValLeu	140
DB	361	GGGAAATAATGGCGAGGTGATTTCAAAGAGCGCTTCMAATAGTGCTCTMAAGATTG	420
QY	141	PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrrTyPheThr	160
DB	421	TTGAGTGGCTCACTTGCGCTAAAGACAAATGATCTGTCAGCGTGGATTTTCA	480
QY	161	PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlLeuAspGln	180
DB	481	TTCAATGAGACTGCAAGCTTCAGAGACTCTTCCCATGAGATTAATTAATTATTTGACCA	540
QY	181	GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu	200
DB	541	GGAGCGCTGCAATGAAATTCACCAATTAATTCATCCCATCTTCTGTGTGAGAGCACTT	600
QY	201	CysGluGlyTyrlLeuValAlaGlyLeuValAspValAlaIleTPValGlyTyThrCysSerAsp	220
DB	601	TGTGAAGAAATGTGTCTGATTAATGAGATGTGTCTATCTGGATTTGGCATTTGTTCAGAT	660
QY	221	TyProGlySerGlyAspAlaSerThrGlyTyTPAsnSerValSerArgIleIleIleGluGlu	240
DB	661	TACCCAAAAGAGATCTCTTACTGATGTGAAATTCAGTTTCTCCGATCATTAATTGAGAA	720
QY	241	LeuProTyrS 243	

```
Db      721 CTACCAAAA 729
|||||
RESULT 4
US-10-124-805-511
; Sequence 511, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C12
; CURRENT APPLICATION NUMBER: US/10/124,805
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 511
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-511

Alignment Scores:
Pred. No.:      1,07e-144      Length:      729
Score:          1301.00        Matches:      243
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels:      0
DB:             15           Gaps:         0

US-10-063-734-122 (1-243) x US-10-124-805-511 (1-729)
Qy      1 MetArgProGInGlyProAlaAlaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20
Db      1 ATGGACCCCGAGGGGCGCGCGCTCCCGCAGCGCGCTCCGCGCTCTGCTGCTCTG 60
Qy      21 LeuLeuGInLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGInLysAla 40
Db      61 CTGGCTGAGAGTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGCAAAAGGCG 120
Qy      41 GInLeuArgGInArgGluValAlaLeuLeuTyraAnglyMetCysLeuGInLysProAla 60
Db      121 CAGCTCCGCGAGAGGAGGTGTGAGCTGTATATGATGTGCTTACAAAGGCCAGCA 180
Qy      61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db      181 GGAAGTCTGTGTCAGACGGAGGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGATC 240
Qy      81 ProGlyArgAspGlyPheLysGlyGluLysGlyCysLeuArgGlySerPheGInGlu 100
Db      241 CCAGGTGGGATGATTCAAAGAGAAAGGGGAGATGTCTGAGGAAAGCTTTGAGAG 300
Qy      101 SerTrpThrProAsnTyrlLysGInCysSerTrpSerSerLeuAsnTyrlLysLeu 120
Db      301 TCCGGAACACCACTACAGAGAGTTCATGAGATTCATGAATTAATGAGCATAGATCT 360
Qy      121 GlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
Db      361 GGGAAATTCGGAGAGTTCATTTTACAAAGATGCTTCAAAATGAGCTTAAAGATTTTG 420
Qy      141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGInArgTrpThrPheThr 160
Db      421 TTCAAGTGGCTCACTTCGGCTAAATGCAAAATGATCTGTCAAGCTTGGATTTTCA 480
Qy      161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlLeuAspGln 180
Db      481 TTCATGAGAGCTGATGATTCAGAGACCTCTTCCCATGGAAGCATATTAATTTTGAACAA 540
Qy      181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGInGlyLeu 200
Db      541 GAAAGCCTGAAATGAATTCACAACTTAATTAATTCACACTTCTTGTGGAGAGACTT 600
```

```
Qy      201 CysGInGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db      601 TGTGAAGAAATTTGGTGGATGTAGATGTTGCTATCTGGGTGGACCTTGTTCAGAT 660
Qy      221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGInGlu 240
Db      661 TACCCAAAAGAGATGCTTCTACTGATGATGAATTCAGTTCTCGCATCATTAATGAAGAA 720
Qy      241 LeuProLys 243
Db      721 CTACCAAAA 729

RESULT 5
US-09-834-759-510
; Sequence 510, Application US/09834759
; Publication No. US20020085998A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 510
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-510

Alignment Scores:
Pred. No.:      1,07e-144      Length:      732
Score:          1301.00        Matches:      243
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%       Indels:      0
DB:             9           Gaps:         0

US-10-063-734-122 (1-243) x US-09-834-759-510 (1-732)
Qy      1 MetArgProGInGlyProAlaAlaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20
Db      1 ATGGACCCCGAGGGGCGCGCGCTCCCGCAGCGCGCTCCGCGCTCTGCTGCTCTG 60
Qy      21 LeuLeuGInLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGInLysAla 40
Db      61 CTGCTGAGCTGCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGAAAGGCG 120
Qy      41 GInLeuArgGInArgGluValAlaLeuLeuTyraAnglyMetCysLeuGInLysProAla 60
Db      121 CAGCTCCGCGAGAGGAGGTGTGAGCTGTATTAAGAGATGTGCTTACAAAGGCCAGCA 180
Qy      61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db      181 GGAAGTCTGTGTCAGACGGAGGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGATC 240
Qy      81 ProGlyArgAspGlyPheLysGlyGluLysGlyCysLeuArgGlySerPheGInGlu 100
Db      241 CCAGGTGGGATGATTCAAAGAGAAAGGGGAGATGTCTGAGGAAAGCTTTGAGAG 300
Qy      101 SerTrpThrProAsnTyrlLysGInCysSerTrpSerSerLeuAsnTyrlLysLeu 120
Db      301 TCCGGAACACCACTACAGAGAGTTCATGAGATTCATGAATTAATGAGCATAGATCTT 360
Qy      121 GlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
```



```

Db 361 GGGAAATTGGCGAGGTGATCATTTACAAAGATCCGTTCAAAATAGTCTCTAAGATTGG 420
Qy 141 PheSerGlySerLeuArgLeuLysCySarGabaAlaCyCyGlnArgTrpTyrrPheThr 160
Db 421 TTCAGTGGCTCATTCTGGCTAAATGCAAAATGCAATGCTGTCAGCGGTGGATTTCACA 480
Qy 161 PheArgGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrrLeuAspGln 180
Db 481 TTCAAATGGAGCTGAATGTTTCAGAGACTCTCCCATTTGAAGCTATTAATTTATTTGACCA 540
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 541 GGAAGCCCTGGAATGATTCACAAATTATTCATCGACACTTCTGTGGAGAGACTT 600
Qy 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 601 TGTGAAGGATTTGCTGCTGATTAAGTGAATGTTGCTATCTGGCTGGCACTTGTTCAGAT 660
Qy 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 661 TACCCAAAAGAGATCTTCTACTGATGAGATGCAATTCAGTTCTGCAATCATTTATGAAGA 720
Qy 241 LeuProLys 243
Db 721 CTACCAAAA 729

```

## RESULT 6

```

US-10-007-805-510
; Sequence 510, Application US/10007805
; Publication No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C10
; CURRENT APPLICATION NUMBER: US/10/007,805
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 510
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-510

```

## Alignment Scores:

```

Pred. No.: 1.07e-144 Length: 732
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

```

US-10-063-734-122 (1-243) x US-10-007-805-510 (1-732)

```

Qy 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 1 ATGCGAGCCCGAGGCCCCCGCCCTCCCGCAGCGGCTCCGCGCCCTCCGCTGCTCTG 60
Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyGlyGlnValAla 40
Db 61 CTGCTCAGCTGCGCCGCGCTGAGGCGCTCTGAGATCCCAAGGGAAGCAAAAGGCC 120

```

```

Qy 41 GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 121 CAGCTCCGCGCAGAGGAGGTGGTGGACCTGTTATTAATGAAATGTCTTACAGGGCCAGCA 180
Qy 61 GlyAlaProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 181 GGAGTGGCTGGTGCAGAGGGAGGCCCTGGGGCAATGTATTCCGGGTACACCTGGGATC 240
Qy 81 ProGlyArgAspGlyPheLysGlyGluLysGlyGluCysLeuArgGlySerPheGluGlu 100
Db 241 CCAGTCCGGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 101 SerTrpTrpProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
Db 301 TCTTGACACCCCACTACACAGCAGTTCATGAGATTCATTAATTAATTAATTAATTAAT 360
Qy 121 GlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
Db 361 GGGAAATTGGCGAGGTGATCATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTG 420
Qy 141 PheSerGlySerLeuArgLeuLysCySarGabaAlaCyCyGlnArgTrpTyrrPheThr 160
Db 421 TTCAGTGGCTCATTCTGGCTAAATGCAAAATGCAATGATGCTGTACAGCTTGTGATTACA 480
Qy 161 PheArgGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrrLeuAspGln 180
Db 481 TTCAAATGAGCTGAATGTTTCAGAGACTCTCCCATTTGAAGCTATTAATTTATTTGACCA 540
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 541 GGAAGCCCTGGAATGATTCACAAATTATTCATCGACACTTCTGTGGAGAGACTT 600
Qy 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 601 TGTGAAGGATTTGCTGCTGATTAAGTGAATGTTGCTATCTGGCTGGCACTTGTTCAGAT 660
Qy 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 661 TACCCAAAAGAGATCTTCTACTGATGAGATGCAATTCAGTTCTGCAATCATTTATGAAGA 720
Qy 241 LeuProLys 243
Db 721 CTACCAAAA 729

```

## RESULT 7

```

US-10-076-622-510
; Sequence 510, Application US/10076622
; Publication No. US20030023036A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C11
; CURRENT APPLICATION NUMBER: US/10/076,622
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 510
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-076-622-510

```

## Alignment Scores:

```

Pred. No.: 1.07e-144 Length: 732
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

```

```

US-10-063-734-122 (1-243) x US-10-076-622-510 (1-732)
QY      1 MetArpProGlnGlyProAlaIaIaSerProGlnArGluLeuArgGlyLeuLeuLeuLeu 20
      1 ATGCGACCCCAAGGCCCCCGCTCCCGCAGCGGCTCCGCGCTCCGCTGCTGCTCG 60
QY      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyGlyGlnGlnAla 40
      61 CTGCTGACAGCTGCCCCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGGG 120
QY      41 GlnLeuArgGlnArgGlnValValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
      121 CAGCTCCGCGACAGGAGGAGGTGTGACCTGTATTAAGATGCTTACAAAGGCGCAGCA 180
QY      61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
      181 GGAGTGGCTGTGAGACGCGAGCCCTGGGGCCCAAGTTATTCGGGTACACCTGGGATC 240
QY      81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
      241 CCAGGTCCGGATGATTCAAAGAGAAAGGGGAATGTCTGAGGAAAGCTTTGAGGAG 300
QY      101 SerTrpThrProAsnTyrIleGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
      301 TCTTGACACCCCACTACAGCAGGTGTGATGAGATTCATTAATTAATGCAATAGATCTT 360
QY      121 GlyIleIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
      361 GGGAATAATGCGGAGGTATCATTTACAAAGATGCGTTCAATAGTCTTAAAGATTTTG 420
QY      141 PheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTrpTyrPheThr 160
      421 TTCATGTGCTCACTTCGCTGCTAAATGCAAAATGATGCTGTGAGGTGTGATTTACA 480
QY      161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
      481 TTCATGAGCTGATGATGTTCAAGACCTCTTCCCATTTGAAGCTATTAATTTGAGCCAA 540
QY      181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
      541 GGAAGCCTGAATGAATTCACATTAATTAATTCATGCACTTCTTCTGTGAAAGACTT 600
QY      201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
      601 TGTGAAGAAATGTGTGTGATTAAGATGATGATGATGATGATGATGATGATGATGAT 660
QY      221 TyrProGlyGlyAspAlaSerThrGlyTyrPheAsnSerValSerArgIleIleIleGln 240
      661 TACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 720
QY      241 LeuProlys 243
      721 CTACCAAAA 729
Db

```

## RESULT 8

```

US-10-060-036-4556
; Sequence 4556, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060.036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 4556
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-4556

```

## Alignment Scores:

Pred. No.:	1-07e-144	Length:	732
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatch:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-063-734-122 (1-243) x US-10-060-036-4556 (1-732)

```

QY      1 MetArpProGlnGlyProAlaIaIaSerProGlnArGluLeuArgGlyLeuLeuLeuLeu 20
      1 ATGCGACCCCAAGGCCCCCGCTCCCGCAGCGGCTCCGCGCTCCGCTGCTGCTCG 60
Db
QY      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyGlyGlnGlnAla 40
      61 CTGCTGACAGCTGCCCCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAAAGGG 120
Db
QY      41 GlnLeuArgGlnArgGlnValValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
      121 CAGCTCCGCGACAGGAGGAGGTGTGACCTGTATTAAGATGCTTACAAAGGCGCAGCA 180
Db
QY      61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
      181 GGAGTGGCTGTGAGACGCGAGCCCTGGGGCCCAAGTTATTCGGGTACACCTGGGATC 240
QY      81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
      241 CCAGGTCCGGATGATTCAAAGAGAAAGGGGAATGTCTGAGGAAAGCTTTGAGGAG 300
Db
QY      101 SerTrpThrProAsnTyrIleGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
      301 TCTTGACACCCCACTACAGCAGGTGTGATGAGATTCATTAATTAATGCAATAGATCTT 360
Db
QY      121 GlyIleIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
      361 GGGAATAATGCGGAGGTATCATTTACAAAGATGCGTTCAATAGTCTTAAAGATTTTG 420
QY      141 PheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTrpTyrPheThr 160
      421 TTCATGTGCTCACTTCGCTGCTAAATGCAAAATGATGCTGTGAGGTGTGATTTACA 480
Db
QY      161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180
      481 TTCATGAGCTGATGATGTTCAAGACCTCTTCCCATTTGAAGCTATTAATTTGAGCCAA 540
QY      181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
      541 GGAAGCCTGAATGAATTCACATTAATTAATTCATGCACTTCTTCTGTGAAAGACTT 600
Db
QY      201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
      601 TGTGAAGAAATGTGTGTGATTAAGATGATGATGATGATGATGATGATGATGATGAT 660
QY      221 TyrProGlyGlyAspAlaSerThrGlyTyrPheAsnSerValSerArgIleIleIleGln 240
      661 TACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 720
Db
QY      241 LeuProlys 243
      721 CTACCAAAA 729
Db

```

## RESULT 9

```

US-10-124-805-510
; Sequence 510, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:

```

APPLICANT: Houghton, Raymond L.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Piersing, David H.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.470C12  
CURRENT APPLICATION NUMBER: US/10/124, 805  
CURRENT FILING DATE: 2002-04-15  
NUMBER OF SEQ ID NOS: 627  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 510  
LENGTH: 732  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-124-805-510

Alignment Scores:  
Pred. No.: 1,07e-144 Length: 732  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-063-734-122 (1-243) x US-10-124-805-510 (1-732)

QY 1 MetArgProGlnGlyProAlaIAserProGlnArgLeuArgGlyLeuLeuLeuLeu 20  
DB 1 ATGCGACCCCGAGGGCCCGCCGCTCCGCGACGGCTCCGCGCTCCGCTGCTCCG

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyLeuGln 40  
DB 61 CTGCTGACAGTCCGCGCCGCGCTGACGCTGACGCTGACGCTGACGCTGACGCTG

QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyraGlyMetCysLeuGlnGlyProAla 60  
DB 121 CAGCTCCGCGAGGAGGTGTGAGCTGTATATGAAATGTGCTTACAGGGCCAGCA 180

QY 61 GlyValProGlnArgArgGlySerProGlnAlaAsnValIleProGlyThrProGlyIle 80  
DB 181 GGGATCCCTGCTGACACGGGACCTGGGGCCAAATGTTATCCGGGTACACCTGGGATC 240

QY 81 ProGlnArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
DB 241 CCGAGTCCGGATGATTCAGAGCAAGAAAGGGAATGTGAGGAAAGCTTGGAGAG 300

QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120  
DB 301 TCCTGACACCCCAATCAAGAGTGTATGAGTTCAATTAATGATGATGATGATGAT 360

QY 121 GlyValIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140  
DB 361 GGGAAATTCGGAGGTGATCAATTAAGATGCTCAATATGCTCTCAAGAGTTTGG 420

QY 141 PheSerGlnSerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpPheThr 160  
DB 421 TTGAGGTGCTCACTGCTGAAATGCAAGATGCAAGTGTGAGGTGAGTTTCAACA 480

QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrlsLeuAspGln 180  
DB 481 TTCAATGAGAGCTGAATGTTCAAGACCTCTCCCATTTGAAGCTATATTTATTTGAACCA 540

QY 181 GlySerProGlnLysCysAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200  
DB 541 GGAAGCCCTGAATGATTCACAAATTAATTCATGCACTTCTGAGGAAAGACCTT 600

QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220  
DB 601 TGTGAAGAAATGCTGCTGATTAAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTG 660

QY 221 TyrlsProGlyAlaAspAlaSerThrGlyTyrlsAsnSerValSerArgIleIleIleGlnGln 240  
DB 661 TACCAAAAGAGATGCTTCTACTGATGAGATTCAGTTTCTGCAATCATTAATTTGAAGA 720

QY 241 LeuProLys 243  
DB 721 CTACCAAAA 729

RESULT 10  
US-09-834-759-512  
Sequence 512, Application US/09834759  
Publication No. US2002008598A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yugu  
APPLICANT: Dillon, David C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jianshun  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.470C9  
CURRENT APPLICATION NUMBER: US/09/834,759  
CURRENT FILING DATE: 2001-04-13  
NUMBER OF SEQ ID NOS: 547  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 512  
LENGTH: 837  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-834-759-512

Alignment Scores:  
Pred. No.: 1,28e-144 Length: 837  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-063-734-122 (1-243) x US-09-834-759-512 (1-837)

QY 1 MetArgProGlnGlyProAlaIAserProGlnArgLeuArgGlyLeuLeuLeuLeu 20  
DB 106 ATGCGACCCCGAGGGCCCGCCGCTCCGCGACGGCTCCGCGCTCCGCTGCTCCG

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProGlyGlyLeuGln 40  
DB 166 CTGCTGACAGTCCGCGCCGCGCTGACGCTGACGCTGACGCTGACGCTGACGCTG

QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyraGlyMetCysLeuGlnGlyProAla 60  
DB 226 CAGCTCCGCGAGGAGGTGTGAGCTGTATATGAAATGTGCTTACAGGGCCAGCA 285

QY 61 GlyValProGlnArgAspGlySerProGlnAlaAsnValIleProGlyThrProGlyIle 80  
DB 286 GGAATCCCTGCTGACACGGGACCTGGGGCCAAATGTTATCCGGGTACACCTGGGATC 345

QY 81 ProGlnArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
DB 346 CCGAGTCCGGATGATTCAGAGCAAGAAAGGGAATGTGAGGAAAGCTTGGAGAG 405

QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120  
DB 406 TCCTGACACCCCAATCAAGAGTGTATGAGTTCAATTAATGATGATGATGATGAT 465

QY 121 GlyValIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140  
DB 466 GGAAGAAATTCGGAGGTGATCAATTAAGATGCTCAATATGCTCTCAAGAGTTTGG 525

QY 141 PheSerGlnSerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpPheThr 160  
DB 526 TTCAAGGTGCTCACTGCTGAAATGCAAGATGCAAGTGTGAGGTGAGTTTCAACA 585

QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrlsLeuAspGln 180

Db 586 TTCATGGAGCTGAATGTTACAGACCTCTCCCATGGAAGCTATTAATTATTGGACCAA 645  
Qy 181 GYSerProGluMetLaserThrIleAsnIleHisArgThSerSerValGluGluLeu 200  
Db 646 GGAAGCCCTGAATGATTAATCAACAAATTAATTCATCGACCTCTCTGGGAAGACTT 705  
Qy 201 CysGluGlyIleGlyValaGlyLeuValaAspValaIleTyrValaGlyThrCysSerAsp 220  
Db 706 TGTGAAGGAATTGGTGTGCTGATTAAGCATGTTGCTATCTGGTGGCACTTGTTCAGAT 765  
Qy 221 TyrProLysGlyAspAlaSerThrGlyTyrPasnSerValSerArgIleIleIleGluGlu 240  
Db 766 TACCAAAAAGAGATGCTTCTACTGATGAAATTCAGTTTCTGCATCATTAATTAAGAA 825  
Qy 241 LeuProLys 243  
Db 826 CTACCAAAA 834  
RESULT 11  
US-09-834-759-513  
; Sequence 513, Application US/09834759  
; Publication No. US20020085998A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C9  
; CURRENT APPLICATION NUMBER: US/09/834,759  
; CURRENT FILING DATE: 2001-04-13  
; NUMBER OF SEQ ID NOS: 547  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 513  
; LENGTH: 837  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-834-759-513  
Alignment Scores:  
Pred. No.: 1,28e-144 Length: 837  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-10-063-734-122 (1-243) x US-09-834-759-513 (1-837)  
Qy 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20  
Db 106 ATGGAGCCCGAGGGGCGCGCCGCTCCCGCAGCGCTCCCGGGCGCTCTGCTGCTCTG 165  
Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnLysAla 40  
Db 166 CTGCTGCAAGCTGCCCGCCCGCTCGAGCCGCTCTGAGATCCCAAGGGAGCAAAAGGCG 225  
Qy 41 GlnLeuArgGlnArgGlyValaValaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60  
Db 226 CAGCTCCGGCAGAGGAGAGGTGTGAGCTGTATATGAGATGTGCTTCAAGGGGCACACA 285  
Qy 61 GlyValProGlyArgAspGlySerProGlyValaAsnValIleProGlyThrProGlyIle 80  
Db 286 GGAATGCTGCTGTGAGACGAGGAGCCCTGGGCGCAATGTATTCCCGGTACACCTGGGATC 345  
Qy 81 ProGlyArgAspGlyPheLysGlyGlyLysGlyGlyCysLeuArgGluSerPheGlnGlu 100  
Db 346 CCAAGTGGGAGTGAATTCAAAGAGAAAGGGGAGATGTCTGAGGAGAAAGCTTTGAGGAG 405

Qy 101 SerTyrThrProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120  
Db 406 TCTTGACACCCCACTACAGACAGTGTTCATGAGGATTCATTGAATTTGACATAGACTT 465  
Qy 121 GlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140  
Db 466 GGGAAATTTGGGAGTGTACATTTCAAAGATGCGCTTCAATATGCTCTTAAGATTTTG 525  
Qy 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160  
Db 526 TTCAGTGTCTACCTCGGCTAAATGCAAGAAATCAGCTGTGCGCTGTGATTTTCACA 585  
Qy 161 PheAsnGlyValaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180  
Db 586 TTCATGGAGCTGAATGTTCAAGACCTCTTCCCATTAAGCTATTAATTTTGGACCAA 645  
Qy 181 GYSerProGluMetLaserThrIleAsnIleHisArgThSerSerValGluGlyLeu 200  
Db 646 GGAAGCCCTGAATGATTAATCAACAAATTAATTCATCGCACTTCTGTGGAAGACTT 705  
Qy 201 CysGluGlyIleGlyValaGlyLeuValaAspValaIleTyrValaGlyThrCysSerAsp 220  
Db 706 TGTGAAGGAATTGGTGTGCTGATTAAGCATGTTGCTATCTGGTGGCACTTGTTCAGAT 765  
Qy 221 TyrProLysGlyAspAlaSerThrGlyTyrPasnSerValSerArgIleIleIleGluGlu 240  
Db 766 TACCAAAAAGAGATGCTTCTACTGATGAAATTCAGTTTCTGCATCATTAATTAAGAA 825  
Qy 241 LeuProLys 243  
Db 826 CTACCAAAA 834  
RESULT 12  
US-10-007-805-512  
; Sequence 512, Application US/10007805  
; Publication No. US20020150581A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Vedrick, Thomas S.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Durham, Margalita  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.470C10  
; CURRENT APPLICATION NUMBER: US/10/007,805  
; CURRENT FILING DATE: 2001-12-07  
; NUMBER OF SEQ ID NOS: 593  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 512  
; LENGTH: 837  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-007-805-512  
Alignment Scores:  
Pred. No.: 1,28e-144 Length: 837  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-10-063-734-122 (1-243) x US-10-007-805-512 (1-837)  
Qy 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20

```

Db      106 ATGCGACCCAGAGGCCCGCCGCTCCCGCAGCGGCTCCGCGCTCCGCTCCTG 165
Qy      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProlysglylysglnlysa1a 40
Db      166 CTGCTGCACACTGCGCCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAGCAAGGGCG 225
Qy      41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGluMetCysLeuGlnGlyProAla 60
Db      226 CAGCTCCGGGAGAGGAGGTGTGACCTGTATATGAAATGTGCTTACAGGGCCAGCA 285
Qy      61 G1yValProG1yArgAspG1ySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
Db      286 GAGAGTCCCTGCTGAGACCGGAGCCCTGGGGCCAATGTTATTCGGGTACACTGGGATC 345
Qy      81 ProG1yArgAspG1yPheIySg1yGlyGlyGlyGluCysLeuArgGluSerPheGluGlu 100
Db      346 CCAGGTCCGGATGATTCAAAGAGAAAGGGGGAATGTCTGAGGAAAGCTTGTAGAGAG 405
Qy      101 SerTrpThrProAsnTyrIySg1yCysSerTrpSerSerLeuAsnTyrG1yIleAspLeu 120
Db      406 TCTTGACACCCCACTACAGACAGTGTTCATGAGATTGATTAATGACATAGATCTT 465
Qy      121 G1yIyS11eAlaGluCysThrPheThrIySmetArgSerAsnSerAlaLeuArgValIleu 140
Db      466 GGGAAATTTGGGAGTGTACATTTACAAAGATCGCTTCAAAATGCTCTAAGAGTTTGG 525
Qy      141 PheSerG1ySerLeuArgLeuIySArgAsnAlaCysG1yGlnArgTyrPheThr 160
Db      526 TTCAGTGGCTCACTTGGCTTAAATGCAAAATGCAATGCTGTCAGCGTGTGTATTTCA 585
Qy      161 PheAsnG1yAlaGluCysSerG1yProIleuProIleGluAlaIleIleTyrLeuAspGln 180
Db      586 TTCAAATGAGCTGAATGTTCAAGACCTCTTCCATGAGCAATTAATTTATTTGAGCAA 645
Qy      181 G1ySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValG1yGlyLeu 200
Db      646 GGAAGCCCTGGAATGATTCACAAATTAATTAATTCATCGACCTTCTGTGGAAGACTT 705
Qy      201 CysGluG1yIleG1yAlaGlyLeuValAspValAlaIleTrpValG1yThrCysSerAsp 220
Db      706 TGTGAAGGAATGTGCTGCTGATTAAGTGTGATGTTGCTATCTGCGCTTGTCAAGAT 765
Qy      221 TyrProIyG1yAspAlaSerThrG1yTrpAsnSerValSerArgIleIleIleGluGlu 240
Db      766 TACCCAAAAGGAATGCTTCTACTGATGAGATTCAGTTTCTGCATCATTTATTAAGA 825
Qy      241 LeuProIyS 243
Db      826 CTACCAAAA 834

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-513

Alignment Scores:
pred. No.:      1,286-144      Length:      837
Score:          1301.00      Matches:      243
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              13          Gaps:          0

US-10-063-734-122 (1-243) x US-10-007-805-513 (1-837)
Qy      1 MetArgProGlnGlyProAlaAspProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db      106 ATGCGACCCAGAGGCCCGCCGCTCCCGCAGCGGCTCCGCGCTCCGCTCCTG 165
Qy      21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProlysglylysglnlysa1a 40
Db      166 CTGCTGCACACTGCGCCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAGCAAGGGCG 225
Qy      41 GlnLeuArgGlnArgGlnValValAspLeuTyrAsnGluMetCysLeuGlnGlyProAla 60
Db      226 CAGCTCCGGGAGAGGAGGTGTGACCTGTATATGAAATGTGCTTACAGGGCCAGCA 285
Qy      61 G1yValProG1yArgAspG1ySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
Db      286 GAGAGTCCCTGCTGAGACCGGAGCCCTGGGGCCAATGTTATTCGGGTACACTGGGATC 345
Qy      81 ProG1yArgAspG1yPheIySg1yGlyGlyGlyGluCysLeuArgGluSerPheGluGlu 100
Db      346 CCAGGTCCGGATGATTCAAAGAGAAAGGGGGAATGTCTGAGGAAAGCTTGTAGAGAG 405
Qy      101 SerTrpThrProAsnTyrIySg1yCysSerTrpSerSerLeuAsnTyrG1yIleAspLeu 120
Db      406 TCTTGACACCCCACTACAGACAGTGTTCATGAGATTGATTAATGACATAGATCTT 465
Qy      121 G1yIyS11eAlaGluCysThrPheThrIySmetArgSerAsnSerAlaLeuArgValIleu 140
Db      466 GGGAAATTTGGGAGTGTACATTTACAAAGATCGCTTCAAAATGCTCTAAGAGTTTGG 525
Qy      141 PheSerG1ySerLeuArgLeuIySArgAsnAlaCysG1yGlnArgTyrPheThr 160
Db      526 TTCAGTGGCTCACTTGGCTTAAATGCAAAATGCAATGCTGTCAGCGTGTGTATTTCA 585
Qy      161 PheAsnG1yAlaGluCysSerG1yProIleuProIleGluAlaIleIleTyrLeuAspGln 180
Db      586 TTCAAATGAGCTGAATGTTCAAGACCTCTTCCATGAGCAATTAATTTATTTGAGCAA 645
Qy      181 G1ySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValG1yGlyLeu 200
Db      646 GGAAGCCCTGGAATGATTCACAAATTAATTAATTCATCGACCTTCTGTGGAAGACTT 705
Qy      201 CysGluG1yIleG1yAlaGlyLeuValAspValAlaIleTrpValG1yThrCysSerAsp 220
Db      706 TGTGAAGGAATGTGCTGCTGATTAAGTGTGATGTTGCTATCTGCGCTTGTCAAGAT 765
Qy      221 TyrProIyG1yAspAlaSerThrG1yTrpAsnSerValSerArgIleIleIleGluGlu 240
Db      766 TACCCAAAAGGAATGCTTCTACTGATGAGATTCAGTTTCTGCATCATTTATTAAGA 825
Qy      241 LeuProIyS 243
Db      826 CTACCAAAA 834

RESULT 14
US-10-076-622-512
; Sequence 512, Application US/1007622
; Publication No. US20030023036A1

```

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/ GENERAL INFORMATION:
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Sleath, Paul R.
/ APPLICANT: Persing, David H.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ AND DIAGNOSIS OF BREAST CANCER
/ FILE REFERENCE: 210121.470C11
/ CURRENT APPLICATION NUMBER: US/10/076,622
/ CURRENT FILING DATE: 2002-02-13
/ NUMBER OF SEQ ID NOS: 627
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 512
/ LENGTH: 837
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-076-622-512

Alignment Scores:
Pred. No.: 1,28e-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-076-622-512 (1-837)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 106 ATGGACCCCAAGGCGCCGCCCTCCCGACGCGCTCCGCGCTCTGCTCTCTG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnGlyAla 40
DB 166 CTGCTGCAGCTGCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAACAAAGCGG 225
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyraSnglMecCysLeuGlnGlyProAla 60
DB 226 CAGCTCCGGCAGAGGAGGTGTGACCTGTATTAATGATGTCTTACAAAGGCCAGCA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 286 GAGAGCTGCTGTCAGACGCGAGCCCTGGGCCAATGTTATTCGGGTACACTGGGATC 345
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 346 CCAAGTCCGGAGTGTCAAAAGAGAAAGGGGGAATGTCTGAGGAAAGCTTTGAGGAG 405
QY 101 SerTrpThrProAsnTyrllysGlnCysSerTrpSerSerLeuAsnTyrllysLeu 120
DB 406 TCCCTGGACACCACTACAGACAGTGTTCATGAGTTCAATTAATTAAGCATAGATCTT 465
QY 121 GlyIysIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 466 GGGAAATTTGGCGAGTGTACATTTTCAAAAGATGCTTCAATATGCTTAAAGACTTTTG 525
QY 141 PheSerGlySerLeuArgLeuIlyCysArgAsnAlaCysCysGlnArgTrpThr 160
DB 526 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGATGCTGCACGTTGGATTTTCA 585
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrllysAspGln 180
DB 586 TTCAATGAGAGCTGAATGTTCAAGACCTCTCCCATTTGAAGCATTAATTAATTTTGAACCA 645
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 646 GGAAGCCCTGAAGATTCACAAATTAATTAATTCACACTTCTTCTGGAAGAGACTT 705
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 706 TGTAAAGAAATTTGTGTGATGTAGTGATGTGTCTATCTGGGTGGCACTTGTTCAGAT 765
QY 221 TyrProIysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGly 240
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DB 766 TACCAAAAGAGATGCTTCTACTGATGATGATTAATCACTTCTGCGATCATTAATGAAGA 825
QY 241 LeuProIys 243
DB 826 CTACCAAAA 834

RESULT 15
US-10-076-622-513
/ Sequence 513, Application US/10076622
/ Publication No. US20030023036A1
/ GENERAL INFORMATION:
/ APPLICANT: Houghton, Raymond L.
/ APPLICANT: Sleath, Paul R.
/ APPLICANT: Persing, David H.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ AND DIAGNOSIS OF BREAST CANCER
/ FILE REFERENCE: 210121.470C11
/ CURRENT APPLICATION NUMBER: US/10/076,622
/ CURRENT FILING DATE: 2002-02-13
/ NUMBER OF SEQ ID NOS: 627
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 513
/ LENGTH: 837
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-076-622-513

Alignment Scores:
Pred. No.: 1,28e-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-076-622-513 (1-837)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 106 ATGGACCCCAAGGCGCCGCCCTCCCGACGCGCTCCGCGCTCTGCTCTCTG 165
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnGlyAla 40
DB 166 CTGCTGCAGCTGCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAACAAAGCGG 225
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyraSnglMecCysLeuGlnGlyProAla 60
DB 226 CAGCTCCGGCAGAGGAGGTGTGACCTGTATTAATGATGTCTTACAAAGGCCAGCA 285
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 286 GAGAGCTGCTGTCAGACGCGAGCCCTGGGCCAATGTTATTCGGGTACACTGGGATC 345
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 346 CCAAGTCCGGAGTGTCAAAAGAGAAAGGGGGAATGTCTGAGGAAAGCTTTGAGGAG 405
QY 101 SerTrpThrProAsnTyrllysGlnCysSerTrpSerSerLeuAsnTyrllysLeu 120
DB 406 TCCCTGGACACCACTACAGACAGTGTTCATGAGTTCAATTAATTAAGCATAGATCTT 465
QY 121 GlyIysIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 466 GGGAAATTTGGCGAGTGTACATTTTCAAAAGATGCTTCAATATGCTTAAAGACTTTTG 525
QY 141 PheSerGlySerLeuArgLeuIlyCysArgAsnAlaCysCysGlnArgTrpThr 160
DB 526 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGATGCTGCACGTTGGATTTTCA 585
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrllysAspGln 180
DB 586 TTCAATGAGAGCTGAATGTTCAAGACCTCTCCCATTTGAAGCATTAATTAATTTTGAACCA 645
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QY	181	GlySerProGluMeAsnSerThrIleAsnIleHisArgThrSerSerValGluGlu	200
Db	646	GGAAACCCCTGAAATGATTAATCAACAAATTAAATTCATCGACCTTCCTGGGAAGGACTT	705
QY	201	CysGluGlyIleGlyValAglyLeuValAspValAlaIleTrpValGlyThrCysSerAsp	220
Db	706	TGTGAAGGAATTGGTGCTGTGATTAGTGAGATGTTGCTATCTGGGTTGGCACTTGTCAAGT	765
QY	221	TyrProPolysGlyAspAlaSerThrGlyTrpPaenSerValSerArgIleIleIleGlu	240
Db	766	TACCCAAAGAGAGATGCTTCTACTGATGGAATTACGTTCTTCGATCATATTGAAGAA	825
QY	241	LeuProLys	243
Db	826	CTACCAAAA	834
RESULT 16			
US-10-060-036-4557			
Sequence 4557, Application US/10060036			
Publication No. US20030073144A1			
GENERAL INFORMATION:			
APPLICANT: Benson, Darin R.			
APPLICANT: Kalos, Michael D.			
APPLICANT: Lodes, Michael J.			
APPLICANT: Persing, David H.			
APPLICANT: Hepler, William T.			
APPLICANT: Jiang, Yugu			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER			
FILE REFERENCE: 210121.566			
CURRENT APPLICATION NUMBER: US/10/060,036			
CURRENT FILING DATE: 2002-01-30			
NUMBER OF SEQ ID NOS: 4560			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 4557			
LENGTH: 837			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-10-060-036-4557			
Alignment Scores:			
Pred. No.: 1,286-144			
Score: 1301.00			
Percent Similarity: 100.00%			
Best Local Similarity: 100.00%			
Query Match: 100.00%			
DB: 14			
Gaps: 0			
US-10-063-734-122 (1-243) x US-10-060-036-4557 (1-837)			
QY	1	MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu	20
Db	106	ATGCGACCCCGAGGGCCCGCCGCTCCCGCGAGGGCTCCGGCCTCCTGCTCTCTG	155
QY	21	LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlyVala	40
Db	166	CTGCTGCGAGCTCCCGCGCCGTCGAGCGCCTCGAGATCCCAAGGGGAAAGGCG	225
QY	41	GlnLeuArgGlnArgGluValValaLeuLysTrpArgGlyMetCysLeuGlnGlyProAla	60
Db	226	CAGCTCCCGCAAGAGGAGGTGTGTGACCTGTATTAAGTAATGTGCTTACCAAGGCGCAGCA	285
QY	61	GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle	80
Db	286	GGAGTGCTGTGTGCGAGACCGGAGCCCTGGGGCCAACTTATTTCCGGGTACCTGGGATC	345
QY	81	ProGlyArgAspGlyPheLysGlyLysGlyLysGlyLysCysLeuArgGlnSerPheGlu	100
Db	346	CCAGTGCGGAGTGGATTCAAGAGGAAAGGGGGGAGATGTCTGAGGAAAGCTTGAAGAG	405
QY	101	SerTrpThrProAsnTrpLysGlnCysSerTrpSerSerLeuAsnTrpGlyIleAspLeu	120
Db	406	TCCTGGACACCCCACTACAGCAGGTGTTCATGTGAGTTCAATTATGTGCATATGATCTT	465

Qy	121	GLYVSLILALAGLNCYethrPheThrlysmcArGserAenserrAlaLeuArVall	149
Db	466	GGAAATAATGGCGAGTGAATTATTCAAAGATGCTTAATAGTCTTAAGATT	522
Qy	141	PheSerGIYserLeuArGleuLysCYsArGAsnAlaCYsCYsGIArGTrPyrPheThr	160
Db	526	TTCAAGTGGCTCACTTCGCTTAATAATGCAAAATGATGCTGTCAAGCTGGTATTTC	585
Qy	161	PheAsnGIYAlaGluCYsSerGIYProLeuPOLLegualAlaIleIleYrLeuAspGln	180
Db	586	TTCAATGGAGCTGAATGTTACAGACCTCTCCATTGAAGCTAATATTATTATTCAGCAA	645
Qy	181	GIYSerProGluwerAmsSerThrIleAsnIleHsaGTrHsSerSerValGluGIYLeu	200
Db	646	GGAAAGCCCTGAATGATTAATTCACAAATTAAATTATTCACACTTCTTCTGTGAAAGCA	705
Qy	201	CysGluGIYIleGIYAlaGluLeuValAspValAlaIleIleIleIleIleGIYThrCYsSerAsp	220
Db	706	TGTGAAGGAATTGGTGTGCTGATTTAGTGAATGTGTCTACTGGTTGGCACTGTTCAGAT	765
Qy	221	TyrProLysGIYAspAlaSerThrGIYTrpAsnSerValSerArGIIleIleIleGluGlu	240
Db	766	TACCCAAAGAGATGCTCTTACTGATGGAATTCAGTTCTCCATCATATTATTAAGAA	825
Qy	241	LeuProLys 243	
Db	826	CTACCAAAA 834	
RESULT 17			
US-10-124-805-512			
; Sequence 512, Application US/10124805			
; Publication No. US20030166022A1			
; GENERAL INFORMATION:			
; APPLICANT: Houghton, Raymond L.			
; APPLICANT: Sleach, Paul R.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER			
; FILE REFERENCE: 210121.470C12			
; CURRENT APPLICATION NUMBER: US/10/124,805			
; CURRENT FILING DATE: 2002-04-15			
; NUMBER OF SEQ ID NOS: 627			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 512			
; LENGTH: 837			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-124-805-512			
Alignment Scores:			
Pred. No.:	1,28e-144	Length:	837
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0
US-10-063-734-122 (1-243) x US-10-124-805-512 (1-837)			
Qy	1	MeArPProGInGInYProAlaAlaSerProGInArGLeuArGInYLeuLeuLeuLeu	20
Db	106	ATGGAGCCCAAGGAGCCCGCCGCTCCCGACAGCGGCTCCGCGGCGTCTGCTCTCTG	165
Qy	21	LeuLeuGInLeuProAlaProSerSerAlaSerGIYIleProLysGIYVbGInLysAla	40
Db	166	CTGCTGAGCTGCCCGCCGCGCTGAGCGCTTGAGATCCCAAGGGAGCAAAAGCGC	225
Qy	41	GIYLeuArGInArGInGIYValValAspLeuYrArAsnGIYMetCYsLeuGInGIYProAla	60
Db	226	CAGCTCCGCGAGGGAGAGTGTGACCTGTATATGAAATGTCTTTCMAAGGCCACGCA	285
Qy	61	GIYValProGIYArGAspGIYSerProGIYAlaAsnValIleProGIYThrProGIYIle	80

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Db      286  GGAGTGCCTGTCGACAGCGGAGCCTCGGGGCCAATGTTATTCGGGTACACTGGGATC
QY      81  ProGlyArgAspGlyPheIysGlyIuIysGlyGlyIuCyIeuAArgIuSerPheGluGlu
Db      346  CCAAGTCGGGATGATTCATTCAAAGAGAAAGAGGGGAAAGTCTGGAGGAAACCTTGGAGAG
QY      101  SerTyrThrProAsnTyrIuSGInCySerTyrSerSerLeuAsnTyrGlyIleAspLeu
Db      406  TCCTGGACACCCCAACTACAGACAGTGTTCATGAGTTCAATTGATTTATGGCATAGATCTT
QY      121  GlyIysIleAlaIuGlySerThrPheThrIysMetArgSerAsnSerAlaIeuArgValIeu
Db      466  GGGAAAAATTGGCGAGAGTGTCATTACAAAGATCGCTTCAATATGTGCTCTAAAGATTTCG
QY      141  PheSerGlySerLeuArgLeuIuIysCyArgAsnAlaCySerGlyIuArgTyrPheThr
Db      526  TTCAGTGCCTCACTTGCGCTTAATATGCAAGATGCAAGATGCAAGTCTGACAGGTGGATATTCACA
QY      161  PheAsnGlyAlaIuGlyCySerSerGlyProLeuProIleGluAlaIleIleTyrIleAspGln
Db      586  TTCAAAGGAGACTGAATGTTGACAGACCTCTCCCATTTGAAGCTAATATTATTTGGACCAA
QY      181  GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyIeu
Db      646  GGAAGCCCTGAATTAATTAATTCAAATTAATTAATTCATGCACTTCTCTGGGAAGACATT
QY      201  CySGluGlyIleGlyAlaGlyIeuValAspValAlaIleTyrValGlyThrCySerAsp
Db      706  TGTGAAGGAATGTGCTGCTGGATTAGTGAATGTTGCTATCTGGGTGGCACTTGTTCAGAT
QY      221  TyrProIysGlyAspAlaSerThrGlyTyrPheSerValSerArgIleIleIleGluGlu
Db      766  TACCCAAAAGAGATCTTCTACTGATGATGAATTCAGTTCTTCGCAATCATTAATTGAAGAA
QY      241  LeuProIys 243
Db      826  CTACCAAAA 834

RESULT 18
US-10-124-805-513
; Sequence 513, Application US/10124805
; Publication No. US20030166022A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleach, Paul R.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470612
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-124-805-513

Alignment Scores:
Pred. No.: 1,286-144 Length: 837
Score: 1301.00 Matches: 243
Percent Similarity: 100.00%
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-063-734-122 (1-243) x US-10-124-805-513 (1-837)
QY      1  MetaArgProGlnGlyProAlaIaSerProGlnArgLeuArgGlyIuLeuLeuLeuLeu
Db      106  ATGGACACCCCAAGGCCCGCGCTCTCCCGCAGCGGCTCCGGGGCTCTGCTGCTCTG

```

QY	21	LeuLeuGluLeuProAlaProSerSerAlaSerGluIleProIleGlyLeuGluIleVala	4
Db	166	CTGGCTGACGCTGCCCGGCCGTGAGGCGCTTGATCCCAAGGAGGAGCAAAAGCCG	22
QY	41	GluIleuArgGlnArgGluValaIleAlaPleuTyTAsnGlyMetCysLeuGlnGlyProAla	60
Db	226	CAGCTCCGGCAGAGGAGGAGGTGGACCTGTATAAAGGAATGTCTTACAAAGGGCACCA	28
QY	61	GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyTThrProGlyIle	80
Db	286	GGAGTGCCTGGTGGAGACGGGAGCCCTGGGGCCAAATGTTATTCGGGATACACTGGATC	34
QY	81	ProGlyArgAspGlyPheIleGlyGlyIleGlyCysLeuArgGluSerPheGlu	100
Db	346	CCAGGTGGGATGATTCAAAGAGAAAAGGGGGAATGTCTGAGGAAAAGCTTTGAGGAG	40
QY	101	SerTrpThrProAsnTyrluysGlnCysSerTPSerSerLeuAsnTyrluysAspLeu	120
Db	406	TCTCGGACACCCAACTACAGACGTTCTATGGAGTTCAATGAATTAATGATGATCTT	46
QY	121	GlyIleValIleAlaGluCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu	140
Db	466	GGGAAAATTCGGGAGTGTACATTTACAAAGATGCTTCAATAATAGCTCTTAAGATTTCG	52
QY	141	PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTrpTyPheThr	160
Db	526	TTCACTGGCTCACTTCGGCTAAATCAAAATGCAATGCTGACGCTGGATTTTCA	58
QY	161	PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyLeuAspGln	180
Db	586	TTCAATGAGACTGAATGTTACAGACCTTCCCATTTGAAGCTAATATTATTGGACAA	64
QY	181	GlySerProGluMetLeuSerThrIleAsnIleHisArgTrpSerSerValGluGlyLeu	200
Db	646	GGAAGCCCTAAATGATTCACAAATTAATATTCATCGACTCTTCGTGGAAAGACTT	70
QY	201	CysGluGlyIleGlyAlaGlyLeuValaIleAlaIleIleProValGlyThrCysSerAsp	220
Db	706	TGTGAAGAAATGTGTCTGGATTAAGATGTTGTGTATCTGGTTGGCACTTGTCAGAT	76
QY	221	TyrProIleGlyAspAlaSerThrGlyTTPAsnSerValSerArgIleIleGluGlu	240
Db	766	TACCAAAAGAAATCTTCTTCACTGATGGAATTCAGTTCTCGCATCATTAATGAAGAA	82
QY	241	LeuProIleys 243	
Db	826	CTACCAAAA 834	
RESULT 19			
US-09-938-418-2			
Sequence 2, Application US/09938418			
Patent No. US20020161199A1			
GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi J.			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul			
APPLICANT: Garney, Austin L.			
APPLICANT: Polakis, Paul			
APPLICANT: Williams, P. Mickey			
APPLICANT: Wood, William I.			
APPLICANT: Wu, Thomas D.			
APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND			
TREATMENT OF TUMOR			
FILE REFERENCE: P5009R1			
CURRENT APPLICATION NUMBER: US/09/938,418			
CURRENT FILING DATE: 2001-08-23			
PRIOR APPLICATION NUMBER: 60/081,071			
PRIOR FILING DATE: 1998-04-07			
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; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 10
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; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-938-418-2

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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Db 198 CTGCTCAGCTGCGCCGCGCGCTGAGCGGCTTGAAGTCCCAAGGGAAGCAAGGCG 257
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Db 258 CAGCTCCGCGAGGAGGAGGTGTGACCTGTATTAATGGAATGTCTTACAAAGGCCAGCA 317
QY 61 GlyValProGlyArgSerGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GAGGTCCCTGCTGCAACGGGACCTCTGGGGCCAAATGTTTCTCGGGTACACCTGGGATC 377
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QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160
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QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db 618 TTCATGAGCTGAATGTTTCAAGACCTCTTCCCATTTGAAGCTTATTAATTTTGGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
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QY 221 TyrProGlyValAspAlaSerThrGlyTyrPheAsnSerValSerArgIleIleIleGlu 240
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; Publication No. US20030073129A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlyGlyGly 40  
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QY 61 GlyValProGlyTyrArgAspGlySerProGlyValAsnValLeuProGlyTyrProGlyTyr 80  
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DB 378 CCGAGTCCGAGTGCATTCAGAGAGAAAGCGGGAATGTTGAGGAGAAAGCTTTGAGAG 437  
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QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgLeuLeuLeuGlnGly 240

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RESULT 21  
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; Sequence 121, Application US/10006867  
; Publication No. US20020119130A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Guiney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William L.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/006,867  
; PRIOR FILING DATE: 2001-12-06  
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Alignment Scores:
Pred. No.: 2 21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-063-734-122 (1-243) x US-10-066-867-121 (1-1257)
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DB 378 CCAGGTCCGAGATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
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DB 678 GGAAGCCCTGAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 737
QY 201 CysGluGlyLeuGlyAlaGlyLeuValaLeuValaLeuLeuLeuLeuLeu 220
DB 738 TGTGAAGGATTCGCTGATTAAGGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProGlyGlyAspAlaSerTrpGlyTrpAsnSerValSerArgLeuLeu 240
DB 798 TACCCAAAAGAGATCTCTACTGATGATGATGATGATGATGATGATGATGAT 857
QY 241 LeuProLeu 243
DB 858 CTACCAAAA 866

RESULT 22
US-10-052-586-365
; Sequence 365, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/07450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
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;; PRIOR FILING DATE: 1998-04-21  
;; PRIOR APPLICATION NUMBER: 60/082569  
;; PRIOR FILING DATE: 1998-04-21  
;; PRIOR APPLICATION NUMBER: 60/082704  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082797  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083495  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083496  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083499  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083559  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
;; PRIOR APPLICATION NUMBER: 60/084414  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084639  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084640  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084643  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085582  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/086023  
;; PRIOR FILING DATE: 1998-05-18  
;; PRIOR APPLICATION NUMBER: 60/086392  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/086486  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087098  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087208  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087609  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087759  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087827  
;; PRIOR FILING DATE: 1998-06-03  
;; PRIOR APPLICATION NUMBER: 60/088025  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088029  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088167  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088202  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088212  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088326  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088655  
;; PRIOR FILING DATE: 1998-06-09

;; PRIOR APPLICATION NUMBER: 60/088722  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088738  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088740  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088811  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088824  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088825  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088826  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088861  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088863  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088876  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089090  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089105  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089512  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089514  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089538  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089598  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089908

## Alignment Scores:

Pred. No.: 2,21e-144 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-063-734-122 (1-243) x US-10-052-586-365 (1-1257)

QY 1 MetArgProGInuPProAlaIaSerProGInuArgLeuArgLyLeuLeuLeuLeu 20  
Db 138 ATGGACCCCGAGGCGCCCGCTCCCGACGGGCTCCGCGCTGCTGCTCTG 197  
QY 21 LeuLeuGInuPProAlaIaSerProGInuArgLeuArgLyLeuLeuLeuLeu 40  
Db 198 CTGCTGACGCTGCGCCCGCTGACGCGCTGACGCTGACGCTGACGCTGACG 257  
QY 41 GInLeuArgGInuArgGInuArgGInuArgGInuArgGInuArgGInuArgGInu 60  
Db 258 CAGCTCCGCGACAGAGGAGGTGTGACCTGTATATATGATGCTTACAGGGCCAGCA 317  
QY 61 GInValProGInuArgGInuArgGInuArgGInuArgGInuArgGInuArgGInu 80  
Db 318 GGAAGTCCCTGTCAAGAGCGGAGCCCTGGGGCCAAATGTATTTCCGGGTACCTGGGATC 377  
QY 81 ProGInuArgGInuArgGInuArgGInuArgGInuArgGInuArgGInuArgGInu 100  
Db 378 CCAGTCCGAGTGTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437  
QY 101 SerTyrProArgGInuArgGInuArgGInuArgGInuArgGInuArgGInuArgGInu 120  
Db 438 TCCTGACACCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCTT 497  
QY 121 GInValLeuArgGInuArgGInuArgGInuArgGInuArgGInuArgGInuArgGInu 140  
Db 498 GGGAAATTCGGAGAGTGTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557

```
QY 141 PheSerGlySerLeuArgLeuValaCysArgAsnAlaCysCysGlnArgTrpTyrPheThr 160
DB 558 TTCAGTGGCTCACTTGGCTAAATATGCAAAATGCTGTCAGGGTGGATTTTTCACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 618 TTCATGAGAGCTGAAATGTTCAAGACCTCTCCCATTTGAAGCTTATTTATTTGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAAGCCCTGAAATGAAATTCACAAATTAATTCATGACACTTCTCTGGAGAGACTT 737
QY 201 CysGluGlyIleGluValaGlyLeuValaAspValaIleTrpValaGlyThrCysSerAsp 220
DB 738 TGTGAAGGAAATGCTGCTGATTAAGAGATGTTGCTATCTGGTGGCACTGTGTCAAGAT 797
QY 221 TyrProLySGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGln 240
DB 798 TACCCAAAAGAGATCTTCTACTGATGAAATTCAGTTTCTCGCATCATTAATTAAGAA 857
QY 241 LeuProLyS 243
DB 858 CTACCAAAA 866

RESULT 23
US-10-063-547-121
; Sequence 121, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-547-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-063-734-122 (1-243) x US-10-063-547-121 (1-1257)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGACCCCGAGGGCCCGCGCTCCCGCAGCGGCTCGCGGCTCCTCGTGTCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProLySGlyValaGlnVala 40
DB 198 CTGCTCAGCTGCGCGCGCGCTGAGAGCTCTGAGATTCCTCCCAAGGGAAGCAAAAGCG 257
QY 41 GlnLeuArgGlnArgGlnValaIlePLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGAGAGAGAGTGTGTGACCTGTATTAATGAAATGTGTTCACAGGCGCAGCA 317
```

```
QY 61 GlyValaProGlyValArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAAGTCTGCTGAGAGCGGAGCCCTGGGCAATGTTATTCGGGATCACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLySGlyGluValySGlyGluCysLeuArgGluSerPheGluGln 100
DB 378 CCAAGTCGGGATGAGATTCAAAGAGAAAGGGGAGATGCTCAGGGAAGCTTTGAGGAG 437
QY 101 SerTrpThrProAsnTyrLySGlyCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCCTGAGACACCAACTACAGCAGTGTTCATGAGTTCATTAATTAATGCAATGACTT 497
QY 121 GlyValIleAlaGluCysThrPheThrThrIysMetArgSerAsnSerAlaLeuArgValaLeu 140
DB 498 GGAAGAAATGCGGAGATGATTCATTACAAAGATGCGTTCAATATAGTCTTAAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuValaCysArgAsnAlaCysCysGlnArgTrpTyrPheThr 160
DB 558 TTCAGTGGCTCACTTGGCTAAATGCAAAATGCAATGATGCTGTACAGCTTTGATTTTACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 618 TTCATGAGAGCTGAAATGTTCAAGACCTCTCCCATTTGAAGCTATTAATTTGACCAA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAAGCCCTGAAATGAAATTCACAAATTAATTCATGACACTTCTCTGGAGAGACTT 737
QY 201 CysGluGlyIleGlyValaGlyLeuValaAspValaIleTrpValaGlyThrCysSerAsp 220
DB 738 TGTGAAGGAAATGCTGCTGATTAAGAGATGTTGCTATCTGGTGGCACTGTTCAGAT 797
QY 221 TyrProLySGlyAspAlaSerThrGlyTyrPAsnSerValSerArgIleIleIleGluGln 240
DB 798 TACCCAAAAGAGATCTTCTACTGATGAAATTCAGTTTCTCGCATCATTAATTAAGAA 857
QY 241 LeuProLyS 243
DB 858 CTACCAAAA 866

RESULT 24
US-10-063-551-121
; Sequence 121, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0  
 US-10-063-734-122 (1-243) x US-10-063-551-121 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20  
 DB 138 ATGCGACCCAGAGGCGCCCGCCCTCCCGACGGCTCCGGGCTCTGCTGCTCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnVal 40  
 DB 198 CTGCTGACACTGCCCGCCGCTGAGGCGCTCTGAGATCCCAAGGGAAGCAAAAGGG 257

QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyraSnglyMetCysLeuGlnGlyProAla 60  
 DB 258 CAGCTCCGCGAGAGGAGGAGGTGTGACCTGTATATAGATGCTTACAGGCGCAGCA 317

QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValLeuProGlyThrProGlyIle 80  
 DB 318 GAGTGCTGTGTGAGACGAGGAGCCCTGGGGCAATGTATCCGGGTACACCTGGGATC 377

QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
 DB 378 CAGGTCCGGAGTGTATCAAGAGAAAGGGGAATGTCTAGGAAAGCTTTGAGAG 437

QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120  
 DB 438 TCCGTGACACCACTACAGAGAGGTGTATGATGATGATGATGATGATGATGATGAT 497

QY 121 GlyValIleAlaGlyCysSerThrPheThrIleMetArgSerSerSerAlaLeuArgValLeu 140  
 DB 488 GGGAAATTTGCGAGAGTGTATCAAGAGAGGTGTATGATGATGATGATGATGATGAT 557

QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTrpPheThr 160  
 DB 558 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGCAATGCTGTGAGGTTGATTTTCA 617

QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyrlsLeuAspGln 180  
 DB 618 TTCATGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 677

QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200  
 DB 678 GGAAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 737

QY 201 CysGlnGlyIleGlyValGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220  
 DB 738 TGTGAAGAAATGTGTGTGATTAATGATGATGATGATGATGATGATGATGATGAT 797

QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlnGlu 240  
 DB 798 TACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 857

QY 241 LeuProLys 243  
 DB 858 CTACCAAAA 866

RESULT 25  
 US-10-174-590-365  
 ; Sequence 365, Application US/10174590  
 ; Publication No. US20030008352A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Yian  
 ; APPLICANT: Deenoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430R1C42  
 ; CURRENT APPLICATION NUMBER: US/10/174,590  
 ; PRIOR APPLICATION DATE: 2002-06-18  
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 365  
 ; LENGTH: 1257  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-174-590-365

Alignment Scores:  
 Pred. No.: 2,21e-144 Length: 1257  
 Score: 1301.00 Matches: 243  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-174-590-365 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20  
 DB 138 ATGCGACCCAGAGGCGCCCGCCCTCCCGAGGAGGTCCGGGCTCTGCTGCTCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyGlyGlnVal 40  
 DB 198 CTGCTGACACTGCCCGCCGCTGAGGCGCTCTGAGATCCCAAGGGAAGCAAAAGGG 257

QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyraSnglyMetCysLeuGlnGlyProAla 60  
 DB 258 CAGCTCCGCGAGAGGAGGAGGTGTGACCTGTATATAGATGCTTACAGGCGCAGCA 317

QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValLeuProGlyThrProGlyIle 80  
 DB 318 GAGTGCTGTGTGAGACGAGGAGCCCTGGGGCAATGTATTCGGGTACACCTGGGATC 377

QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
 DB 378 CAGGTCCGGAGTGTATCAAGAGAAAGGGGAATGTCTAGGAAAGCTTTGAGAG 437

QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120  
 DB 438 TCCGTGACACCACTACAGAGAGGTGTATGATGATGATGATGATGATGATGATGAT 497

QY 121 GlyValIleAlaGlyCysSerThrPheThrIleMetArgSerSerSerAlaLeuArgValLeu 140  
 DB 498 GGGAAATTTGCGAGAGTGTATCAAGAGATGCTTCAAAATGATGCTCTTAAGAGTTTG 557

QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTrpPheThr 160  
 DB 558 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGCAATGCTGTGAGGTTGATTTTCA 617

QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleIleTyrlsLeuAspGln 180  
 DB 618 TTCATGAGAGCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 677

QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200  
 DB 678 GGAAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 737

QY 201 CysGlnGlyIleGlyValGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220  
 DB 738 TGTGAAGAAATGTGTGTGATTAATGATGATGATGATGATGATGATGATGATGAT 797

QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlnGlu 240  
 DB 798 TACCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 857

QY 241 LeuProLys 243  
 DB 241 LeuProLys 243



DB 858 CTACCAAAA 866

RESULT 26

US-10-176-758-365

/ Sequence 365, Application US/10176758

/ Publication No. US20030008353A1

/ GENERAL INFORMATION:

/ APPLICANT: Baker, Kevin P.

/ APPLICANT: Chen, Jian

/ APPLICANT: Desnoyers, Luc

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.

/ APPLICANT: Gurney, Austin L.

/ APPLICANT: Pan, James

/ APPLICANT: Smith, Victoria

/ APPLICANT: Watanabe, Colin K.

/ APPLICANT: Wood, William I.

/ APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

/ FILE REFERENCE: P3430R1C104

/ CURRENT APPLICATION NUMBER: US/10/176,758

/ PRIOR FILING DATE: 2002-06-21

/ Prior Application removed - See File Wrapper or Palm

/ NUMBER OF SEQ ID NOS: 612

/ SEQ ID NO 365

/ LENGTH: 1257

/ TYPE: DNA

/ ORGANISM: Homo Sapien

US-10-176-758-365

Alignment Scores:

Pred. No.:	2,21e-144	Length:	1257
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-063-734-122 (1-243) x US-10-176-758-365 (1-1257)

QY 1 MetArpProGlnGlyProAlaAlaSerProGlnArGLeuArgGlyLeuLeuLeuLeu 20

DB 138 ATCCGACCCCGAGGGCCCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGlyGly 40

DB 198 CTGCTCAGCTGCGCGCGCTGAGCGCTGAGATCCCAAGGGGAAGCAAGGCG 257

QY 41 GlnLeuArgGlnArgGlnValValAlaPleuTyrAsnGlyMetCysLeuGlnGlyProAla 60

DB 258 CAGCTCCGGAGGGAGGGAGGTGTGACCTGTATTAATGGAATGTGTACAAAGGCCAGCA 317

QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80

DB 318 GAGGTGCTGTGTGAGACGGGAGCCCTGGGGCCAAATGTTATTCGGGTACACTGGGATC 377

QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100

DB 378 CCAGGTCCGGATGATTCAAAAGAGAAAGGGGAATGTCTGAGGAAAGCTTTGAGGAG 437

QY 101 SerTrpThrProAsnTyrIleGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120

DB 438 TCTTGACACCCCACTACAGAGGTGTCTAGAGTTCATTGAATTAATGCAATAGATCTT 497

QY 121 GlyIleValIleGlnCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValIle 140

DB 498 GGGAAATTCGGAGGTACATTACAAAGATCCGTTCAAAATGCTCTCAAGATTTC 557

QY 141 PheSerGlySerLeuArgLeuLeuGlyCysArgAsnAlaCysCysGlnArgTyrPheThr 160

DB 558 TTCAGTGCTCACTTGGCTAAATATCAGAAATGATGCTGTGACGGGTGTGATTTCACA 617

QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGluValIleIleTyrLeuAspGln 180

DB 618 TTCATGAGCTGGAATGTTCAAGACCTCTCCCATTTGAAGCATATATTATTGAGCAAA 677

QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200

DB 678 GGAAGCCCTGAATATCAACAATTAATTCATTCGACCTTCCTGTGTGAGACACTT 737

QY 201 CysGlnGlyIleGlyValGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220

DB 738 TGTGAAGGAATGTGTGATGATTAAGATGTGTCTATCTGGGTGGCACTTGTCAGAT 797

QY 221 TyrProGlyArgAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGlnGlu 240

DB 798 TACCCAAAGAGAGCTTCTTACTGATGAGATTCAGTTCTTCGATCATTTATTGAGAA 857

QY 241 LeuProGly 243

DB 858 CTACCAAAA 866

RESULT 27

US-10-175-737-365

/ Sequence 365, Application US/10175737

/ Publication No. US20030013153A1

/ GENERAL INFORMATION:

/ APPLICANT: Baker, Kevin P.

/ APPLICANT: Chen, Jian

/ APPLICANT: Desnoyers, Luc

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.

/ APPLICANT: Gurney, Austin L.

/ APPLICANT: Pan, James

/ APPLICANT: Smith, Victoria

/ APPLICANT: Watanabe, Colin K.

/ APPLICANT: Wood, William I.

/ APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

/ FILE REFERENCE: P3430R1C50

/ CURRENT APPLICATION NUMBER: US/10/175,737

/ PRIOR FILING DATE: 2002-06-19

/ Prior Application removed - See File Wrapper or Palm

/ NUMBER OF SEQ ID NOS: 612

/ SEQ ID NO 365

/ LENGTH: 1257

/ TYPE: DNA

/ ORGANISM: Homo Sapien

US-10-175-737-365

Alignment Scores:

Pred. No.:	2,21e-144	Length:	1257
Score:	1301.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-10-063-734-122 (1-243) x US-10-175-737-365 (1-1257)

QY 1 MetArpProGlnGlyProAlaAlaSerProGlnArGLeuArgGlyLeuLeuLeuLeu 20

DB 138 ATCCGACCCCGAGGGCCCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 197

QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGlyGly 40

DB 198 CTGCTCAGCTGCGCGCGCTGAGCGCTGAGATCCCAAGGGGAAGCAAGGCG 257

QY 41 GlnLeuArgGlnArgGlnValValAlaPleuTyrAsnGlyMetCysLeuGlnGlyProAla 60

DB 258 CAGCTCCGGAGGGAGGGAGGTGTGACCTGTATTAATGGAATGTGTACAAAGGCCAGCA 317

QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80

Db 318 GGAGTGCCTGTGAGACGGAGCCCTGGGGCCCATGATTATCCGGGTACACCTGGGATC 377  
Qy 81 ProglYATGAPGlyPheLySGlyGlyuLySGlyuCyLeuArgLysSerPheGluGlu 100  
Db 378 CCAAGTCCGGATGAGATTCAAGAGAGAAAGGGGAATGCTCGAGGAGAAAGCTTTGAGAG 437  
Qy 101 SerTPThrProAsnTyLySGlyuCySerTrpSerSerLeuAsnTyLyGlyLeuAspLeu 120  
Db 438 TCCTGACACCCCACTACAGAGCAGTGTTCATGAGATTCAATGATTAATGACATGATCTT 497  
Qy 121 GlyLySIIealGlyuCySerThyPheThyLysMetArgSerAsnSerAlaLeuArgValLeu 140  
Db 498 GGGAAATTTGGAGAGTACATTACAAAGATGCTGTAATGCTCTCAAGAGCTTTG 557  
Qy 141 PheSerGlySerLeuArgLeuLysCySerAsnAlaCySerGlnArgTrpTrpPheThr 160  
Db 558 TTCATGCGCTGACTTCGCGCTAAATGCAAAATGCAATGCTGAGCGTGGATTTGACA 617  
Qy 161 PheAsnGlyAlaGlyuCySerGlyProLeuProIleGluAlaIleIleTyLeuAspGln 180  
Db 618 TTCATGAGAGCTGAAATGTTCAAGACCTCTCCCATGGAAGCTAATTTTGGACCA 677  
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThySerSerValGlyuGlyLeu 200  
Db 678 GGAAGCCCTGAATGAAATGAAATTCACAAATTAATTCATCGCACTTCTGTGAGAGACTT 737  
Qy 201 CysGlyGlyIleGlyValaGlyLeuValaAspValaIleTrpValGlyThyCysSerAsp 220  
Db 738 TGTGAAGAAATGCTGCTGAGATTAGTGATGTTGCTGATCGGTGGACCTGTTCAGAT 797  
Qy 221 TyrProLySGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240  
Db 798 TACCCAAAGAGATGCTTCTACTGATGAAATTCAGTTCTCGCATCATATTGAAGA 857  
Qy 241 LeuProLyS 243  
Db 858 CTACCAAAA 866

RESULT 28  
US-10-063-616-121  
; Sequence 121, Application US/10063616  
; Publication No. US20030013855A1  
GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gutney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,616  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 121  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-063-616-121

Alignment Scores:  
Pred. No.: 2,21e-144 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-063-616-121 (1-1257)  
Qy 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20  
Db 138 ATGCATCCCGAGGGGCGCGCGCTCCCGCAGCGGGCTCCGCGCTCTGCTGCTCTG 197  
Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleLeuProLySGlyuLySGlyu 40  
Db 198 CTGCTGACAGCTCCCGCGCGCTGAGGCGCTCTGAGATCCCAAGGGGAGAGCAAGCGC 257  
Qy 41 GlnLeuArgGlnArgGlyValaIleAspLeuTyArgAsnGlyMetCysLeuGlnGlyProAla 60  
Db 258 CAGCTCCCGCAGAGGAGAGCTGTGAGCCTGTATATAGAAATGCTTACAGAGGCCAGCA 317  
Qy 61 GlyValProGlyArgAspGlySerProGlyValaAsnValIleProGlyThyProGlyIle 80  
Db 318 GGAGTGCCTGTGAGAGAGGGAGCCCTGGGGCCCATGATTATTCGGGTACACCTGGGATC 377  
Qy 81 ProglYATGAPGlyPheLySGlyGlyuLySGlyuCyLeuArgLysSerPheGluGlu 100  
Db 378 CCAAGTCCGGATGAGATTCAAGAGAGAAAGGGGAATGCTCGAGGAGAAAGCTTTGAGAG 437  
Qy 101 SerTPThrProAsnTyLySGlyuCySerTrpSerSerLeuAsnTyLyGlyLeuAspLeu 120  
Db 438 TCCTGACACCCCACTACAGAGCAGTGTTCATGAGATTCAATGATTAATGACATGATCTT 497  
Qy 121 GlyLySIIealGlyuCySerThyPheThyLysMetArgSerAsnSerAlaLeuArgValLeu 140  
Db 498 GGGAAATTTGGAGAGTACATTACAAAGATGCTGTAATGCTCTCAAGAGCTTTG 557  
Qy 141 PheSerGlySerLeuArgLeuLysCySerAsnAlaCySerGlnArgTrpTrpPheThr 160  
Db 558 TTCATGCGCTGACTTCGCGCTAAATGCAAAATGCAATGCTGAGCGTGGATTTGACA 617  
Qy 161 PheAsnGlyAlaGlyuCySerGlyProLeuProIleGluAlaIleIleTyLeuAspGln 180  
Db 618 TTCATGAGAGCTGAAATGTTCAAGACCTCTCCCATGGAAGCTAATTTTGGACCA 677  
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThySerSerValGlyuGlyLeu 200  
Db 678 GGAAGCCCTGAATGAAATGAAATTCACAAATTAATTCATCGCACTTCTGTGAGAGACTT 737  
Qy 201 CysGlyGlyIleGlyValaGlyLeuValaAspValaIleTrpValGlyThyCysSerAsp 220  
Db 738 TGTGAAGAAATGCTGCTGAGATTAGTGATGTTGCTGATCGGTGGACCTGTTCAGAT 797  
Qy 221 TyrProLySGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240  
Db 798 TACCCAAAGAGATGCTTCTACTGATGAAATTCAGTTCTCGCATCATATTGAAGA 857  
Qy 241 LeuProLyS 243  
Db 858 CTACCAAAA 866

RESULT 29  
US-10-174-581-365  
; Sequence 365, Application US/10174581  
; Publication No. US20030017540A1  
GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, J'ian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gutney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C41

PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081838
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082568
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082569
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082704
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082797
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/083495
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083496
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083499
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083559
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/084366
PRIOR FILING DATE:	1998-05-05
PRIOR APPLICATION NUMBER:	60/084414
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084639
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084640
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084643
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085573
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085579
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085580
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085582
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085700
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/086023
PRIOR FILING DATE:	1998-05-18
PRIOR APPLICATION NUMBER:	60/086392
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/086486
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/087098
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087208
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/087609
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087759
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/087827
PRIOR FILING DATE:	1998-06-03
PRIOR APPLICATION NUMBER:	60/088025
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088028
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088029
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088033
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088167
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088202
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088212
PRIOR FILING DATE:	1998-06-05
PRIOR APPLICATION NUMBER:	60/088217
PRIOR FILING DATE:	1998-06-05

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PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088722
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088740
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088811
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088825
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088863
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089090
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653

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## Alignment Scores:

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Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

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US-10-063-734-122 (1-243) x US-10-174-581-365 (1-1257)

```

QY 1 MetArgProGInGlyProAlaAlaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGATCCCGAGGAGGCGCCGCCCTCCCGCAGCGGCTCCGGGCGCTCTGCTGCTCTG 197
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProGlyGlyLeuGInLeu 40
DB 198 CTGCTGAGCTGCGCCGCCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGCAAAAGCG 257
QY 41 GInLeuArgGInArgGInValValAlaSplLeuTYraGInGlyMetCysLeuGInGlyProAla 60
DB 258 CAGCTCCGCGAGAGGAGGAGTGTGAGCTGTATATGAAATGCTTCAAGGGCCACAGA 317
QY 61 G1yValProG1yArgAspG1ySerProG1yAlaAsnVal11leProG1yThPhProG1y1le 80
DB 318 GGAATGCTGTGTCAAGACGAGACCCCTGGGGCCAATGTTATTCGCGGTACACTGGGATC 377
QY 81 ProG1yArgAspG1yPheLeuG1yG1uLysG1yG1uG1yCysLeuArgG1uSerPheG1uG1u 100
DB 378 CCAGGTGCGGATGATTCAGAAAGAGAAAGGGGAGATGTGAGGAGAAAGCTTTGAGAG 437
QY 101 SerThPhrProAsnTYrLysG1uG1uG1uG1uG1uG1uG1uG1uG1uG1uG1uG1u 120
DB 438 TCCGGAACCCCACTACAGACAGATGTCATGAGATTCATGAAATATGAGCATATGATCTT 497
QY 121 G1yLys11leAlaG1uG1yThPhrThLysMetArgSerAsnSerAlaLeuArgValLeu 140

```

```

DB 498 GGGAAATTGGCGATGTACATTATCAAGATGCGTTCAATATGCTTAAGGTTTG 557
QY 141 PheSerG1ySerLeuArgLeuLysCysArgAsnAlaCysCysGInArgTYrPheThr 160
DB 558 TTCAGTGGCTCACTTCGGCTAAATGCAAGAAATCAGTCTGACGCTTGATTTTACA 617
QY 161 PheArgG1yAlaG1uCysSerG1yProLeuPro11leGInAl1le11eTYrLeuAspG1n 180
DB 618 TTCATGAGCTGAATGTTCAGACCTCTTCCATGTAGATATATTAATTTGGACAA 677
QY 181 G1ySerProG1uMetAsnSerThr11eAsn11eHisArgThrSerSerValG1uG1yLeu 200
DB 678 GGAAGCCCTGAATGAATTCAACAAATTATTCATGCACTTCTTGAGAAAGACTT 737
QY 201 CysG1uG1y11leG1yAlaG1yLeuValAspValAla11eTYrPValG1yThrCysSerAsp 220
DB 738 TGTGAAGAAATGTGTGCTGATGTAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
QY 221 TYrProLysG1yAspAlaSerThrG1yTYrAsnSerValSerArg11e11e11eG1uG1u 240
DB 798 TACCCAAAGAGATGCTTCTTACTGATGAGATTCAGTTCTGCACTATTAATTAAGAA 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866

```

## RESULT 30

```

US-10-176-483-365
Sequence 365, Application US/10176483
Publication No. US20030017541A1

```

## GENERAL INFORMATION:

```

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P343081C68
CURRENT FILING DATE: 2002-06-20
Prior application removed - See file wrapper or Pam
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 365
LENGTH: 1257
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-483-365

```

## Alignment Scores:

```

Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

```

US-10-063-734-122 (1-243) x US-10-176-483-365 (1-1257)

```

QY 1 MetArgProGInGlyProAlaAlaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGATCCCGAGGAGGCGCCGCCCTCCCGCAGCGGCTCCGGGCGCTCTGCTGCTCTG 197
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProGlyGlyLeuGInLeu 40
DB 198 CTGCTGAGCTGCGCCGCCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGCAAAAGCG 257

```

```
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGGCAGAGGAGGAGGTGGACCTGTATTAATGGAATGTGCTTACAGGGCCAGCA 317
QY 61 G1yValProG1yArgAspG1ySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
DB 318 GGAGTCCCTGCTGACAGCCGAGACCTCGGGGCCAATGTTATTCTCGGGTACACTGGGATC 377
QY 81 ProG1yArgAspG1yPheIyGlyGluValCysLeuArgGluSerPheGluGlu 100
DB 378 CCAGGTCGGAGTGAATTCAGAGAGAGAAAGGGGGAATGCTGAGGAGAAAGCTTTGAGAG 437
QY 101 SerTrpThrProAsnTyrIyGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCTTGACACCCCACTACAGACAGTGTTCATGAGATTCATTGAATTAATGACATAGATCTT 497
QY 121 G1yIyValAlaGluCysThrPheThrIyMetArgSerAsnSerAlaLeuArgValIleu 140
DB 498 GGGAAATTTGGGAGGTGATCATTACAAAGATGCGTTCAATATGCTCTTAAGAGTTTGG 557
QY 141 PheSerGlySerLeuArgLeuIySyrValArgAsnAlaCysCysGlnArgTrpIyPheThr 160
DB 558 TTCAGTGGCTCACTTCGGCTAAATGACAGAAATGCAATGCTGTCAGCGTTGGTATTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrIleuAspGln 180
DB 618 TTCATAGAGAGCTGAATGTTCAAGACCTCTCCATTAAGCTATTAATTTATTTGGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAAGCCCTGGAATGATTCACAAATTAATTCATCGCACTTCTCTGGAGAGACTT 737
QY 201 CysGluGlyIleGlyValaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAATGGTCTGCTGATTAAGTGAATGTTGCTATCTGCTGCTGCACTTGTACAG 797
QY 221 TyrProIyGlyAspAlaSerThrGlyTTPanSerValSerArgIleIleIleGluGlu 240
DB 798 TACCCAAAAGAGATGCTTCTACTGATGAGATTCAGTTCTGCAATCATTATTGAAGAA 857
QY 241 LeuProIyS 243
DB 858 CTACCAAAA 866
RESULT 31
US-10-176-749-365
; Sequence 365, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-749-365
```

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Alignment Scores:
Pred. No.: 2 216-144
Score: 1301.00 Matches: 1257
Percent Similarity: 100.00% Conservative: 243
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Gaps: 0
DB: 14

US-10-063-734-122 (1-243) x US-10-176-749-365 (1-1257)
QY 1 MetArgProGlnGlyProAlaIleAspProGlnArgLeuArgGlyLeuLeuLeuLeu 20
DB 138 ATGCGACCCCAAGGGCCCGCCGCTCCCGGACGGGCTCGGGGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProIyGlyGlyGlnValAla 40
DB 198 CTGCTGCACTCCCGCCGCTCGAGCCGCTCTGAGATCCCAAGGGGAGAGAGGGCG 257
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGGCAGAGGAGGTGGACCTGTATTAATGGAATGTGCTTACAGGGCCAGCA 317
QY 61 G1yValProG1yArgAspG1ySerProG1yAlaAsnValIleProG1yThrProG1yIle 80
DB 318 GGAGTCCCTGCTGACAGCCGAGACCTCGGGGCCAATGTTATTCCGGGTACACTGGGATC 377
QY 81 ProG1yArgAspG1yPheIyGlyGluValCysLeuArgGluSerPheGluGlu 100
DB 378 CCAGGTCGGAGTGAATTCAGAGAGAGAAAGGGGGAATGCTGAGGAGAAAGCTTTGAGAG 437
QY 101 SerTrpThrProAsnTyrIyGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCTTGACACCCCACTACAGACAGTGTTCATGAGATTCATTGAATTAATGACATAGATCTT 497
QY 121 G1yIyValAlaGluCysThrPheThrIyMetArgSerAsnSerAlaLeuArgValIleu 140
DB 498 GGGAAATTTGGGAGGTGATCATTACAAAGATGCGTTCAATATGCTCTTAAGAGTTTGG 557
QY 141 PheSerGlySerLeuArgLeuIySyrValArgAsnAlaCysCysGlnArgTrpIyPheThr 160
DB 558 TTCAGTGGCTCACTTCGGCTAAATGACAGAAATGCAATGCTGTCAGCGTTGGTATTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrIleuAspGln 180
DB 618 TTCATAGAGAGCTGAATGTTCAAGACCTCTCCATTAAGCTATTAATTTATTTGGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAAGCCCTGGAATGATTCACAAATTAATTCATCGCACTTCTCTGGAGAGACTT 737
QY 201 CysGluGlyIleGlyValaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAATGGTCTGCTGATTAAGTGAATGTTGCTATCTGCTGCTGCACTTGTACAG 797
QY 221 TyrProIyGlyAspAlaSerThrGlyTTPanSerValSerArgIleIleIleGluGlu 240
DB 798 TACCCAAAAGAGATGCTTCTACTGATGAGATTCAGTTCTGCAATCATTATTGAAGAA 857
QY 241 LeuProIyS 243
DB 858 CTACCAAAA 866
RESULT 32
US-10-176-914-365
; Sequence 365, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
```

APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C83  
CURRENT APPLICATION NUMBER: US/10/176, 914  
CURRENT FILING DATE: 2002-06-20  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 365  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-176-914-365

Alignment Scores:  
Pred. No.: 2,21e-144 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-176-914-365 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20  
DB 138 ATGCCACCCCGAGGCGCCCGCCCTCCCGACGCGCTCCGCGGCTCCGCTGCTCCG 197  
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlnGlyGlnGlnVal 40  
DB 198 CTGCTGCGAGCTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAAGGAGCG 257  
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyraAsnGlyMetCysLeuGlnGlyProAla 60  
DB 258 CAGCTCCGCGAGGAGGAGGTGTGCGCTGTATTAATGAAATGCTTACAGGGCCAGCA 317  
QY 61 GlyValProGlnArgAspGlySerProGlnValAsnValIleProGlnTyrrProGlyIle 80  
DB 318 GAGAGCTGCTGTGAGACGGAGCCCTGGGCGCAATGTAATTCGGGTAACCTGGGATC 377  
QY 81 ProGlnArgAspGlyPheLeuGlyGlnGlyGlnGlyCysLeuArgGlySerPheGlnGlu 100  
DB 378 CAGGTCGAGATGATTAAGAGAAAGGGGAAATGCTAGAGGAAAGCTTTGAGAG 437  
QY 101 SerTrpThrProAsnTyrrGlnGlnCysSerTrpSerSerLeuAsnTyrrGlyIleAspLeu 120  
DB 438 TCCGAGACACCCAACTACAGACAGTGTTCATGAGTTCAATTAATGATAGATCTT 497  
QY 121 GlyValIleAlaGlnCysThrPheThrIleAsnMetArgSerAsnSerAlaLeuArgValLeu 140  
DB 498 GGGAAATTCGGAGATGATTAATTAACAGATGCTTCAATTAATGAGCTTAAAGATTG 557  
QY 141 PheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTrpTyrrPheThr 160  
DB 558 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGATGCTGTCAAGCTTTGATTTTCA 617  
QY 161 PheAsnGlnValArgCysSerGlyProLeuProIleGlnAlaIleIleTyrrLeuAspGln 180  
DB 618 TTCATGAGCTGATGATGTCAGGACCTTCCCATTAAGCTAATTAATTAATTTGAGCA 677  
QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200  
DB 678 GGAAGCCCTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 737  
QY 201 CysGlnGlyIleGlyValGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220  
DB 738 TGTGAAGAAATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 797

QY 221 TyrProGlyValAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlnGlu 240  
DB 798 TACCCAAAAGAGAGCTTCTACGATGAAATTCAGTTCTCCCATTAATTAAGAA 857  
QY 241 LeuProGly 243  
DB 858 CTACCAAA 866

RESULT 33

US-10-176-915-365  
Sequence 365, Application US/10176915  
Publication No. US20030017544A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C110  
CURRENT APPLICATION NUMBER: US/10/176, 915  
CURRENT FILING DATE: 2002-06-21  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 365  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-176-915-365

Alignment Scores:  
Pred. No.: 2,21e-144 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-176-915-365 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20  
DB 138 ATGCCACCCCGAGGCGCCCGCCCTCCCGACGCGCTCCGCGGCTCCGCTGCTCCG 197  
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlnGlyGlnGlnVal 40  
DB 198 CTGCTGCGAGCTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAAGGAGCG 257  
QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyraAsnGlyMetCysLeuGlnGlyProAla 60  
DB 258 CAGCTCCGCGAGGAGGAGGTGTGCGCTGTATTAATGAAATGCTTACAGGGCCAGCA 317  
QY 61 GlyValProGlnArgAspGlySerProGlnValAsnValIleProGlnTyrrProGlyIle 80  
DB 318 GAGAGCTGCTGTGAGACGGAGCCCTGGGCGCAATGTAATTCGGGTAACCTGGGATC 377  
QY 81 ProGlnArgAspGlyPheLeuGlyGlnGlyGlnGlyCysLeuArgGlySerPheGlnGlu 100  
DB 378 CAGGTCGAGATGATTAAGAGAAAGGGGAAATGCTAGAGGAAAGCTTTGAGAG 437  
QY 101 SerTrpThrProAsnTyrrGlnGlnCysSerTrpSerSerLeuAsnTyrrGlyIleAspLeu 120  
DB 438 TCCGAGACACCCAACTACAGACAGTGTTCATGAGTTCAATTAATGATAGATCTT 497  
QY 121 GlyValIleAlaGlnCysThrPheThrIleAsnMetArgSerAsnSerAlaLeuArgValLeu 140

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DB 498 GGAATAATTCGCGAGTGTACATTTACMAAGATCGCTTCAATAGTCTTAAGATTGTTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAnaAlaCysCysGlyAlaRgrTrpYrPheThr 160
DB 558 TTCAGTGGCTCCTCGCTGCTAAATGCAAAATGACAGTGTGACGGTGGATTTTACACA 617
QY 161 PheAnGlyAlaGlyCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 618 TTCATATGAGCTGATGTTTCAAGACCTCTTCCATTTGAAGCTATATTATTGAGCCAA 677
QY 181 GlySerProGluMeCAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAACCCCTGGAATGATTCACAAATTAATTCATCGACCTTCTCTGGAGAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGGATGTGCTGCTGATTAAGATGATGATGCTGATGCTGAGCTTGTTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
DB 798 TACCCAAAAGAGATGCTTCTACTGATGATGATTCAGTTCTTCGATCATTTATTGAGAA 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866

RESULT 34
US-10-063-569-121
; Sequence 121, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Bilen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; PRIORITY FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-063-569-121 (1-1257)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeuLeu 20
DB 138 ATGCCAGCCCGAGGGCCCGCCGCTCCCGCAGCGGCTCCGGGCTCTCTGCTGCTCCG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnValAla 40
DB 198 CTGCTGCACTGCGCGCGCGCTGACGCGCTCTGACATCCCAAGGAGAAAGGAGGCG 257
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
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DB 258 CAGCTCCGCGAGAGGAGGTGTGACCTGTATTAATGAAATGTGCTTACMAAGGCCACGA 317
QY 61 GlyValProGlyValArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAAGTCCGTGCGAGACGGAGCGCTGGGCGCAATGTTATTCGGGATCACCTGGAGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGluLysGlyGluCysLeuArgGluSerPheGluGlu 100
DB 378 CCAAGTCCGGAGATTTCAAGAGAAAGAGGAGATGTCTGAGGAAAGCTTTGAGGAG 437
QY 101 SerTrpThrProAsnTyrIleGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCCTGAGACCCCACTACAGACAGATGTTCAAGCTTCAATTAATTAATGAGCATGATCTT 497
QY 121 GlyValIleAlaGlyCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
DB 498 GGAATAATTCGCGAGTGTACATTACAAAGATCGCTTCAATATGCTCTTAAGATTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAnaAlaCysCysGlnArgTrpYrPheThr 160
DB 558 TTCAGTGGCTCCTCGCTGCTAAATGCAAAATGACAGTGTGACGGTGGATTTTACACA 617
QY 161 PheAnGlyAlaGlyCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 618 TTCATATGAGCTGATGTTTCAAGACCTCTTCCATTTGAAGCTATATTATTGAGCCAA 677
QY 181 GlySerProGluMeCAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAACCCCTGGAATGATTCACAAATTAATTCATCGACCTTCTCTGGAGAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
DB 738 TGTGAAGGATGTGCTGCTGATTAAGATGATGCTGATGCTGAGCTTGTTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
DB 798 TACCCAAAAGAGATGCTTCTACTGATGATGATTCAGTTCTTCGATCATTTATTGAGAA 857
QY 241 LeuProLys 243
DB 858 CTACCAAAA 866

RESULT 35
US-10-063-513-121
; Sequence 121, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Bilen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; PRIORITY FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
```

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-063-513-121 (1-1257)

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QY 1 MetAaPProGInGlyProAlaAaSerProGInaArgLeuArgGlyLeuLeuLeuLeu 20
Db 138 ATGCAACCCCAAGGGGCCCCCGCCCTCCCGCAGCGGCTCCGGGGCTCTGCTGCTCGT 197
QY 21 LeuLeuGInLeuProAlaAProSerSerAlaSerGluLeuProGlyGlyGlyGlyGly 40
Db 198 CTGCTGAGCTCCCGCCGCGCTGAGCGCTCTGAGATCCCAAGGGGAGCAAAAGGGG 257
QY 41 GInLeuAArgGInaArgGluValValAspLeuTyraSerGlyMetCysLeuGInGlyProAla 60
Db 258 CAGCTCCGGCAGAGGAGGTGTGAGCTGTATATAGATGTGCTTACAAAGGCCACAGA 317
QY 61 GlyValPProGlyAraAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GAGGTGCTGTGAGACGGGAGCCCTGGGGCCAAATGTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyAraAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 378 CCAAGTCCGGATGATGATTCAAAGAGAAAGGGGAAATGCTGAGGAAAGCTTTAGAGAG 437
QY 101 SerTrpThrProAsnTyrluGInCysSerTrpSerSerLeuAsnTyrluIleAspLeu 120
Db 438 TCCTGACACCCCACTACAGAGAGTTCATGATGATTCATTAATGAGCATATGATCTT 497
QY 121 GlyIleIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATTCGGAGATGTACATTTCAAAGAGCCCTTCAAAATAGCTTAAAGAGTTTGG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlyAraTrpPheThr 160
Db 558 TTCACTGGCTCACTTCGGCTAAATGCAAGAAATGATGCTGACAGCTTGGATTTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrluAspGln 180
Db 618 TTCATGAGAGCTGATGATTCAGAGACCTCTCCCATTTGAAGCTATATATTATGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAATGAATTCACATTAATATTCATTCACACTTCTCTGTGGAAAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGAAATGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 798 TACCCAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 857
QY 241 LeuProLys 243
Db 858 CTACCAAAA 866

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-063-513-121 (1-1257)

QY 1 MetAaPProGInGlyProAlaAaSerProGInaArgLeuArgGlyLeuLeuLeuLeu 20
Db 138 ATGCAACCCCAAGGGGCCCCCGCCCTCCCGCAGCGGCTCCGGGGCTCTGCTGCTCGT 197
QY 21 LeuLeuGInLeuProAlaAProSerSerAlaSerGluLeuProGlyGlyGlyGlyGly 40
Db 198 CTGCTGAGCTCCCGCCGCGCTGAGCGCTCTGAGATCCCAAGGGGAGCAAAAGGGG 257
QY 41 GInLeuAArgGInaArgGluValValAspLeuTyraSerGlyMetCysLeuGInGlyProAla 60
Db 258 CAGCTCCGGCAGAGGAGGTGTGAGCTGTATATAGATGTGCTTACAAAGGCCACAGA 317
QY 61 GlyValPProGlyAraAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GAGGTGCTGTGAGACGGGAGCCCTGGGGCCAAATGTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyAraAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 378 CCAAGTCCGGATGATGATTCAAAGAGAAAGGGGAAATGCTGAGGAAAGCTTTAGAGAG 437
QY 101 SerTrpThrProAsnTyrluGInCysSerTrpSerSerLeuAsnTyrluIleAspLeu 120
Db 438 TCCTGACACCCCACTACAGAGAGTTCATGATGATTCATTAATGAGCATATGATCTT 497
QY 121 GlyIleIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATTCGGAGATGTACATTTCAAAGAGCCCTTCAAAATAGCTTAAAGAGTTTGG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlyAraTrpPheThr 160
Db 558 TTCACTGGCTCACTTCGGCTAAATGCAAGAAATGATGCTGACAGCTTGGATTTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrluAspGln 180
Db 618 TTCATGAGAGCTGATGATTCAGAGACCTCTCCCATTTGAAGCTATATATTATGACCA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAATGAATTCACATTAATATTCATTCACACTTCTCTGTGGAAAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGAAATGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 798 TACCCAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGATGATGAT 857
QY 241 LeuProLys 243
Db 858 CTACCAAAA 866

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RESULT 37
US-10-063-512-121
; Sequence 121, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-121

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-063-512-121 (1-1257)
QY 1 MetArgProGlnGlyProAlaIAserProGlnArgLeuArgGlyLeuLeuLeu 20
DB 138 ATGCGACCCGAGGGCCCCCGCGCTCCCGACGGGCTCCGCGCTCTGCTCTCG 197
QY 21 LeuLeuGlnLeuProAlaIAserSerAlaSerGluIleProGlyGlyGlnVala 40
DB 198 CTGCTCGACGTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGCGC 257
QY 41 GlnLeuArgGlnArgGluValaIAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGCAGAGGAGGTGTGACCTGTATATGAAATGCTTACAAAGGCCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAGTCCCTGTGTGAGACCGGAGCCCTGGGGCCAATGTTATCCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyCysLeuArgGlyLeuSerPheGluGlu 100
DB 378 CCAAGCTCGGATGATTTCAAAGAGAAAGGGGAATGTCTGAGGAAGCTTTGAGAG 437
QY 101 SerTyrThrProAsnTyrIleGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCTGTGACACCCAACTACAAGCAGTGTTCATGAGTTCAATTGAATATGCAATAGATCTT 497
QY 121 GlyIleIleAlaGlyCysThrPheThrIleMetArgSerAsnSerAlaLeuValLeu 140
DB 498 GGAATAATGGAGAGTACATTACAAAGATCGTTCAATAGTCTCTCAAGAGTTTGG 557
QY 141 PheSerGlySerLeuArgLeuLeuValAspAsnAlaCysCysGlnArgTyrPheThr 160
DB 558 TTCAGTGGCTCACTTGGCTTAATAATGCAAAATGCAATGCTGTGAGGCTTGATTTTCA 617
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
DB 618 TTCAAATGAGAGTGAATGTTCAAGACCTTCCCATTTGAAGCTATATTTATTTGAGCA 677
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QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
DB 678 GGAAGCCCTGGAATGATTAATCAACATTAATATTCATCGACTTCTTGTGAGAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValaIAspValaIleTyrValGlyThrCysSerAsp 220
DB 738 TGTGAAGGAATGGTGGCTGATTAAGTGAATGTTGATCTGTGAGTGTGCACTTGTTCAGAT 797
QY 221 TyrProIleGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGlu 240
DB 798 TACCCAAAGAGAGTCTTCTACTGATGAGAAATGATGTTCTGCAATCATTAATGAAGA 857
QY 241 LeuProIle 243
DB 858 CTATCCAAA 866

RESULT 38
US-10-173-706-365
; Sequence 365, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-706-365

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-173-706-365 (1-1257)
QY 1 MetArgProGlnGlyProAlaIAserProGlnArgLeuArgGlyLeuLeuLeu 20
DB 138 ATGCGACCCGAGGGCCCCCGCGCTCCCGACGGGCTCCGCGCTCTGCTCTCG 197
QY 21 LeuLeuGlnLeuProAlaIAserSerAlaSerGluIleProGlyGlyGlnVala 40
DB 198 CTGCTCGACGTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGCGC 257
QY 41 GlnLeuArgGlnArgGluValaIAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGCAGAGGAGGTGTGACCTGTATATGAAATGCTTACAAAGGCCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GGAGTCCCTGTGTGAGACCGGAGCCCTGGGGCCAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyCysLeuArgGlyLeuSerPheGluGlu 100
```

Db 378 CCAAGTCGGAGATGATTCAGAGAGAAAGGGGGAATGCTGAGGAGAAAGCTTTGAGAG 437  
QY 101 SerTPthrProAsnThrLysGlnCysSerTrpSerLeuAsnThrGlyIleAspLeu 120  
Db 438 TCCTGGACACCCAACTACAGACAGGTTCATGAGATTGATTAATGACATAGATCTT 497  
QY 121 GlyValIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140  
Db 498 GGGAAATATGCGAGATGATCATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTG 557  
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpIlePheThr 160  
Db 558 TTCAGTGGCTCACTTCGCTTAAATGCAAAATGCAATGCTGTCAGCGTTGATTTTCACA 617  
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleIleIleLeuAspGln 180  
Db 618 TTCATGAGAGCTGAAATGTTCAAGACCTCTTCCCATGAAAGCTAATTAATTTGACCAA 677  
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200  
Db 678 GGAAGCCCTGAAATGATTCACAAATTAATTCATGCACTTCTCTGGAAGACCTT 737  
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220  
Db 738 TGTGAAGAAATGCTGCTGATTAAGATGTTGCTATCTGGGTGGCACTTGTTCAAGAT 797  
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240  
Db 798 TACCCAAAGAGATGCTTCTTACTGATGGAATTCAGTTTCTGCAATCAATTTGAAGA 857  
QY 241 LeuProLys 243  
Db 858 CTACCAAAA 866

RESULT 39  
US-10-175-738-365  
; Sequence 365, Application US/10175738  
; Publication No. US20030022294A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C45  
; CURRENT APPLICATION NUMBER: US/10/175,738  
; CURRENT FILING DATE: 2002-06-19  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 365  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-175-738-365

Alignment Scores:  
Pred. No.: 2,21e-144 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-175-738-365 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20  
Db 138 ATGCAACCCAGAGGCCCGCCGCTCCCGAGGCGCTCCGCGGCTCTGCTGCTCTG 197  
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnValAla 40  
Db 198 CTGCTGCAAGCTGCGCGCGCGCTCGAGCGCTCTGATAGTCCCAAGGGGAAAGCAAGCGC 257  
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60  
Db 258 CAGCTCCCGACAGAGGAGGTGTGACCTGTATATGAAATGTGCTTACAAAGGCGCAGCA 317  
QY 61 GlyValProGlyArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80  
Db 318 GGAGTGCTGCTGTCAGACAGGAGGCCCTGGGSCAATGTTATTCGGGTACACCTGGGATC 377  
QY 81 ProGlyArgAspGlyPheLysGlyGluLysGlyLysCysLeuArgGlySerPheGluGlu 100  
Db 378 CCAAGTCGGAGATGATTCAAAGAGAAAGGGGGAATGCTGAGAGGAAAGCTTTGAGAG 437  
QY 101 SerTPthrProAsnThrLysGlnCysSerTrpSerLeuAsnThrGlyIleAspLeu 120  
Db 438 TCCTGGACACCCAACTACAGACAGGTTCATGAGATTGATTAATGACATAGATCTT 497  
QY 121 GlyValIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140  
Db 498 GGGAAATATGCGAGATGATCATTTACAAAGATGCGTTCAAAATAGTCTCTAAGAGTTTG 557  
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpIlePheThr 160  
Db 558 TTCAGTGGCTCACTTCGCTTAAATGCAAAATGCAATGCTGTCAGCGTTGATTTTCACA 617  
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleIleIleLeuAspGln 180  
Db 618 TTCATGAGAGCTGAAATGTTCAAGACCTCTTCCCATGAAAGCTAATTAATTTGACCAA 677  
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200  
Db 678 GGAAGCCCTGAAATGATTCACAAATTAATTCATGCACTTCTCTGGAAGACCTT 737  
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220  
Db 738 TGTGAAGAAATGCTGCTGATTAAGATGTTGCTATCTGGGTGGCACTTGTTCAAGAT 797  
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240  
Db 798 TACCCAAAGAGATGCTTCTTACTGATGGAATTCAGTTTCTGCAATCAATTTGAAGA 857  
QY 241 LeuProLys 243  
Db 858 CTACCAAAA 866

RESULT 40  
US-10-175-752-365  
; Sequence 365, Application US/10175752  
; Publication No. US20030022295A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C60  
; CURRENT APPLICATION NUMBER: US/10/175,752

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/ CURRENT FILING DATE: 2002-06-19
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 365
/ LENGTH: 1257
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-175-752-365

Alignment Scores:
Pred. No.: 2, 21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-175-752-365 (1-1257)
QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20
DB 138 ATGCGACCCGAGGAGCCCGCGCTCCCGACGCGCTCCGCGCTCTGCTGCTG 137
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProGlyGlyGlnYsAla 40
DB 198 CTGCTGACGCTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGluValIaIaLeuLeuTyraGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGAGGAGGAGGTGTGACCTGTATATGATGTGCTTACAAAGGCGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GAGGTCTGTGTGAGAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 378 CCAAGTCCGGATGATTTCAAGAGAGAAAGGGGAAATGCTGAGGAAAGCTTTGAGAG 437
QY 101 SerTyrThrProAsnTyrIysGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCCTGACACCCCAATCAAGACAGTGTTCATGAGTTCAATTAATGATGATGATCTT 497
QY 121 GlyIleIleAlaIuGlySerThrPheThrIleMetArgSerSerSerAlaLeuArgValIleu 140
DB 498 GGAAGAAATGCGAGGTGTACATTACAAAGATCGTTCAATATGCTCAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLeuYsCysArgAsnAlaCysCysGlnArgTyrPyrPheThr 160
DB 558 TTCAGTGGCTCACTTGGCTTAAATGCAAAATGCAATGCTGCAAGCTTGTGATTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleIleIleLeuAspGln 180
DB 618 TTCAAATGAGACTGAATGTTCAAGACCTCTCCATGAACTAATTAATTTTGACCAA 677
QY 181 GlySerProGlnMetLeuSerThrIleAsnIleHisArgThrSerSerValIleGluGlyLeu 200
DB 678 GGAAGCCCTGAATGAATTCACAAATTAATTAATTCATGCACTTCTGAGAGAGACTT 737
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220
DB 738 TGTGAAGAAATTTGCTGTGATTAAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTG 737
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGln 240
DB 798 TACCCAAAGAGAAATGCTTCTACTGATGATGAATTCAGTTTCTGCAATCATTAATGAAGA 857
QY 241 LeuProIys 243
DB 858 CTACCAAAA 866

RESULT 41
US-10-176-482-365
```

```
/ Sequence 365, Application US/10176482
/ Publication No. US20030022296A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C70
/ CURRENT APPLICATION NUMBER: US/10/176,482
/ CURRENT FILING DATE: 2002-06-20
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 365
/ LENGTH: 1257
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-176-482-365

Alignment Scores:
Pred. No.: 2, 21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-176-482-365 (1-1257)
QY 1 MetArgProGlnGlyProAlaIaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20
DB 138 ATGCGACCCGAGGAGCCCGCGCTCCCGACGCGCTCCGCGCTCTGCTGCTGCTG 137
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProGlyGlyGlnYsAla 40
DB 198 CTGCTGACGCTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGluValIaIaLeuLeuTyraGlyMetCysLeuGlnGlyProAla 60
DB 258 CAGCTCCGCGAGGAGGAGGTGTGACCTGTATATGATGTGCTTACAAAGGCGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 318 GAGGTCTGTGTGAGAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
DB 378 CCAAGTCCGGATGATTTCAAGAGAGAAAGGGGAAATGCTGAGGAAAGCTTTGAGAG 437
QY 101 SerTyrThrProAsnTyrIysGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120
DB 438 TCCTGACACCCCAATCAAGACAGTGTTCATGAGTTCAATTAATTAATGATGATCTT 497
QY 121 GlyIleIleAlaIuGlySerThrPheThrIleMetArgSerSerSerAlaLeuArgValIleu 140
DB 498 GGAAGAAATGCGAGGTGTACATTACAAAGATCGTTCAATATGCTCAAGAGTTTG 557
QY 141 PheSerGlySerLeuArgLeuLeuYsCysArgAsnAlaCysCysGlnArgTyrPyrPheThr 160
DB 558 TTCAGTGGCTCACTTGGCTTAAATGCAAAATGCAATGCTGCAAGCTTGTGATTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleIleIleLeuAspGln 180
DB 618 TTCAAATGAGACTGAATGTTCAAGACCTCTCCATGAACTAATTAATTTTGACCAA 677
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QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAAATGATTAATCAACATTAATATTCATCGACCTTCTGTGGAGAGACTT 737
QY 201 CysGluGlyIleGlyValGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGGAATGGTGTGATTAAGAGATGGTTCATCGGGTGGCACTGTGTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 798 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTGCAATCATTAATTGAAGA 857
QY 241 LeuProLys 243
Db 858 CTACCAAAA 866

RESULT 42
US-10-176-757-365
; Sequence 365, Application US/10176757
; Publication No. US20030022297A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C86
; CURRENT APPLICATION NUMBER: US/10/176,757
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-757-365

Alignment Scores:
Pred. No.: 2,216-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-176-757-365 (1-1257)
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 138 ATGGCAAGCCCGAGGGGCGCCGCGCTCCCGCAGCGCTCCGGGGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluIleProLysGlyLysGlnValAla 40
Db 198 CTGCTGCAAGCTCCCGCGCCCTCGAGCGCTCTGAGATCCCAAGGAGGCAAAAGCG 257
QY 41 GlnLeuArgGlnArgGlnValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGGGAGAGAGAGAGTGTGAGCTGTATATATGAGATGCTTCAAGGGGCAACA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyTle 80
Db 318 GGAATGGCTGTGTGAGAGAGAGCGCTGGGGCAATGTATATCCCGGTACACCTGGGATC 377
QY 81 ProGlyArgAspGlyPheLysGlyGluLysGlyGluCysLeuArgGluSerPheGluIle 100
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Db 378 CCAGTCGGGATGATTCAAAGAGAAAAAGGGGGAATGCTGAGGGAAGCTTTGAGAG 437
QY 101 SerTrpThrProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120
Db 438 TCTTGAGACCCCACTACAGAGAGTTCATGAGGATTCATTAAGATTAATGATGATCTT 497
QY 121 GlyLysIleAlaGlyCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATATGCGAGATGTCATTTACAAAGATGCGTTCAAAATAGCTCTTAAGATTG 557
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpTyrPheThr 160
Db 558 TTCAGTGGCTCATTGCGCTAAATGCGAAATCATGCTGTACGCGTGGATATTACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180
Db 618 TTCATGAGAGCTGAATGTTCAGAGACTTCTCCATGAGCTAATTAATTTATTTGGACAA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAAATGATTAATCAACATTAATATTCATCGACCTTCTGTGGAGAGACTT 737
QY 201 CysGluGlyIleGlyValGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGGAATGGTGTGATTAAGAGATGGTTCATCGGGTGGCACTGTGTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGlu 240
Db 798 TACCCAAAAGAGAGTCTTACTGAGATGGAATTCAGTTTCTGCAATCATTAATTGAAGA 857
QY 241 LeuProLys 243
Db 858 CTACCAAAA 866

RESULT 43
US-10-176-913-365
; Sequence 365, Application US/10176913
; Publication No. US20030022298A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C66
; CURRENT APPLICATION NUMBER: US/10/176,913
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-913-365

Alignment Scores:
Pred. No.: 2,216-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-176-913-365 (1-1257)
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```
QY 1 MetArpProGlnGlyProAlaIaSerProGlnArGlyLeuLeuLeu 20
Db 138 ATGCCAAGCCAGGGCCCGCCCTCCCGACGGCTCCGGGCTTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGly 40
Db 198 CTGCTGCAGCTGCCCGCCGCTGAGCGCTCTGAGATCCCCAAGGGGAAGCAAGGGCG 257
QY 41 GlnLeuArGlnArGlnValValAlaPleuTyraGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGGCAGAGGAGGTGGTGAACCTGTAAAGAAATGCTTAACAAGGGCCAGCA 317
QY 61 GlyValProGlyArGAspGlySerProGlyAlaAsnValLeuProGlyThrProGlyIle 80
Db 318 GGAAGTCCCTGGTGGAGACGGGACCTCGGGCCAAATGTTATTCGGGTACACCTGGAGATC 377
QY 81 ProGlyArGAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 378 CCAGGTCCGGATGATTCAGAAAGAGAAAGGGGGAATGCTGAGGAAAGCTTTGAGAG 437
QY 101 SerTPThrProAsnTyrlsGlnCysSerTPSerSerLeuAsnTyrlsIleAlaPleu 120
Db 438 TCCTGGACACCCCAACTACAGAGCTGTTCAATGAGATTCATGAAATATGCAATAGATCTT 497
QY 121 GlyValIleAlaGluCysThrPheThrIleMetArGSerAsnSerAlaLeuArGValLeu 140
Db 498 GGGAAATATGGAGAGTGTACATTTACAAAGATCGCTTCAATATGCTCTTAAGAGTTTGG 557
QY 141 PheSerGlySerLeuArGLeuLysCysArGAsnAlaCysCysGlnArGTrpTyrlPheThr 160
Db 558 TTCAGTGGCTCACTTGGCTTAAATGCAAAATGCAATGCTGAGGCTTGATTTTCAACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlLeuAspGln 180
Db 618 TTCAATGGAGTGAAGTTCAGAGACCTCTCCATTTGAAGCTAATATTTATTTGAGCCAA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAAATGATTCACAAATTAATTCATCGCATCTTCTGAGAGGACTT 737
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGAAATGGTCTGCTGATTAAGTGAATGTTGCTATCGGGTGGCACTTGTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGln 240
Db 798 TACCCAAAAGAGAGTCTTCTACTGATGGAATTCAGTTTCTCGCATCATTTATGAAGAA 857
QY 241 LeuProLys 243
Db 858 CTACCAAAA 866
RESULT 44
US-10-180-552-365
; Sequence 365, Application US/10180552
; Publication No. US20030022300A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Ausetin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C153
; CURRENT APPLICATION NUMBER: US/10/180,552
; CURRENT FILING DATE: 2002-06-25
```

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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO. 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-180-552-365
Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-063-734-122 (1-243) x US-10-180-552-365 (1-1257)
QY 1 MetArpProGlnGlyProAlaIaSerProGlnArGlyLeuLeuLeu 20
Db 138 ATGCCAAGCCAGGGCCCGCCCTCCCGACGGCTCCGGGCTTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGly 40
Db 198 CTGCTGCAGCTGCCCGCCGCTGAGCGCTCTGAGATCCCCAAGGGGAAGCAAGGGCG 257
QY 41 GlnLeuArGlnArGlnValValAlaPleuTyraGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGGCAGAGGAGGTGGTGAACCTGTAAAGAAATGCTTAACAAGGGCCAGCA 317
QY 61 GlyValProGlyArGAspGlySerProGlyAlaAsnValLeuProGlyThrProGlyIle 80
Db 318 GGAAGTCCCTGGTGGAGACGGGACCTCGGGCCAAATGTTATTCGGGTACACCTGGAGATC 377
QY 81 ProGlyArGAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100
Db 378 CCAGGTCCGGATGATTCAGAAAGAGAAAGGGGGAATGCTGAGGAAAGCTTTGAGAG 437
QY 101 SerTPThrProAsnTyrlsGlnCysSerTPSerSerLeuAsnTyrlsIleAlaPleu 120
Db 438 TCCTGGACACCCCAACTACAGAGCTGTTCAATGAGATTCATGAAATATGCAATAGATCTT 497
QY 121 GlyValIleAlaGluCysThrPheThrIleMetArGSerAsnSerAlaLeuArGValLeu 140
Db 498 GGGAAATATGGAGAGTGTACATTTACAAAGATCGCTTCAATATGCTCTTAAGAGTTTGG 557
QY 141 PheSerGlySerLeuArGLeuLysCysArGAsnAlaCysCysGlnArGTrpTyrlPheThr 160
Db 558 TTCAGTGGCTCACTTGGCTTAAATGCAAAATGCAATGCTGAGGCTTGATTTTCAACA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlLeuAspGln 180
Db 618 TTCAATGGAGTGAAGTTCAGAGACCTCTCCATTTGAAGCTAATATTTATTTGAGCCAA 677
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCCTGAAATGATTCACAAATTAATTCATCGCATCTTCTGAGAGGACTT 737
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220
Db 738 TGTGAAGAAATGGTCTGCTGATTAAGTGAATGTTGCTATCGGGTGGCACTTGTCAGAT 797
QY 221 TyrProLysGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGln 240
Db 798 TACCCAAAAGAGAGTCTTCTACTGATGGAATTCAGTTTCTCGCATCATTTATGAAGAA 857
QY 241 LeuProLys 243
Db 858 CTACCAAAA 866
RESULT 45
US-10-180-557-365
; Sequence 365, Application US/10180557
```

```

Publication No. US2003002301A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Ylan
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P343081C147
CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 365
LENGTH: 1257
TYPE: DNA
ORGANISM: Homo Sapien
US-10-180-557-365

```

```
Db 438 TCCTGGACACCCAACTACAGAGCTGTTCATGAGTTCAATTAATGACATAGATCTT 497
Qy 121 G1ylysl1a1aG1uCystrPhetrlyrMetArSerArSerArAlaLeuArVal1leu 140
Db 498 GGGAAAATTGCGAGATGTCATTATTAACAAGATGCTTCAAAATAGTCTCTAAGAGTTTGG 557
Qy 141 PheSerG1Ser1euArSer1euArSer1euArSer1euArSer1euArSer1euArSer1eu 160
Db 558 TTCAGTGGCTCACTTCTGGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 617
Qy 161 PheAsnG1yAlaG1uCySerG1yPro1euPro1leuAla1le1le1le1le1le1le1le1 180
Db 618 TTCAAATGGAGCTGAATGTTCAAGACCTCTTCCCATTTGAAGCTATATTATTATTTGACCAA 677
Qy 181 G1ySerProG1uMeArSerThrl1eAn1le1eArG1ThSerSerVal1G1uG1y1leu 200
Db 678 GGAAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 737
Qy 201 CySG1uG1y1leG1yAlaG1yLeuValAspValAla1le1le1le1le1le1le1le1le1 220
Db 738 TGTGAAGGAAATGCTGCTGATTAAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 797
Qy 221 TyrProLyG1yAspAlaSerThrG1yTTPAsnSerValSerArg1le1le1le1le1le1 240
Db 798 TACCCAAAAGAGAGATCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATG 857
Qy 241 LeuProLy 243
Db 858 CTACCAAAA 866
```

## RESULT 47

```
US-10-173-700-365
; Sequence 365, Application US/10173700
; Publication No. US20030027262A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C14
; CURRENT APPLICATION NUMBER: US/10/173,700
; PRIOR APPLICATION DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-700-365
```

## Alignment Scores:

```
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
```

US-10-063-734-122 (1-243) x US-10-173-700-365 (1-1257)

```
Qy 1 MetArProG1nG1yPro1a1aSerProG1nArG1yLeuArG1yLeuArG1yLeuArG1yLeu 20
Db 138 ATCGACACCCAGGAGCCCGCGCTCCCGGACAGGAGCTCCGCGGCTCCGCTGCTGCTCCTG 197
```

```
Qy 21 LeuLeuG1nLeuPro1a1aProSerSer1aSerG1u1leProLyG1yLyseG1nLyseAla 40
Db 198 CTGCTGACAGCTGCCCGCCCGCTCGAGCCCTCTGAGATCCCAAGGAGAGAGAGAGAGAGAG 257
Qy 41 G1nLeuArG1nArG1yAlaVala1aPleuArSer1eArSer1eArSer1eArSer1eArSer1e 60
Db 258 CAGCTCCCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 317
Qy 61 G1yAlaProG1yArG1yArG1ySerProG1yAlaArVal1le1le1le1le1le1le1le1le 80
Db 318 GGAAGGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 377
Qy 81 ProG1yArG1yArG1yPhyLyseG1yG1yLyseG1yG1yLyseG1yG1yLyseG1yG1yLyse 100
Db 378 CAGGCTGGAGATGATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
Qy 101 SerTrpThrProAsnTyrLyseG1nCySerTrpSerSer1eArSer1eArSer1eArSer1e 120
Db 438 TCCTGGACACCCAACTACAGAGCTGTTCATGAGTTCAATTAATTAATTAATTAATTAATTAAT 497
Qy 121 G1ylysl1a1aG1uCystrPhetrlyrMetArSerArSerArAlaLeuArVal1leu 140
Db 498 GGGAAAATTGCGAGATGTCATTATTAACAAGATGCTTCAAAATAGTCTCTAAGAGTTTGG 557
Qy 141 PheSerG1Ser1euArSer1euArSer1euArSer1euArSer1euArSer1euArSer1eu 160
Db 558 TTCAGTGGCTCACTTCTGGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 617
Qy 161 PheAsnG1yAlaG1uCySerG1yPro1euPro1leuAla1le1le1le1le1le1le1le1le 180
Db 618 TTCAAATGGAGCTGAATGTTCAAGACCTCTTCCCATTTGAAGCTATATTATTATTTGACCAA 677
Qy 181 G1ySerProG1uMeArSerThrl1eAn1le1eArG1ThSerSerVal1G1uG1y1leu 200
Db 678 GGAAGCCCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 737
Qy 201 CySG1uG1y1leG1yAlaG1yLeuValAspValAla1le1le1le1le1le1le1le1le1 220
Db 738 TGTGAAGGAAATGCTGCTGATTAAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 797
Qy 221 TyrProLyG1yAspAlaSerThrG1yTTPAsnSerValSerArg1le1le1le1le1le1 240
Db 798 TACCCAAAAGAGAGATCTTCTACTGATGATGATGATGATGATGATGATGATGATGATGATG 857
Qy 241 LeuProLy 243
Db 858 CTACCAAAA 866
```

## RESULT 48

```
US-10-174-572-365
; Sequence 365, Application US/10174572
; Publication No. US20030027263A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C40
; CURRENT APPLICATION NUMBER: US/10/174,572
; PRIOR APPLICATION DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
```

```

; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-572-365

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-174-572-365 (1-1257)
QY 1 MetATpProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 138 ATGCAACCCCAAGGCCCCCGCTCCCGACGCGCTCCGCGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGlyAla 40
Db 198 CTGCTGACGCTCCCGCGCTCGAGCGCTCTGAGATGCCCAAGGGAAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValAlaLeuLeuTyrrAsnGlyMetCysLeuGlnGlyProAla 60
Db 258 CAGCTCCGACAGAGGAGGTGTGACCTGTATTAATGAGATGCTTACAGGCGCAGCA 317
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
Db 318 GGAAGTCCGTGTGAGACGGGAGCCCTGGGCGCAATGTTATTCGGGTACACTGGGATC 377
QY 81 ProGlyArgAspGlyPheIysGlyGlyGlyCysLeuArgGlnSerPheGlnGlu 100
Db 378 CCAGGTCCGGAGATTCAAAGAGAGAAAGGGGAGATGTCTGAGGGAAGCTTTGAGAG 437
QY 101 SerTPTrProAsnTyrrIysGlnCysSerTPSerSerLeuAsnTyrrGlyIleAspLeu 120
Db 438 TCCTGGACACCACTACAGCAAGTGTTCATGAGATTCATTAATTAATGCAATGATCTT 497
QY 121 GlyIysIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATTGGCGAGTGTATCATTTCAAAAGATCGCTTCAAAATGCTTAAAGATTTTG 557
QY 141 PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTPTrPheThr 160
Db 558 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGATGCTGTACAGGTGGTATTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrrLeuAspGln 180
Db 618 TTCAATGAGAGCTGATGTTCAAGACCTCTTCCCATTTGAAGCTATTAATTTGAGACCA 677
QY 181 GlySerProGlnMetArgSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCTGAATTAATTCACAAATTAATTAATTCATTCGACATCTTCTGTGAAAGACTT 737
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTPTrValGlyThrCysSerAsp 220
Db 738 TGTAAAGAAATGTGTGTGATTAATGATGTTGCTATCTGGGTGGGCACTTGTTCAGAT 797
QY 221 TyrProIysGlyAspAlaSerThrGlyTyrrAsnSerValSerArgIleIleIleGlnGlu 240
Db 798 TACCAAAAGAGATGCTTCTACTGATGATGATTCAGATTTCTCGCATATTAATTAAGA 857
QY 241 LeuProIys 243
Db 858 CTACCAAAA 866

RESULT 49
US-10-174-579-365
; Sequence 365, Application US/10174579
; Publication No. US20030027264A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

```

```

; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C31
; CURRENT APPLICATION NUMBER: US/10/174,579
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-579-365

Alignment Scores:
Pred. No.: 2,21e-144 Length: 1257
Score: 1301.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-174-579-365 (1-1257)
QY 1 MetATpProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20
Db 138 ATGCAACCCCAAGGCCCCCGCTCCCGACGCGCTCCGCGCTCTGCTGCTCTG 197
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGlyAla 40
Db 198 CTGCTGACGCTCCCGCGCTCGAGCGCTCTGAGATGCCCAAGGGAAGCAAGGCG 257
QY 41 GlnLeuArgGlnArgGlnValAlaLeuLeuTyrrAsnGlyMetCysLeuGlnGlyProAla 60
Db 318 GGAAGTCCGTGTGAGACGGGAGCCCTGGGCGCAATGTTATTCGGGTACACTGGGATC 377
QY 81 ProGlyArgAspGlyPheIysGlyGlyGlyCysLeuArgGlnSerPheGlnGlu 100
Db 378 CCAGGTCCGGAGTGTATTCAAAGAGAGAAAGGGGAGATGTCTGAGGGAAGCTTTGAGAG 437
QY 101 SerTPTrProAsnTyrrIysGlnCysSerTPSerSerLeuAsnTyrrGlyIleAspLeu 120
Db 438 TCCTGGACACCACTACAGCAAGTGTTCATGAGATTCATTAATTAATGCAATGATCTT 497
QY 121 GlyIysIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140
Db 498 GGGAAATTGGCGAGTGTATCATTTCAAAAGATCGCTTCAAAATGCTTAAAGATTTTG 557
QY 141 PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTPTrPheThr 160
Db 558 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGATGCTGTACAGGTGGTATTTCA 617
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrrLeuAspGln 180
Db 618 TTCAATGAGAGCTGATGTTCAAGACCTCTTCCCATTTGAAGCTATTAATTTGAGACCA 677
QY 181 GlySerProGlnMetArgSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200
Db 678 GGAAGCCTGAATTAATTCACAAATTAATTAATTCATTCGACATCTTCTGTGAAAGACTT 737

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QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220  
Db 738 TGTGAAGGAATGCTGCTGATTAAGTGAATGCTATCTGATCTGCTGCACTTGTTCAGAT 797  
QY 221 TyrProLysGlyAspAlaSerThrGlyTyrPaenSerValSerArgIleIleIleGlu 240  
Db 798 TACCCAAAAGGAGATCTTCTACTGATGATGAAATTCAGTTTCGCATCATTAATGAAGA 857  
QY 241 LeuProLys 243  
Db 858 CTACCAAAA 866

## RESULT 50

US-10-174-582-365  
; Sequence 365, Application US/10174582  
; Publication No. US20030027265A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C36  
; CURRENT APPLICATION NUMBER: US/10/174,582  
; CURRENT FILING DATE: 2002-06-18  
; Prior Application removed - See file wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 365  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-174-582-365

Alignment Scores:  
Pred. No.: 2,21e-144 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-063-734-122 (1-243) x US-10-174-582-365 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeuLeu 20  
Db 138 ATGCGACCCCGAGGCGCCCGCGCTCCCGCAGCGGCTCCGCGCTGCTGCTCTG 197  
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnIleProLysGlyLysGlnLysAla 40  
Db 198 CTGCTGAGCTGCCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGGAAGCAAAAGCG 257  
QY 41 GlnLeuArgGlnArgGlnValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60  
Db 258 CAGCTCCGCGAGAGGAGGAGTGTGAGACTGTATATATGAAATGTCTTACAAAGGCCAGCA 317  
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80  
Db 318 GGAGTGTCTGTGAGAGCGGAGCCCTGGGGCCAATGTATTCGGGGTACACCTGGGATC 377  
QY 81 ProGlyArgAspGlyPheLysGlyGlnLysGlyGlnCysLeuArgGlyLysPheGlnGlu 100  
Db 378 CCAAGTGGGATGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437  
QY 101 SerTyrProAsnTyrLysGlnCysSerTyrSerSerLeuAsnTyrGlyIleAspLeu 120

Db 438 TCCGTGACACCCCACTACAGAGATGTCATGAGACTTCATTAATTAAGCATTAATCTT 497  
QY 121 GlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140  
Db 498 GGGAAATTTGCGAGATGTCATTTTCAAAAGATGCTTCAAAATAGCTCTTAAGATTGG 557  
QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTyrPheThr 160  
Db 558 TTCAGTGGCTCACTTCGGCTAAATGCAAAATGCAATGATGCTGTCAGCTGTGATTTACA 617  
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGlnAlaIleIleTyrLeuAspGln 180  
Db 618 TTCAATGGAGCTGAATGTCAGAGACTTCCCATTTGAAGCTAATTAATTTATTTGAACCA 677  
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200  
Db 678 GGAAGCCCTGAAATGATTAACAATTAATTAATTCATTCGACATTTCTTGTGTGAAGACTT 737  
QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220  
Db 738 TGTGAAGGAATTGGTGTGATTAAGTGAATGCTATCTGATCTGCTGCACTTGTTCAGAT 797  
QY 221 TyrProLysGlyAspAlaSerThrGlyTyrPaenSerValSerArgIleIleIleGlu 240  
Db 798 TACCCAAAAGGAGATCTTCTACTGATGATGAAATTCAGTTTCGCATCATTAATGAAGA 857  
QY 241 LeuProLys 243  
Db 858 CTACCAAAA 866

Search completed: December 25, 2004, 07:59:55  
Job time : 562 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 23:00:19 ; Search time 736.Seconds  
(without alignments)  
9509.805 Million cell updates/sec

Title: US-10-063-734-121

Perfect score: 1257

Sequence: 1 ggaagagagcgcgcggtgta.....aataaataattccacaa 1257

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA.\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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; Patent No. US20020161199A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Polakis, Paul
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5009R1
; CURRENT APPLICATION NUMBER: US/09/938,418
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/081,071
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/085,697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/097,022
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/101,922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/103,679
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; PRIOR FILING DATE: 1999-03-08
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; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28

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; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-938-418-2

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; Sequence 430, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tuma, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCES: P2830P1C1  
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; CURRENT FILING DATE: 2001-09-04  
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 PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1257; DB 10; Length 1257;  
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 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 61 CGAGCCAGACGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
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 121 CCGGCGAGCGCGGAGCCATGAGACCCAGAGGCCCGCGCGCTCTCGGAGCGCGCTCGG 180  
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Db 901 TTATTATGCTTGAATGCTTCACTTAATTAATGCTTAATTAATGCTTAATGCTT 960  
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Qy 1141 TTTGTTTTTCTCTTAGTATAGATTTTAAAAAATATAAAGTACCAATCTTTGAC 1200  
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Qy 1201 AATTGTAATGTAAGATTTTATTTATCTGTTAAATTAATTTATTTCCACA 1257  
Db 1201 AATTGTAATGTAAGATTTTATTTATCTGTTAAATTAATTTATTTCCACA 1257

RESULT 3  
US-10-006-867-121  
Sequence 121, Application US/10006867  
Publication No. US20020119130A1  
GENERAL INFORMATION:  
APPLICANT: Baton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/006, 867  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: 60/063435  
PRIOR FILING DATE: 1997-10-29  
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PRIOR FILING DATE: 1997-10-29  
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Query Match 100.0%; Score 1257; DB 13; Length 1257;  
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61	CGAGCCAGACGCTGACCAAGTTCCTCTCTCGGTCTCTCCGCTCAAGCTCCGCGCTG	120					
61	CGAGCCAGACGCTGACCAAGTTCCTCTCTCGGTCTCTCCGCTCAAGCTCCGCGCTG	120					
121	CCGGGACGCGGGAGGACATGCAATCCCAAGGCCCCCGCGCTCCCGGACGGGCTCCGCG	180					
121	CCGGGACGCGGGAGGACATGCAATCCCAAGGCCCCCGCGCTCCCGGACGGGCTCCGCG	180					
181	GCCCTCGCTGCTCTCGCTGCTGCAAGTCCCGCGCGCTCGAGGCGCTCGAGATCCCA	240					
181	GCCCTCGCTGCTCTCGCTGCTGCAAGTCCCGCGCGCTCGAGGCGCTCGAGATCCCA	240					
241	AGGGAGAGCAAAAGGCGCAGCTCCGCGAGAGGAGTGTGACCTGTATATGATGAT	300					
241	AGGGAGAGCAAAAGGCGCAGCTCCGCGAGAGGAGTGTGACCTGTATATGATGAT	300					
301	GCTTACAAAGGCGCAGAGAGTGGCTGGTGGAGAGGGAGCCCTCGGGGCCAATGTTATTC	360					
301	GCTTACAAAGGCGCAGAGAGTGGCTGGTGGAGAGGGAGCCCTCGGGGCCAATGTTATTC	360					
361	CGGGTACACCTGGGATCCCAAGGTGGGATGATTCATTAAGAGAAAAGGGGAGATGCTGA	420					
361	CGGGTACACCTGGGATCCCAAGGTGGGATGATTCATTAAGAGAAAAGGGGAGATGCTGA	420					
421	GGGAAGCTTTGAGAGGCTCTGAGACCCCACTACAGCGATGTTATGAGAGTCTATGGA	480					
421	GGGAAGCTTTGAGAGGCTCTGAGACCCCACTACAGCGATGTTATGAGAGTCTATGGA	480					
481	ATTATGGCATAGTCTTGGGAAAATTGCGAGTGTATCATTTACAAAGATGCGTCAATA	540					
481	ATTATGGCATAGTCTTGGGAAAATTGCGAGTGTATCATTTACAAAGATGCGTCAATA	540					
541	GTGCTCTAAGAGTTTGTTCAGTGGCTCATCTCGGCTTAAATGCAAAATGATGATCTGTC	600					
541	GTGCTCTAAGAGTTTGTTCAGTGGCTCATCTCGGCTTAAATGCAAAATGATGATCTGTC	600					
601	AGGTTGGAATTTCAATTCATGGAAGTGAATGTTGAGAGCTCTTCCCATTTGAAGCTA	660					
601	AGGTTGGAATTTCAATTCATGGAAGTGAATGTTGAGAGCTCTTCCCATTTGAAGCTA	660					
661	TAAATTTATTTGAGCAAGAGAGCCCTGAAATGAAATTCACAAATTAATTTATTCGCACTT	720					
661	TAAATTTATTTGAGCAAGAGAGCCCTGAAATGAAATTCACAAATTAATTTATTCGCACTT	720					
721	CTTCTGTGAGAGACTTTGTGAAGAAATGGTGTGATTAATGAGATGTTGCTATCTGAG	780					
721	CTTCTGTGAGAGACTTTGTGAAGAAATGGTGTGATTAATGAGATGTTGCTATCTGAG	780					
781	TTGGCACTGTTCAATTAACCAAGAGAGTGTCTTACTGGAATGGAATTCAGTTCTTC	840					

Db 781 TTGGCACTTGTTCAGATTACCCAAAGAGAGTCTTCTACTGATGGAATTCAGTTTC 840  
QY 841 GGATCATTTATGAAGAACTACCAAAATATGCTTAATTTTCATTTGCTACTCTTTT 900  
Db 841 GCATCATTTATGAAGAACTACCAAAATATGCTTAATTTTCATTTGCTACTCTTTT 900  
QY 901 TTATTAAGCTTGAAGTGTTCCTTAATTAATGATTTAAATAGTTATGATACATCT 960  
Db 901 TTATTAAGCTTGAAGTGTTCCTTAATTAATGATTTAAATAGTTATGATACATCT 960  
QY 961 GAATGAAAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTCACTGTTTTAA 1020  
Db 961 GAATGAAAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTCACTGTTTTAA 1020  
QY 1021 ACTACATTAATTCATTTGCTTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
Db 1021 ACTACATTAATTCATTTGCTTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
QY 1081 AGAATACCTTCTCATAGTACATCTCTCAACCTTAATTTGGAATATTTGTGCT 1140  
Db 1081 AGAATACCTTCTCATAGTACATCTCTCAACCTTAATTTGGAATATTTGTGCT 1140  
QY 1141 TTTGTTTTCTCTAGTATGATGCAATTTTAAAAAATATAAGCTACCAATCTTTGAC 1200  
Db 1141 TTTGTTTTCTCTAGTATGATGCAATTTTAAAAAATATAAGCTACCAATCTTTGAC 1200  
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTTCCACA 1257  
Db 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTTCCACA 1257

## RESULT 5

US-10-063-547-121  
Sequence 121, Application US/10063547  
Publication No. US20020182638A1  
GENERAL INFORMATION:  
APPLICANT: Ealon, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Malanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,547  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 121  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-063-547-121

Query Match 100.0%; Score 1257; DB 13; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3,4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGGCGCGGGGTAAAGCCGATGATGCAAGCTGCGCGCGGCTCGAGAGCGG 60  
Db 1 GGAGAGAGGCGCGGGGTAAAGCCGATGATGCAAGCTGCGCGCGGCTCGAGAGCGG 60  
QY 61 CGAGAGCAGAGCGCTGACCAAGCTTCTCTCGGCTCTCGGCTCAGCTCGGCGCTG 120  
Db 61 CGAGAGCAGAGCGCTGACCAAGCTTCTCTCGGCTCTCGGCTCAGCTCGGCGCTG 120  
QY 121 CCGGAGCGCGGAGCGATCGAAGCCGAGGCGCGCGCGCTCCGCGAGCGGCTCGCG 180  
Db 121 CCGGAGCGCGGAGCGATCGAAGCCGAGGCGCGCGCGCTCCGCGAGCGGCTCGCG 180

QY 181 GCCTCTGCTGCTCTGCTGCTGCAAGCTGCCGCGCGCTCGAGCGCTCGAGATCCCA 240  
Db 181 GCCTCTGCTGCTCTGCTGCTGCAAGCTGCCGCGCGCTCGAGCGCTCGAGATCCCA 240  
QY 241 AGGGAGAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGACCTGTATTAATGAAATG 300  
Db 241 AGGGAGAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGACCTGTATTAATGAAATG 300  
QY 301 GCTTACAAAGGCGCAGAGAGTCCGCTGCGAGCGGAGCCCTGGGCGCAATGTAATC 360  
Db 301 GCTTACAAAGGCGCAGAGAGTCCGCTGCGAGCGGAGCCCTGGGCGCAATGTAATC 360  
QY 361 CGGCTACCTGAGATCCAGAGTGGAGTGAATTCAAAGAGAAAGGAGGAAATGCTGA 420  
Db 361 CGGCTACCTGAGATCCAGAGTGGAGTGAATTCAAAGAGAAAGGAGGAAATGCTGA 420  
QY 421 GGAGAAAGCTTTGAGAGTCTTGACACCCCACTACAGAGAGTTCATGAGATTCGA 480  
Db 421 GGAGAAAGCTTTGAGAGTCTTGACACCCCACTACAGAGAGTTCATGAGATTCGA 480  
QY 481 ATTAAGGCAATGATCTTGGGAAATTTGGGAGGTATCATTTACAAAGATGCCTTCAA 540  
Db 481 ATTAAGGCAATGATCTTGGGAAATTTGGGAGGTATCATTTACAAAGATGCCTTCAA 540  
QY 541 GTGCTCTAAGATTTGTTCAAGTGTCTCACTTCGCTTAAATGCAAGATGATGCTGTC 600  
Db 541 GTGCTCTAAGATTTGTTCAAGTGTCTCACTTCGCTTAAATGCAAGATGATGCTGTC 600  
QY 601 AGCGTGTATTTCAATTCATTAAGAGTGAATGTTCAAGAGCTCTTCCATTTGAAGTA 660  
Db 601 AGCGTGTATTTCAATTCATTAAGAGTGAATGTTCAAGAGCTCTTCCATTTGAAGTA 660  
QY 661 TAATTTATTTGACCAAGAGAGCCCTGAATGATTCACCAATTAATTTATTCATGCACT 720  
Db 661 TAATTTATTTGACCAAGAGAGCCCTGAATGATTCACCAATTAATTTATTCATGCACT 720  
QY 721 CTTCTGAGAGAGACTTGTGAAGAAATGGTGTGATGATGATGATGATGATGATG 780  
Db 721 CTTCTGAGAGAGACTTGTGAAGAAATGGTGTGATGATGATGATGATGATGATG 780  
QY 781 TTGGCACTTGTTCAGATTACCCAAAGAGAGTCTTCACTGATGAGAAATTCAGTTCTC 840  
Db 781 TTGGCACTTGTTCAGATTACCCAAAGAGAGTCTTCACTGATGAGAAATTCAGTTCTC 840  
QY 841 GCATCATTTATGAAGAACTACCAAAATATGCTTAATTTTCATTTGCTACTCTTTT 900  
Db 841 GCATCATTTATGAAGAACTACCAAAATATGCTTAATTTTCATTTGCTACTCTTTT 900  
QY 901 TTATTAAGCTTGAAGTGTTCCTTAATTAATGATTTAAATAGTTATGATACATCT 960  
Db 901 TTATTAAGCTTGAAGTGTTCCTTAATTAATGATTTAAATAGTTATGATACATCT 960  
QY 961 GAATGAAAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTCACTGTTTTAA 1020  
Db 961 GAATGAAAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTTCACTGTTTTAA 1020  
QY 1021 ACTACATTAATTCATTTGCTTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
Db 1021 ACTACATTAATTCATTTGCTTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
QY 1081 AGAATACCTTCTCATAGTACATCTCTCAACCTTAATTTGGAATATTTGTGCT 1140  
Db 1081 AGAATACCTTCTCATAGTACATCTCTCAACCTTAATTTGGAATATTTGTGCT 1140  
QY 1141 TTTGTTTTCTCTAGTATGATGCAATTTTAAAAAATATAAGCTACCAATCTTTGAC 1200  
Db 1141 TTTGTTTTCTCTAGTATGATGCAATTTTAAAAAATATAAGCTACCAATCTTTGAC 1200  
QY 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTTCCACA 1257  
Db 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTTCCACA 1257

```
RESULT 6
US-10-063-551-121
; Sequence 121, Application US/10063551
; Publication No. US20020183494A1
GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 121
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-121

Query Match      100.0%; Score 1257; DB 13; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAGAGCGCGCGGCTGAAAAGCGCATTTGAGAGCTGCGCGCGCTCGAGAGCGCG 60
DB 1 GAGAGAGCGCGCGGCTGAAAAGCGCATTTGAGAGCTGCGCGCGCTCGAGAGCGCG 60
QY 61 CGAGAGCGAGCGCTACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGAGCGAGCGCTACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCGCGAGCGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 180
DB 121 CCGCGAGCGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 180
QY 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGAGAGCGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 300
DB 241 AGGAGAGCGAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 300
QY 301 GCTTACAGAGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 360
DB 301 GCTTACAGAGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 360
QY 361 CGGAGTACCTGGAGTCCAGGTGCGAGTGAATTCAGAGAGAGAGAGAGAGAGAG 420
DB 361 CGGAGTACCTGGAGTCCAGGTGCGAGTGAATTCAGAGAGAGAGAGAGAGAGAG 420
QY 421 GGGAGAGCTTGGAGAGTCTGAGACCCCACTAACACAGTTCATGAGAGTTCATGA 480
DB 421 GGGAGAGCTTGGAGAGTCTGAGACCCCACTAACACAGTTCATGAGAGTTCATGA 480
QY 481 ATTATGCGATGATCTTGGAGAGAGTTCAGAGTGAATTCAGAGAGAGAGAGAGAG 540
DB 481 ATTATGCGATGATCTTGGAGAGAGTTCAGAGTGAATTCAGAGAGAGAGAGAGAG 540
QY 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGAGAGATGATCTGTC 600
DB 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGAGAGATGATCTGTC 600
QY 601 AGCGTTGGTATTTCACATTCATGAGAGTGAATGTTTCAGAGCTCTTCCCATGAGCTA 660
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DB 601 AGCGTTGGTATTTCACATTCATGAGAGTGAATGTTTCAGAGCTCTTCCCATGAGCTA 660
QY 661 TAATTTATTTGGAGCAGAGAGAGCGCTGAAATGAAATTCACATTAATATTCATGCACTT 720
DB 661 TAATTTATTTGGAGCAGAGAGAGCGCTGAAATGAAATTCACATTAATATTCATGCACTT 720
QY 721 CTCTGTGAGAGAGCTTGTGAGAGAGATGGTGTGAGTGAAGTGTGATGCTATCTGGG 780
DB 721 CTCTGTGAGAGAGCTTGTGAGAGAGATGGTGTGAGTGAAGTGTGATGCTATCTGGG 780
QY 781 TTGGCAGCTTGTGAGATTCACCAAGAGAGATGCTTCTACGTGATGAGATTCAGTTCTC 840
DB 781 TTGGCAGCTTGTGAGATTCACCAAGAGAGATGCTTCTACGTGATGAGATTCAGTTCTC 840
QY 841 GCATATATTTGAGAGATTCACCAAGATGCTTCTACGTGATGAGATTCAGTTCTC 900
DB 841 GCATATATTTGAGAGATTCACCAAGATGCTTCTACGTGATGAGATTCAGTTCTC 900
QY 901 TTATATATCTTGGAGATGCTTCACTTAATGACATTTTAATAGTTAATGATATGATCT 960
DB 901 TTATATATCTTGGAGATGCTTCACTTAATGACATTTTAATAGTTAATGATATGATCT 960
QY 961 GAATGAGAGAGAGAGCTTAATATGTTTACAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GAATGAGAGAGAGAGCTTAATATGTTTACAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 ATCTAGCATTTATTCATTTTGTCTCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 AGAATACCTTCTTCAATGATGACATTTCTCAACCTTATATTTGAGATATGTTGTGCT 1140
DB 1081 AGAATACCTTCTTCAATGATGACATTTCTCAACCTTATATTTGAGATATGTTGTGCT 1140
QY 1141 TTTGTTTTTCTCTTATGATGATTTTAAATTAATTAATTAATTAATTAATTAATTA 1200
DB 1141 TTTGTTTTTCTCTTATGATGATTTTAAATTAATTAATTAATTAATTAATTAATTA 1200
QY 1201 AATTTGTAATGTTAAGATTTTATTAATGTTAATTAATTAATTAATTAATTAATTA 1257
DB 1201 AATTTGTAATGTTAAGATTTTATTAATGTTAATTAATTAATTAATTAATTAATTA 1257

RESULT 7
US-10-174-590-365
; Sequence 365, Application US/10174590
; Publication No. US2003008352A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-365
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Query Match 100.0%; Score 1257; DB 14; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTCGCGCGGCTCGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTCGCGCGGCTCGAGCGCG 60
QY 61 CGAGAGCAGACGCTGACGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGAGCAGACGCTGACGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCGGAGCGCGGAGCGCATGCGACCCCGAGGCGCGCGCTCCCGAGCGGCTCGCG 180
DB 121 CCGGAGCGCGGAGCGCATGCGACCCCGAGGCGCGCGCTCCCGAGCGGCTCGCG 180
QY 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 GCTTACAAAGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 GCTTACAAAGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 CGGAGTACACCTGGAGATCCAGAGTGGAGATGATTCAGAGAGAGAGAGAGAGAG 420
DB 361 CGGAGTACACCTGGAGATCCAGAGTGGAGATGATTCAGAGAGAGAGAGAGAGAG 420
QY 421 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 ATTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ATTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 GTGCTCTGAAGAGTTTGTTCAGTGGCTCACTTCGAGTAAATGACAGAAATGAC 600
DB 541 GTGCTCTGAAGAGTTTGTTCAGTGGCTCACTTCGAGTAAATGACAGAAATGAC 600
QY 601 AGCGTGGATTTTCAATTCATGAGAGCTGAGATGTTTCAAGACCTCTTCCCAT 660
DB 601 AGCGTGGATTTTCAATTCATGAGAGCTGAGATGTTTCAAGACCTCTTCCCAT 660
QY 661 TAATTTATTTGAGCAAGAGAGCGCTGAATGAAATCAATTAATTAATTCAGACT 720
DB 661 TAATTTATTTGAGCAAGAGAGCGCTGAATGAAATCAATTAATTAATTCAGACT 720
QY 721 CTTCCTGAGAGAGCTTTTGAAGAGATTTGCTGATGATGATGATGATGATGATG 780
DB 721 CTTCCTGAGAGAGCTTTTGAAGAGATTTGCTGATGATGATGATGATGATGATG 780
QY 781 TTGGCAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 TTGGCAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 GGATCATTTATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GGATCATTTATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 TTATTTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 TTATTTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 ATCTAGCATTTATTTGCTTCAATCAAAAGTGGTTCAATTAATTTTATTTAGT 1080
  
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DB 1021 ATCTAGCATTTATTTGCTTCAATCAAAAGTGGTTCAATTAATTTTATTTAGT 1080
QY 1081 AGAATATTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 AGAATATTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 TTTGTTTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 TTTGTTTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 AATTTGTAATTTGTAAGATTTTATTTATCTGTTAATATAAATTAATTTTCA 1257
DB 1201 AATTTGTAATTTGTAAGATTTTATTTATCTGTTAATATAAATTAATTTTCA 1257

```

RESULT 8  
 US-10-176-758-365  
 ; Sequence 365, Application US/10176758  
 ; Publication No. US20030008353A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430R1C104  
 ; CURRENT APPLICATION NUMBER: US/10/176,758  
 ; PRIORITY FILING DATE: 2002-06-21  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 365  
 ; LENGTH: 1257  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-176-758-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTCGCGCGGCTCGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTCGCGCGGCTCGAGCGCG 60
QY 61 CGAGAGCAGACGCTGACGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGAGCAGACGCTGACGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCGGAGCGCGGAGCGCATGCGACCCCGAGGCGCGCGCTCCCGAGCGGCTCGCG 180
DB 121 CCGGAGCGCGGAGCGCATGCGACCCCGAGGCGCGCGCTCCCGAGCGGCTCGCG 180
QY 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 GCTTACAAAGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 GCTTACAAAGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
  
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QY 361 CCGGTAACCTGGATCCAGTCGGATGATTCAGAGAGAAAAGGGGAATGCTGA 420
DB 361 CCGGTACACCTGGATCCAGTCGGATGATTCAGAGAGAAAAGGGGAATGCTGA 420
QY 421 GGGAAAGCTTGGAGTCTTGACACCCCACTACAGAGCTGTTCAATGAGTCAATGA 480
DB 421 GGGAAAGCTTGGAGTCTTGACACCCCACTACAGAGCTGTTCAATGAGTCAATGA 480
QY 481 ATTATGCAATAGATCTTGGGAAAATTCGGAGTGTACATTTACAAAGATCGTTCAAA 540
DB 481 ATTATGCAATAGATCTTGGGAAAATTCGGAGTGTACATTTACAAAGATCGTTCAAA 540
QY 541 GTGCTTAAGAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 GTGCTTAAGAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 AGCGTTGATTTTCAATTCAGATGAGCTGAAATGTTTCAAGACCTGTTCCATTTGAAG 660
DB 601 AGCGTTGATTTTCAATTCAGATGAGCTGAAATGTTTCAAGACCTGTTCCATTTGAAG 660
QY 661 TAAATTAATTTGACCAAGAGAGCCCTGAATGAAATCAATTAATTAATTCATCGCACT 720
DB 661 TAAATTAATTTGACCAAGAGAGCCCTGAATGAAATCAATTAATTAATTCATCGCACT 720
QY 721 CTTCGTGGAAGAGCTTGTGGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 CTTCGTGGAAGAGCTTGTGGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 TTGGCACTGCTCAGATTCACCAAGAGAGAGCTTCACTGAGATGGAATTCAGATTC 840
DB 781 TTGGCACTGCTCAGATTCACCAAGAGAGAGCTTCACTGAGATGGAATTCAGATTC 840
QY 841 GCATCAATTAATGAGAACTACCAAAATTAATGCTTAATTTTCAATGCTGCTGCTGCT 900
DB 841 GCATCAATTAATGAGAACTACCAAAATTAATGCTTAATTTTCAATGCTGCTGCTGCT 900
QY 901 TTATTAATGCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 TTATTAATGCTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GAATGAAAAGCAAGCACTAAATATGTTTACAGACCAAGAGTGTATTCACATGTTT 1020
DB 961 GAATGAAAAGCAAGCACTAAATATGTTTACAGACCAAGAGTGTATTCACATGTTT 1020
QY 1021 ATCTAGCAATTAATTCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 ATCTAGCAATTAATTCATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 AGAATACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 AGAATACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 TTGCTTTTCTCTAGATAGCATTTTAAAAAATTAATTAATTAATTAATTAATTAAT 1200
DB 1141 TTGCTTTTCTCTAGATAGCATTTTAAAAAATTAATTAATTAATTAATTAATTAAT 1200
QY 1201 AATTTGTAAGTGAATTTTATCTGTTAATTAATTAATTAATTAATTAATTAAT 1257
DB 1201 AATTTGTAAGTGAATTTTATCTGTTAATTAATTAATTAATTAATTAATTAAT 1257

```

## RESULT 9

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US-10-175-737-365
; Sequence 365, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James

```

```

; APPLICANT: Smith, Victoria
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-737-365

```

```

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGAAGAGGCGCGGGTGAAGGCGCATTTGATGACCTTCCGCGGCTCGAGGCGCG 60
DB 1 GGAAGAGGCGCGGGTGAAGGCGCATTTGATGACCTTCCGCGGCTCGAGGCGCG 60
QY 61 CGAGACCGAGCTGACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGAGACCGAGCTGACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCGGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB 121 CCGGCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 181 GCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGGAAGCAAAAGGCGCAGCTCCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
DB 241 AGGGAAGCAAAAGGCGCAGCTCCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 301 GCTTACAGAGGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
DB 301 GCTTACAGAGGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 CGGGAACCTGGGATCCGAGTCCGAGTGGATTTCAAGAGAAAAGGGGAATGCTGA 420
DB 361 CGGGAACCTGGGATCCGAGTCCGAGTGGATTTCAAGAGAAAAGGGGAATGCTGA 420
QY 421 GGGAAAGCTTGAAGAGTCTTGACACCCCACTACAGAGCTGTTCAATGAGTCAATGA 480
DB 421 GGGAAAGCTTGAAGAGTCTTGACACCCCACTACAGAGCTGTTCAATGAGTCAATGA 480
QY 481 ATTATGCAATAGATCTTGGGAAAATTCGGAGTGTACATTTACAAAGATCGTTCAAA 540
DB 481 ATTATGCAATAGATCTTGGGAAAATTCGGAGTGTACATTTACAAAGATCGTTCAAA 540
QY 541 GTGCTTAAGAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 GTGCTTAAGAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 AGCGTTGATTTTCAATTCAGATGAGCTGAAATGTTTCAAGACCTGTTCCATTTGAAG 660
DB 601 AGCGTTGATTTTCAATTCAGATGAGCTGAAATGTTTCAAGACCTGTTCCATTTGAAG 660
QY 661 TAAATTAATTTGACCAAGAGAGCCCTGAATGAAATCAATTAATTAATTCATCGCACT 720
DB 661 TAAATTAATTTGACCAAGAGAGCCCTGAATGAAATCAATTAATTAATTCATCGCACT 720
QY 721 CTTCGTGGAAGAGCTTGTGGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 CTTCGTGGAAGAGCTTGTGGAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

```

QY 781 TTGGCACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840  
DB 781 TTGGCACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840  
QY 841 GCATCAATTATGGAAGACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900  
DB 841 GCATCAATTATGGAAGACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900  
QY 901 TTATTTGCTTGGATGATGCTTCACTTAATGATCAATTTTAATAAGTTATGATACATCT 960  
DB 901 TTATTTGCTTGGATGATGCTTCACTTAATGATCAATTTTAATAAGTTATGATACATCT 960  
QY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTTCACTGTTTTTAA 1020  
DB 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTTCACTGTTTTTAA 1020  
QY 1021 ATCTAGCAATTATTCATTTTGTCTTCAATCAAAAGTGCTTCAATATTTTAAAGTTT 1080  
DB 1021 ATCTAGCAATTATTCATTTTGTCTTCAATCAAAAGTGCTTCAATATTTTAAAGTTT 1080  
QY 1081 AGAATCTTCTTCATAGTCACATTTCTCAACCTAATTTTGAATATGTTGTGCTT 1140  
DB 1081 AGAATCTTCTTCATAGTCACATTTCTCAACCTAATTTTGAATATGTTGTGCTT 1140  
QY 1141 TTGTTTTTCTCTTAGTATAGCAATTTTAAATTAATTAAGCTACCAATCTTTGATC 1200  
DB 1141 TTGTTTTTCTCTTAGTATAGCAATTTTAAATTAATTAAGCTACCAATCTTTGATC 1200  
QY 1201 AATTGTAAATGTTAAGAAATTTTAAATGTTAATTAATTAATTAATTTTCAACA 1257  
DB 1201 AATTGTAAATGTTAAGAAATTTTAAATGTTAATTAATTAATTAATTTTCAACA 1257

## RESULT 10

US-10-063-616-121  
; Sequence 121, Application US/10063616  
; Publication No. US20030013855A1  
; GENERAL INFORMATION:  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerstlisen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Guirney, Austin L.  
; APPLICANT: Matarabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063, 616  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 121  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-063-616-121

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3 4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGTGAAGCGCATTTGATGACGCTCGCGCGCTCGAGCGCGG 60  
DB 1 GGAGAGAGCGCGCGGTGAAGCGCATTTGATGACGCTCGCGCGCTCGAGCGCGG 60  
QY 61 CGAGAGCAGACGCTGACACGCTTCTCTCGTCTCTCTCGCTCCGCTCCGAGCTCGGCTG 120  
DB 61 CGAGAGCAGACGCTGACACGCTTCTCTCGTCTCTCTCGCTCCGCTCCGAGCTCGGCTG 120  
QY 1201 CCCGAGAGCGCGGAGCATGCAAGCCAGAGGCGCGCGCTCCGCGAGCGGCTCGCG 180

DB 121 CCCGAGAGCGCGGAGCATGCAAGCCAGAGGCGCGCGCTCCGCGAGCGGCTCGCG 180  
QY 181 GCTCTCTGCTGCTCTGCTGCTGCACTGCTCCGCGCGCTCGAGCGCTCTGAGATCCCA 240  
DB 181 GCTCTCTGCTGCTCTGCTGCTGCACTGCTCCGCGCGCTCGAGCGCTCTGAGATCCCA 240  
QY 241 AGGGGAAGCAAAAGCGCAGCTCCGCGCAGAGGAGGTGTGAGCTGTAAATGGAATGT 300  
DB 241 AGGGGAAGCAAAAGCGCAGCTCCGCGCAGAGGAGGTGTGAGCTGTAAATGGAATGT 300  
QY 301 GCTTACAGGCGCAGCAGAGATGCTGTGAGACCGGAGCCCTGGGCGCAATGTTATTC 360  
DB 301 GCTTACAGGCGCAGCAGAGATGCTGTGAGACCGGAGCCCTGGGCGCAATGTTATTC 360  
QY 361 CGGCTACCTCGGAGATCCCAAGTCCGAGATGATTCAGAGAGAAAAGGGGGAATGTCTGA 420  
DB 361 CGGCTACCTCGGAGATCCCAAGTCCGAGATGATTCAGAGAGAAAAGGGGGAATGTCTGA 420  
QY 421 GGGAAAGCTTTGAGAGTCTGGAGACCCCACTACAGAGAGTGTGATGAGATTCATTA 480  
DB 421 GGGAAAGCTTTGAGAGTCTGGAGACCCCACTACAGAGAGTGTGATGAGATTCATTA 480  
QY 481 ATTATGCAATGATCTTGGGAAAATTCGAGATGATCATTTTCAAGATGCGTTCAATA 540  
DB 481 ATTATGCAATGATCTTGGGAAAATTCGAGATGATCATTTTCAAGATGCGTTCAATA 540  
QY 541 GTGCTTAAGAGTTTGTTCAGTGTGCTCACTTGGCTTAAATGCAAGATGCAATGCTGTC 600  
DB 541 GTGCTTAAGAGTTTGTTCAGTGTGCTCACTTGGCTTAAATGCAAGATGCAATGCTGTC 600  
QY 601 AGGCTGTAAAGATTTTCAATCAATGAGCTGAATGTTCAAGAGCTCTTCCCATTTGAAGCTA 660  
DB 601 AGGCTGTAAAGATTTTCAATCAATGAGCTGAATGTTCAAGAGCTCTTCCCATTTGAAGCTA 660  
QY 661 TAATTAATTTGAGCAAGAGAGCCCTGAATGATTCACAAATTAATTAATTCATGCACTT 720  
DB 661 TAATTAATTTGAGCAAGAGAGCCCTGAATGATTCACAAATTAATTAATTCATGCACTT 720  
QY 721 CTTCGTGAGAGACTTTGTGAAGAAATGTTGCTGATGATGATGTTGCTATCTGGG 780  
DB 721 CTTCGTGAGAGACTTTGTGAAGAAATGTTGCTGATGATGATGATGTTGCTATCTGGG 780  
QY 781 TTGGCACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840  
DB 781 TTGGCACTTGTTCAGATTACCCAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840  
QY 841 GCATCAATTATGGAAGACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900  
DB 841 GCATCAATTATGGAAGACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT 900  
QY 901 TTATTTGCTTGGATGATGCTTCACTTAATGATCAATTTTAATAAGTTATGATACATCT 960  
DB 901 TTATTTGCTTGGATGATGCTTCACTTAATGATCAATTTTAATAAGTTATGATACATCT 960  
QY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTTCACTGTTTTTAA 1020  
DB 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTTCACTGTTTTTAA 1020  
QY 1021 ATCTAGCAATTATTCATTTTGTCTTCAATCAAAAGTGCTTCAATATTTTAAAGTTT 1080  
DB 1021 ATCTAGCAATTATTCATTTTGTCTTCAATCAAAAGTGCTTCAATATTTTAAAGTTT 1080  
QY 1081 AGAATCTTCTTCATAGTCACATTTCTCAACCTAATTTTGAATATGTTGTGCTT 1140  
DB 1081 AGAATCTTCTTCATAGTCACATTTCTCAACCTAATTTTGAATATGTTGTGCTT 1140  
QY 1141 TTGTTTTTCTCTTAGTATAGCAATTTTAAATTAATTAATTAATTAATTTTCAACA 1200  
DB 1141 TTGTTTTTCTCTTAGTATAGCAATTTTAAATTAATTAATTAATTTTCAACA 1200  
QY 1201 AATTGTAAATGTTAAGAAATTTTAAATGTTAATTAATTAATTAATTTTCAACA 1257



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Db      1201 AATTGTAATGTTAAGAAATTTTATATCTGTAAATAAATAATTATTCACACA 1257

RESULT 11
US-10-174-581-365
Sequence 365, Application US/10174581
Publication No. US20030017540A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C41
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US/10/174,581
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063564
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
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PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069425
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: 60/069870
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/068017
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
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PRIOR FILING DATE: 1998-04-08
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PRIOR APPLICATION NUMBER: 60/081838
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PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08366
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PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086486
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087098
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087208
PRIOR FILING DATE: 1998-05-28

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1	PRIOR APPLICATION NUMBER: 60/087609
2	PRIOR FILING DATE: 1998-06-02
3	PRIOR APPLICATION NUMBER: 60/087759
4	PRIOR FILING DATE: 1998-06-02
5	PRIOR APPLICATION NUMBER: 60/087827
6	PRIOR FILING DATE: 1998-06-03
7	PRIOR APPLICATION NUMBER: 60/088025
8	PRIOR FILING DATE: 1998-06-04
9	PRIOR APPLICATION NUMBER: 60/088028
10	PRIOR FILING DATE: 1998-06-04
11	PRIOR APPLICATION NUMBER: 60/088029
12	PRIOR FILING DATE: 1998-06-04
13	PRIOR APPLICATION NUMBER: 60/088033
14	PRIOR FILING DATE: 1998-06-04
15	PRIOR APPLICATION NUMBER: 60/088167
16	PRIOR FILING DATE: 1998-06-05
17	PRIOR APPLICATION NUMBER: 60/088202
18	PRIOR FILING DATE: 1998-06-05
19	PRIOR APPLICATION NUMBER: 60/088212
20	PRIOR FILING DATE: 1998-06-05
21	PRIOR APPLICATION NUMBER: 60/088217
22	PRIOR FILING DATE: 1998-06-05
23	PRIOR APPLICATION NUMBER: 60/088326
24	PRIOR FILING DATE: 1998-06-04
25	PRIOR APPLICATION NUMBER: 60/088655
26	PRIOR FILING DATE: 1998-06-09
27	PRIOR APPLICATION NUMBER: 60/088722
28	PRIOR FILING DATE: 1998-06-10
29	PRIOR APPLICATION NUMBER: 60/088738
30	PRIOR FILING DATE: 1998-06-10
31	PRIOR APPLICATION NUMBER: 60/088740
32	PRIOR FILING DATE: 1998-06-10
33	PRIOR APPLICATION NUMBER: 60/088811
34	PRIOR FILING DATE: 1998-06-10
35	PRIOR APPLICATION NUMBER: 60/088824
36	PRIOR FILING DATE: 1998-06-10
37	PRIOR APPLICATION NUMBER: 60/088825
38	PRIOR FILING DATE: 1998-06-10
39	PRIOR APPLICATION NUMBER: 60/088826
40	PRIOR FILING DATE: 1998-06-10
41	PRIOR APPLICATION NUMBER: 60/088861
42	PRIOR FILING DATE: 1998-06-11
43	PRIOR APPLICATION NUMBER: 60/088863
44	PRIOR FILING DATE: 1998-06-11
45	PRIOR APPLICATION NUMBER: 60/088876
46	PRIOR FILING DATE: 1998-06-11
47	PRIOR APPLICATION NUMBER: 60/089090
48	PRIOR FILING DATE: 1998-06-12
49	PRIOR APPLICATION NUMBER: 60/089105
50	PRIOR FILING DATE: 1998-06-12
51	PRIOR APPLICATION NUMBER: 60/089512
52	PRIOR FILING DATE: 1998-06-16
53	PRIOR APPLICATION NUMBER: 60/089514
54	PRIOR FILING DATE: 1998-06-16
55	PRIOR APPLICATION NUMBER: 60/089538
56	PRIOR FILING DATE: 1998-06-17
57	PRIOR APPLICATION NUMBER: 60/089598
58	PRIOR FILING DATE: 1998-06-17
59	PRIOR APPLICATION NUMBER: 60/089653

	Query Match	100.0%	Score 1257	DB 14	Length 1257
	Best Local Similarity	100.0%	Pred. NO. 3,4e-271		
	Matches 1257	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	GSAGAGAGGCGCGCGGTGAAAGGCGCATATGACGCGCGCGCGCTCGAGCGCGG	60		
Db	1	GGAGAGAGGCGCGCGGTGAAAGGCGCATATGACGCGCGCGCGCTCGAGCGCGG	60		
QY	61	CGAGCCAGAGCGTGAACCGCTTCTCTCTCGGTCTCTCGGCTTCAGCTCCGCGGTG	120		
Db	61	CGAGCCAGAGCGTGAACCGCTTCTCTCTCGGTCTCTCGGCTTCAGCTCCGCGGTG	120		
QY	121	CCGGGACGCCGGAACCATGCGACCCCGAGGCGCCCGCGCTCCCGCGAGCGGCTTCGGG	180		

Db	121	CCCCGACCCGGGAGCCATGGAACCCAGGGCCCCGCCCTCCCCCGAGGGCTCCGGC	180
Oy	181	GCCTCTGCTGCTCTGCTGCTGAGCTGCCCGGCCGCTGAGATCCCA	240
Db	181	GCCTCTGCTGCTCTGCTGCTGAGCTGCCCGGCCGCTGAGAGCCTCTAGATCCCA	240
Oy	241	AGGGGAAGCAAAAGCCCACTCCGCGAGAGGGAGTGTGTGACTGTATAATGGAATGT	300
Db	241	AGGGGAAGCAAAAGCCCACTCCGCGAGAGGGAGTGTGTGACTGTATAATGGAATGT	300
Oy	301	GCTTACAAAGGCGCAGCAGAGTGCCTGCTGAGACGGGAGCCCTGGGGCCAAATGTTATTC	360
Db	301	GCTTACAAAGGCGCAGCAGAGTGCCTGCTGAGACGGGAGCCCTGGGGCCAAATGTTATTC	360
Oy	361	CGGGTACACCTGGGATCCAGGTGGGATGTCAAGAGAGAAAGGGGAAATGTCTGA	420
Db	361	CGGGTACACCTGGGATCCAGGTGGGATGTCAAGAGAGAAAGGGGAAATGTCTGA	420
Oy	421	GGGAAAGCTTTGAGGAGTCTTGAGACCCCACTACAGAGCTTTCAATGAGTTCAATGA	480
Db	421	GGGAAAGCTTTGAGGAGTCTTGAGACCCCACTACAGAGCTTTCAATGAGTTCAATGA	480
Oy	481	ATTATGGATATGATCTTGGGAAATTTGGGAGTACATTACAAAGATGGCTCAATA	540
Db	481	ATTATGGATATGATCTTGGGAAATTTGGGAGTACATTACAAAGATGGCTCAATA	540
Oy	541	GTGCTTAAAGTTTGTTCAGTGGCTCACTCCGCTAAATGAGAAATGCATGCTGTC	600
Db	541	GTGCTTAAAGTTTGTTCAGTGGCTCACTCCGCTAAATGAGAAATGCATGCTGTC	600
Oy	601	AGCGTTGGATTTCACTTCATGAGCTGATGTTCAAGACCTTCCATTGAAAGCTA	660
Db	601	AGCGTTGGATTTCACTTCATGAGCTGATGTTCAAGACCTTCCATTGAAAGCTA	660
Oy	661	TAAATTTATTTGSAACCAAGAAAGCCCTGAAATGATTCACAAATTAATATTCATGCACTT	720
Db	661	TAAATTTATTTGSAACCAAGAAAGCCCTGAAATGATTCACAAATTAATATTCATGCACTT	720
Oy	721	CTTCTGTGGAAGACTTTGTGAGAAATTTGGTGTCTGATTAGTGGATGTTGCTATCTGGG	780
Db	721	CTTCTGTGGAAGACTTTGTGAGAAATTTGGTGTCTGATTAGTGGATGTTGCTATCTGGG	780
Oy	781	TTGGCACTTGTTCAGATTAACCAAGAGAGTCTTCTACTGATGGAATTCAGTTCCTC	840
Db	781	TTGGCACTTGTTCAGATTAACCAAGAGAGTCTTCTACTGATGGAATTCAGTTCCTC	840
Oy	841	GCATCATTTATGAAGACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT	900
Db	841	GCATCATTTATGAAGACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACCTCTTTT	900
Oy	901	TTATTTATGCCCTGGAATGTTCACTTTAAATGACATTTTAAATTAAGTTATGATACACT	960
Db	901	TTATTTATGCCCTGGAATGTTCACTTTAAATGACATTTTAAATTAAGTTATGATACACT	960
Oy	961	GAATGAAAGCAAAAGCTAAATATGTTTACAGACCAAGTGTGATTTCAACTGTCTTTTAA	1020
Db	961	GAATGAAAGCAAAAGCTAAATATGTTTACAGACCAAGTGTGATTTCAACTGTCTTTTAA	1020
Oy	1021	ATCTAGCATTAATCAATTTTGTCTTAATCAAAAGTGTTCATAATTTTTTTTAACTGGTT	1080
Db	1021	ATCTAGCATTAATCAATTTTGTCTTAATCAAAAGTGTTCATAATTTTTTTTAACTGGTT	1080
Oy	1081	AGAAATACCTTTCATATGTCATCTCTCAACTATTAATTTGGAATATGTTGGTGTCT	1140
Db	1081	AGAAATACCTTTCATATGTCATCTCTCAACTATTAATTTGGAATATGTTGGTGTCT	1140
Oy	1141	TTTGTCTTTTCTCTTAGATATGCAATTTTAAAAAATATATAAAGCTACCAATCTTTGTAC	1200
Db	1141	TTTGTCTTTTCTCTTAGATATGCAATTTTAAAAAATATATAAAGCTACCAATCTTTGTAC	1200
Oy	1201	AATTTGTAATGTTAAAGATTTTTTTTATATCTGTAAATATAAATTAATTTCCACA	1257

Db 1201 AATTGTAAATGTTAAGAAATTTTATATCTGTAAATAATAATATTCCACACA 1257

RESULT 12  
US-10-176-483-365  
; Sequence 365, Application US/10176483  
; Publication No. US20030017541A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C68  
; CURRENT APPLICATION NUMBER: US/10/176,483  
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 365  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-176-483-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3,4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAGAGGCGCGGGGTGAAGGCGCATTTGATGACGCTGGGGCGCTCCGAGGCGCG 60  
Db 1 GGAGAGAGGCGCGGGGTGAAGGCGCATTTGATGACGCTGGGGCGCTCCGAGGCGCG 60

Qy 61 CGAGACGACGCTGACCACTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Db 61 CGAGACGACGCTGACCACTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120

Qy 121 CCGGCGACCGGGAGGACCATGCGACCCCGAGGCGCGCGCGCTCTCTCTCTCTCTCTCT 180  
Db 121 CCGGCGACCGGGAGGACCATGCGACCCCGAGGCGCGCGCGCTCTCTCTCTCTCTCTCT 180

Qy 181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Db 181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

Qy 241 AGGGAGACCAAAAGGCGGAGCTCCGCGAGAGGAGGTGTGAGCTGTATTAATGGAATGT 300  
Db 241 AGGGAGACCAAAAGGCGGAGCTCCGCGAGAGGAGGTGTGAGCTGTATTAATGGAATGT 300

Qy 301 GCTTAAGAGGCGCGACGAGAGTGTCTGTCTGAGAGGGAAGCCCTGAGGCGCAATGTTATTC 360  
Db 301 GCTTAAGAGGCGCGACGAGAGTGTCTGTCTGAGAGGGAAGCCCTGAGGCGCAATGTTATTC 360

Qy 361 CGGGTACACTGTGGATCCAGAGTGGAGTGTCAAAAGAGAAAGGGGGGAATGTCGA 420  
Db 361 CGGGTACACTGTGGATCCAGAGTGGAGTGTCAAAAGAGAAAGGGGGGAATGTCGA 420

Qy 421 GGGAAAGCTTTGAGAGTCTGAGACCACTACCAAGTTCATGAGATTCATTTGA 480  
Db 421 GGGAAAGCTTTGAGAGTCTGAGACCACTACCAAGTTCATGAGATTCATTTGA 480

Qy 481 AATTAGCATGATCTTGGGAAATTTGGGAGTGTACATTTTCAAAAGATGGCTCAATA 540  
Db 481 AATTAGCATGATCTTGGGAAATTTGGGAGTGTACATTTTCAAAAGATGGCTCAATA 540

Qy 541 GTGCTTAAGAGTGTGTGCTGAGTGTCACTTGGGCTAAATGCAAAATGCAATGCTGTC 600

Db 541 GTGCTTAAGAGTGTGTGCTGAGTGTCACTTGGGCTAAATGCAAAATGCAATGCTGTC 600

Qy 601 AGCGTTGATTTTCACTTCAATGAGAGTGTGAGAGCTCTCTCTCTCTCTCTCTCTCTCT 660  
Db 601 AGCGTTGATTTTCACTTCAATGAGAGTGTGAGAGCTCTCTCTCTCTCTCTCTCTCTCT 660

Qy 661 TAAATTAATTTGACCAAGAGGCGCTGAAATGAATTTCAACATTAATTTATTCGACCTT 720  
Db 661 TAAATTAATTTGACCAAGAGGCGCTGAAATGAATTTCAACATTAATTTATTCGACCTT 720

Qy 721 CTTCTGTGGAAGAGCTTTGTGAGAGATTTGTGCTGATTTAGTGAATGCTTATTCGGG 780  
Db 721 CTTCTGTGGAAGAGCTTTGTGAGAGATTTGTGCTGATTTAGTGAATGCTTATTCGGG 780

Qy 781 TTGGCACTGTTCAAGATTACCAAAAGAGATGCTTCTACTGATGAGAAATTCAGTTCTC 840  
Db 781 TTGGCACTGTTCAAGATTACCAAAAGAGATGCTTCTACTGATGAGAAATTCAGTTCTC 840

Qy 841 GCATCATTTAGAGAACTACCAAAATTAATGCTTTAATTTCTTCTTCTTCTTCTTCTTCT 900  
Db 841 GCATCATTTAGAGAACTACCAAAATTAATGCTTTAATTTCTTCTTCTTCTTCTTCTTCT 900

Qy 901 TTATTATGCTTGTGAGATGTTCACTTAAATGACATTTTAAATAGTTATGATATACCT 960  
Db 901 TTATTATGCTTGTGAGATGTTCACTTAAATGACATTTTAAATAGTTATGATATACCT 960

Qy 961 GAATGAAAGCAAGAGCTTAATATGTTTACAGACCAAGAGTGAATTCACACTGTTTAA 1020  
Db 961 GAATGAAAGCAAGAGCTTAATATGTTTACAGACCAAGAGTGAATTCACACTGTTTAA 1020

Qy 1021 AATTGACATTTATTCATTTTGTCTCAATCAAAAGGTTTCAATATTTTGTGCTT 1080  
Db 1021 AATTGACATTTATTCATTTTGTCTCAATCAAAAGGTTTCAATATTTTGTGCTT 1080

Qy 1081 AGAATACTTCTTCAATGATGACATTTCTCAACCTATTAATTTGAAATATGTTGCTGTC 1140  
Db 1141 TTTGTTTTTCTCTTATGATGATTTTAAAAAATTAAGGCTAACATTTTGTGTC 1200

Qy 1201 AATTGTAAATGTTAAGAAATTTTATATCTGTAAATAATAATATTCCACACA 1257  
Db 1201 AATTGTAAATGTTAAGAAATTTTATATCTGTAAATAATAATATTCCACACA 1257

RESULT 13  
US-10-176-749-365  
; Sequence 365, Application US/10176749  
; Publication No. US20030017542A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C76  
; CURRENT APPLICATION NUMBER: US/10/176,749  
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 365  
; LENGTH: 1257

```

TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-749-365

Query Match      100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGCGGTGAAAGCGCATTTGATGACGCTGCGCGCGCTCGAGGCGCG 60
DB 1 GGAGAGAGCGCGCGCGGTGAAAGCGCATTTGATGACGCTGCGCGCGCTCGAGGCGCG 60
QY 61 CGAGAGCAGACGCTGACACGTTCTCTCGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 CGAGAGCAGACGCTGACACGTTCTCTCGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 CCCGCGAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCTGCTGCGAGCGGCTCGCG 180
DB 121 CCCGCGAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCTGCTGCGAGCGGCTCGCG 180
QY 181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AGGCGGAGGAGGAGGAGCGAGCTCCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 241 AGGCGGAGGAGGAGGAGCGAGCTCCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 301 GCTTACAGAGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 GCTTACAGAGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 CGGCTACACCTGCGGAGTCCGAGGTCGCGAGTGAATCAAGAGAGAGAGAGAGAGAG 420
DB 361 CGGCTACACCTGCGGAGTCCGAGGTCGCGAGTGAATCAAGAGAGAGAGAGAGAGAG 420
QY 421 GGGAAAGCTTTGAGAGGTCCTGAGACCCAACTACAGAGGTCGATGAGGTCATTTGA 480
DB 421 GGGAAAGCTTTGAGAGGTCCTGAGACCCAACTACAGAGGTCGATGAGGTCATTTGA 480
QY 481 ATTATGCGATAGATCTTGGGAAATTTGCGAGTGTACATTTACAAAGATGCGTTCAATA 540
DB 481 ATTATGCGATAGATCTTGGGAAATTTGCGAGTGTACATTTACAAAGATGCGTTCAATA 540
QY 541 GTGCTCTAAGAGTTTGTGTCAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 GTGCTCTAAGAGTTTGTGTCAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AGGCTGTGATTTCAATTCATGAGTGAATGTTGAGGAGCTCTTCCCATTTGAAGCTA 660
DB 601 AGGCTGTGATTTCAATTCATGAGTGAATGTTGAGGAGCTCTTCCCATTTGAAGCTA 660
QY 661 TAATTTATTTGAGCAAGAGAGGCTGAAATGATTTCAACAATTTAATTTATTCATGCA 720
DB 661 TAATTTATTTGAGCAAGAGAGGCTGAAATGATTTCAACAATTTAATTTATTCATGCA 720
QY 721 CTTCGTGGAAGACCTTTGGAAGAAATGTCGTGATTTGATGATGTCATCTGCG 780
DB 721 CTTCGTGGAAGACCTTTGGAAGAAATGTCGTGATTTGATGATGTCATCTGCG 780
QY 781 TTGGGACCTGTCAGATTTACCCAAAGAGAGTCTTCTAGTGAATGAGTTCAGTTTC 840
DB 781 TTGGGACCTGTCAGATTTACCCAAAGAGAGTCTTCTAGTGAATGAGTTCAGTTTC 840
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTGATTCACCTCTTTT 900
DB 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTGATTCACCTCTTTT 900
QY 901 TTATTTATGCTTGAATGTTCACTTAATGACATTTTAATTAATGATTTATGATTA 960
DB 901 TTATTTATGCTTGAATGTTCACTTAATGACATTTTAATTAATGATTTATGATTA 960
QY 961 GAATGAAGAGCAAAAGCGAGCTCCGCGAGAGGAGGAGTGTGACCTGTATTAATG 1020

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DB 961 GAATGAAGAGCAAAAGCTAAATGTTTACAGCCAAAGTGATTTCACTGTTTAA 1020
QY 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGGTTTCAATATTTTGTGTT 1080
DB 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGGTTTCAATATTTTGTGTT 1080
QY 1081 AGAATACCTTTCTTCAATGACATTTCTCAACCTATAATTTGAATATGTTGTC 1140
DB 1081 AGAATACCTTTCTTCAATGACATTTCTCAACCTATAATTTGAATATGTTGTC 1140
QY 1141 TTTGTTTTTCTTCTAGTATGACATTTTAAATAATAAAGCTACCAATCTTTGAC 1200
DB 1141 TTTGTTTTTCTTCTAGTATGACATTTTAAATAATAAAGCTACCAATCTTTGAC 1200
QY 1201 AATTTGTAATGTTAAGATTTTATTTATCTGTTAAATTAATTAATTTTCAACA 1257
DB 1201 AATTTGTAATGTTAAGATTTTATCTGTTAAATAATAAATTAATTTTCAACA 1257

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RESULT 14
US-10-176-914-365
; Sequence 365, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176, 914
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-914-365

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Query Match      100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGTGAAAGCGCATTTGATGACGCTGCGCGCGCTCGAGGCGCG 60
DB 1 GGAGAGAGCGCGCGCGGTGAAAGCGCATTTGATGACGCTGCGCGCGCTCGAGGCGCG 60
QY 61 CGAGAGCAGACGCTGACACGTTCTCTCGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 61 CGAGAGCAGACGCTGACACGTTCTCTCGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 CCCGCGAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCTGCTGCGAGCGGCTCGCG 180
DB 121 CCCGCGAGCGCGGAGCGCATGCGACCCGAGGCGCGCGCTGCTGCGAGCGGCTCGCG 180
QY 181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AGGCGGAGGAGGAGGAGCGAGCTCCGCGAGAGGAGGAGTGTGACCTGTATTAATG 300
DB 241 AGGCGGAGGAGGAGGAGCGAGCTCCGCGAGAGGAGGAGTGTGACCTGTATTAATG 300

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Db 1141 TTGCTTTTCTCTTGTATGATTTTAAATTAATTAAGCTACCAATCTTTGTAC 1200  
Qy 1201 AATTTGTAATGTAAAGATTTTAAATCTGTAAATTAATTAATTTATTTCCACA 1257  
Db 1201 AATTTGTAATGTAAAGATTTTAAATCTGTAAATTAATTAATTTATTTCCACA 1257

RESULT 17  
US-10-063-513-121  
; Sequence 121, Application US/10063513  
; Publication No. US20030018172A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,513  
; PRIOR APPLICATION: 2002-05-01  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 121  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-063-513-121

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAAGAGAGCGCGCGGGTGAAGAGCGCATTTAGCAGCTTGCGCGCGCTTGAGCGCGG 60  
Db 1 GGAAGAGAGCGCGCGGGTGAAGAGCGCATTTAGCAGCTTGCGCGCGCTTGAGCGCGG 60  
Qy 61 CGAGAGCGAGCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Db 61 CGAGAGCGAGCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Qy 121 CCGGAGCGCGGAGCGCATTCGAGCCCGCGCGCTCTCCCGAGCGGCTCCGCG 180  
Db 121 CCGGAGCGCGGAGCGCATTCGAGCCCGCGCGCTCTCCCGAGCGGCTCCGCG 180  
Qy 181 GCT 240  
Db 181 GCT 240  
Qy 241 AGGGGAGCAAAAGCGCGAGCTCCGGGAGAGGAGTGTGAGCTGTATTAATGAAATGT 300  
Db 241 AGGGGAGCAAAAGCGCGAGCTCCGGGAGAGGAGTGTGAGCTGTATTAATGAAATGT 300  
Qy 301 GCTTACAAAGGCGCGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
Db 301 GCTTACAAAGGCGCGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
Qy 361 CGGAGTACCTTGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
Db 361 CGGAGTACCTTGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
Qy 421 GGGAAAGCTTTGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
Db 421 GGGAAAGCTTTGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
Qy 481 AATTAAGCATAGATCTTTGGGAAAATTCGGAAGTGTACATTTTAAAGATGCGTTCAATA 540  
Db 481 AATTAAGCATAGATCTTTGGGAAAATTCGGAAGTGTACATTTTAAAGATGCGTTCAATA 540

Qy 541 GTGCTTAAGAGTTTGTTCAGTGGCTCACTTGCGCTAAATGAGAAATGATGCTGTC 600  
Db 541 GTGCTTAAGAGTTTGTTCAGTGGCTCACTTGCGCTAAATGAGAAATGATGCTGTC 600  
Qy 601 AGCGTTGATTTTACATTCATGAGCTGAGTGTTCAGGACCTCTTCCCATGGAAGCTA 660  
Db 601 AGCGTTGATTTTACATTCATGAGCTGAGTGTTCAGGACCTCTTCCCATGGAAGCTA 660  
Qy 661 TAAATTTTGAAGCAAGGAGCCCTGAAATGAAATTCACATTTAATTCATGCACTT 720  
Db 661 TAAATTTTGAAGCAAGGAGCCCTGAAATGAAATTCACATTTAATTCATGCACTT 720  
Qy 721 CTTCGTGGAAGAGCTTTGTGAAGAAATGCTGTGATGATGATGATGATGATGATGATG 780  
Db 721 CTTCGTGGAAGAGCTTTGTGAAGAAATGCTGTGATGATGATGATGATGATGATGATG 780  
Qy 781 TTGGCACTTGTTCAGATTAACCAAGAGAGTCTTCTACTGATGATGATGATGATGATG 840  
Db 781 TTGGCACTTGTTCAGATTAACCAAGAGAGTCTTCTACTGATGATGATGATGATGATG 840  
Qy 841 GCATCATTTAGAGAGTCACTTAATTAATGCTTTAATTTGATGCTTCTCTCTCTCTCT 900  
Db 841 GCATCATTTAGAGAGTCACTTAATTAATGCTTTAATTTGATGCTTCTCTCTCTCTCT 900  
Qy 901 TTAATTAAGCTTGAAGAGTCACTTAATTAATGATGATGATGATGATGATGATGATG 960  
Db 901 TTAATTAAGCTTGAAGAGTCACTTAATTAATGATGATGATGATGATGATGATGATG 960  
Qy 961 GAATGAAGAGCAAGCTTAATTAATGATGATGATGATGATGATGATGATGATGATG 1020  
Db 961 GAATGAAGAGCAAGCTTAATTAATGATGATGATGATGATGATGATGATGATGATG 1020  
Qy 1021 AATTAAGCTTGAAGAGTCACTTAATTAATGATGATGATGATGATGATGATGATG 1080  
Db 1021 AATTAAGCTTGAAGAGTCACTTAATTAATGATGATGATGATGATGATGATGATG 1080  
Qy 1081 AGAATTAATTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
Db 1081 AGAATTAATTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
Qy 1141 TTTGTTTTTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
Db 1141 TTTGTTTTTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
Qy 1201 AATTTGTAATGTAAAGATTTTAAATCTGTAAATTAATTAATTTATTTCCACA 1257  
Db 1201 AATTTGTAATGTAAAGATTTTAAATCTGTAAATTAATTAATTTATTTCCACA 1257

RESULT 18  
US-10-063-515-121  
; Sequence 121, Application US/10063515  
; Publication No. US20030018173A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,515  
; PRIOR APPLICATION: 2002-05-01  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 121  
; LENGTH: 1257

TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-063-515-121

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGCCGATGATGACCTGCGCGCGCTCGAGGCGCG 60  
DB 1 GGAGAGAGCGCGCGGGTGAAGCCGATGATGACCTGCGCGCGCTCGAGGCGCG 60  
QY 61 CGAGAGCAGACGCTGACACAGTCTCTCTCGAGTCTCTCGAGTCTCTCGAGTCT 120  
DB 61 CGAGAGCAGACGCTGACACAGTCTCTCTCGAGTCTCTCGAGTCTCTCGAGTCT 120  
QY 121 CCGGAGAGCGCGGAGCCATGCGACCCCGAGGCGCGCGCGCTCGCGCGCG 180  
DB 121 CCGGAGAGCGCGGAGCCATGCGACCCCGAGGCGCGCGCGCGCTCGCGCGCG 180  
QY 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 241 AGGAGAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGACCTGTATATGAAATGT 300  
DB 241 AGGAGAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGACCTGTATATGAAATGT 300  
QY 301 GCTTACAGAGGCGCAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
DB 301 GCTTACAGAGGCGCAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
QY 361 CGGCTACCTCGGAGATCCCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
DB 361 CGGCTACCTCGGAGATCCCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
QY 421 GGGAAAGCTTGGAGAGTCTGCGACCACTACCAAGAGTGTGCTGCTGCTGCTG 480  
DB 421 GGGAAAGCTTGGAGAGTCTGCGACCACTACCAAGAGTGTGCTGCTGCTGCTG 480  
QY 481 ATTATGAGCATAGATCTTGGAGAAATGCGAGTGTACATTTACAAAGATCGTTCA 540  
DB 481 ATTATGAGCATAGATCTTGGAGAAATGCGAGTGTACATTTACAAAGATCGTTCA 540  
QY 541 GTGCTCTAAGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 600  
DB 541 GTGCTCTAAGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 600  
QY 601 AGCGTGTATTTACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 660  
DB 601 AGCGTGTATTTACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 660  
QY 661 TAAATTAATTTGACCAAGAGAGCGCTGAAATGAAATTCATTCATTCATTCAT 720  
DB 661 TAAATTAATTTGACCAAGAGAGCGCTGAAATGAAATTCATTCATTCATTCATTC 720  
QY 721 CTCTGCTGAGAGAGCTTGTGAGAGAAATGCTGCTGAGTGTGCTGCTGCTGCT 780  
DB 721 CTCTGCTGAGAGAGCTTGTGAGAGAAATGCTGCTGAGTGTGCTGCTGCTGCT 780  
QY 781 TTGGACATTTGTCAGATTAACCAAAAGAGAGTGTGCTGCTGAGTGTGCTGCTG 840  
DB 781 TTGGACATTTGTCAGATTAACCAAAAGAGAGTGTGCTGCTGAGTGTGCTGCTG 840  
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTGATTTGCTACCTTT 900  
DB 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTGATTTGCTACCTTT 900  
QY 901 TTTATATGCTTGTGAGATGCTTCACTTAATGACATTTTAAATAGTTATGATACAT 960  
DB 901 TTTATATGCTTGTGAGATGCTTCACTTAATGACATTTTAAATAGTTATGATACAT 960  
QY 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGAGTGTGATTTCACTGTTTAA 1020

DB 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGAGTGTGATTTCACTGTTTAA 1020  
QY 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTGTAGTGT 1080  
DB 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTGTAGTGT 1080  
QY 1081 AGAATACCTTCTTCATATGACATTTCTCAACCTTAATATTTGAAATATTTGTGTCT 1140  
DB 1081 AGAATACCTTCTTCATATGACATTTCTCAACCTTAATATTTGAAATATTTGTGTCT 1140  
QY 1141 TTTGTTTCTTCTTATGATATGATTTTAAATATTAATTAAGCTACCATTTGTAC 1200  
DB 1141 TTTGTTTCTTCTTATGATATGATTTTAAATATTAATTAAGCTACCATTTGTAC 1200  
QY 1201 AATTGTAAATGTAAAGATTTTATTTATATCTGTTAAATTAATTAATTTTCAACA 1257  
DB 1201 AATTGTAAATGTAAAGATTTTATTTATATCTGTTAAATTAATTAATTTTCAACA 1257

RESULT 19  
US-10-063-512-121  
Sequence 121, Application US/10063512  
Publication No. US20030018183A1  
GENERAL INFORMATION:  
APPLICANT: Batoni, Dan L.  
APPLICANT: Gerilisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,512  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 121  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-063-512-121

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGCCGATGATGACCTGCGCGCGCTCGAGGCGCG 60  
DB 1 GGAGAGAGCGCGCGGGTGAAGCCGATGATGACCTGCGCGCGCTCGAGGCGCG 60  
QY 61 CGAGAGCAGACGCTGACACAGTCTCTCTCGAGTCTCTCGAGTCTCTCGAGTCT 120  
DB 61 CGAGAGCAGACGCTGACACAGTCTCTCTCGAGTCTCTCGAGTCTCTCGAGTCT 120  
QY 121 CCGGAGAGCGCGGAGCCATGCGACCCCGAGGCGCGCGCGCTCGCGCGCG 180  
DB 121 CCGGAGAGCGCGGAGCCATGCGACCCCGAGGCGCGCGCGCGCTCGCGCGCG 180  
QY 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 241 AGGAGAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGACCTGTATATGAAATGT 300  
DB 241 AGGAGAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGACCTGTATATGAAATGT 300  
QY 301 GCTTACAGAGGCGCAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360



Db 301 GCTTACAAAGGCCACAGAGAGTGCCTGTGTGAGACGGAGACCTTGGGCGCAATGTTATTC 360  
Qy 361 CGGATACACCTGGGATCCAGAGTGGGATGATTTCAAGAGAGAAAGGGGAAATGTCTA 420  
Db 361 CGGATACACCTGGGATCCAGAGTGGGATGATTTCAAGAGAGAAAGGGGAAATGTCTA 420  
Qy 421 GGGAAAGCTTTGAGAGTCTGTGACACCCAACTACAGAGAGTGTTCATGAGATTCATTA 480  
Db 421 GGGAAAGCTTTGAGAGTCTGTGACACCCAACTACAGAGAGTGTTCATGAGATTCATTA 480  
Qy 481 ATTATGCAATAGATCTTGGGAAATTCGGAGATGTATTCATTAAGATGCTTCAATA 540  
Db 481 ATTATGCAATAGATCTTGGGAAATTCGGAGATGTATTCATTAAGATGCTTCAATA 540  
Qy 541 GTGCTCTAAGAGTGTTCAGTGTGCTCACTTGGGCTAATATGCAAGAAATGATGCTGC 600  
Db 541 GTGCTCTAAGAGTGTTCAGTGTGCTCACTTGGGCTAATATGCAAGAAATGATGCTGC 600  
Qy 601 AGCGTTGATTTTCAATTCATTAAGATGAGTGAATGTTTCAAGACCTCTTCCATTTGAAGCTA 660  
Db 601 AGCGTTGATTTTCAATTCATTAAGATGAGTGAATGTTTCAAGACCTCTTCCATTTGAAGCTA 660  
Qy 661 TAAATTTATTTGACCAAGAGAGCCCTGAATGATTAATTCATTAATTCATTCAGACTT 720  
Db 661 TAAATTTATTTGACCAAGAGAGCCCTGAATGATTAATTCATTAATTCATTCAGACTT 720  
Qy 721 CTTCGTGGAAGAGCTTGTGTGAAGAAATGTGTGTGATTAAGTGTGCTATCTGAG 780  
Db 721 CTTCGTGGAAGAGCTTGTGTGAAGAAATGTGTGTGATTAAGTGTGCTATCTGAG 780  
Qy 781 TTGGACATCTTGTCAATTTACCAAAAGAGATGCTTCACTGAGTGAATTCAGATTTCTC 840  
Db 781 TTGGACATCTTGTCAATTTACCAAAAGAGATGCTTCACTGAGTGAATTCAGATTTCTC 840  
Qy 841 GCATCATTTATGAGAACTACCAAAATATATGCTTTAATTTTCACTTGTCTACTCTTTT 900  
Db 841 GCATCATTTATGAGAACTACCAAAATATATGCTTTAATTTTCACTTGTCTACTCTTTT 900  
Qy 901 TTATTTATGCTTGAATGCTTCACTTAATATGATTAATTAATTAATTAATTAATTAAT 960  
Db 901 TTATTTATGCTTGAATGCTTCACTTAATATGATTAATTAATTAATTAATTAATTAAT 960  
Qy 961 GAATGAAAGCAAGAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTAA 1020  
Db 961 GAATGAAAGCAAGAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTAA 1020  
Qy 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATTAATTTTGTAGTGT 1080  
Db 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATTAATTTTGTAGTGT 1080  
Qy 1081 AGAATACCTTCTTCATGATCAATCTCTCAACCTATATTTGAATATGTTGTGTCT 1140  
Db 1081 AGAATACCTTCTTCATGATCAATCTCTCAACCTATATTTGAATATGTTGTGTCT 1140  
Qy 1141 TTGTGTTTCTCTTATGATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1200  
Db 1141 TTGTGTTTCTCTTATGATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1200  
Qy 1201 AATTTGTAATGTTTAAAGATTTTATCTGTTAATTAATTAATTAATTAATTAATTAAT 1257  
Db 1201 AATTTGTAATGTTTAAAGATTTTATCTGTTAATTAATTAATTAATTAATTAATTAAT 1257

RESULT 20  
US-10-173-706-365  
; Sequence 365, Application US/10173706  
; Publication No. US20030022293A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P343081C7  
; CURRENT APPLICATION NUMBER: US/10/173, 706  
; PRIORITY FILING DATE: 2002-06-17  
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 365  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-173-706-365  
Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGAGAGGCGCGCGGTGAAGAGCGCATTAATGACCTTCGAGCGGCTTCGAGCGCG 60  
Db 1 GAGAGAGGCGCGCGGTGAAGAGCGCATTAATGACCTTCGAGCGGCTTCGAGCGCG 60  
Qy 61 CGGAGCCAGAGCTGACCACTTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Db 61 CGGAGCCAGAGCTGACCACTTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Qy 121 CCCGACGCGGAGCCATGAGCACTCCGAGAGGAGCCCGGCGCTCCGAGCGGCTTCGAG 180  
Db 121 CCCGACGCGGAGCCATGAGCACTCCGAGAGGAGCCCGGCGCTCCGAGCGGCTTCGAG 180  
Qy 181 GCTCTCTGCT 240  
Db 181 GCTCTCTGCT 240  
Qy 241 AGGGAGAGCAAAAGGCGGAGCTCCGAGAGGAGGAGTGTGACCTGTATTAATGAATGT 300  
Db 241 AGGGAGAGCAAAAGGCGGAGCTCCGAGAGGAGGAGTGTGACCTGTATTAATGAATGT 300  
Qy 301 GCTTACAAAGGCGCAGAGAGTGTGTGAGAGCGGAGCCCTGAGGCGCAATGTTATTC 360  
Db 301 GCTTACAAAGGCGCAGAGAGTGTGTGAGAGCGGAGCCCTGAGGCGCAATGTTATTC 360  
Qy 361 CGGATACACCTGGGATCCAGAGTGGGATGATTTCAAGAGAGAAAGGGGAAATGTCTGA 420  
Db 361 CGGATACACCTGGGATCCAGAGTGGGATGATTTCAAGAGAGAAAGGGGAAATGTCTGA 420  
Qy 421 GGGAAAGCTTTGAGAGTCTGTGACACCCAACTACAGAGAGTGTTCATGAGATTCATTA 480  
Db 421 GGGAAAGCTTTGAGAGTCTGTGACACCCAACTACAGAGAGTGTTCATGAGATTCATTA 480  
Qy 481 ATTATGCAATAGATCTTGGGAAATTCGGAGATGTATTCATTAAGATGCTTCAATA 540  
Db 481 ATTATGCAATAGATCTTGGGAAATTCGGAGATGTATTCATTAAGATGCTTCAATA 540  
Qy 541 GTGCTCTAAGAGTGTTCAGTGTGCTCACTTGGGCTAATATGCAAGAAATGATGCTGC 600  
Db 541 GTGCTCTAAGAGTGTTCAGTGTGCTCACTTGGGCTAATATGCAAGAAATGATGCTGC 600  
Qy 601 AGCGTTGATTTTCAATTCATTAAGATGAGTGAATGTTTCAAGACCTCTTCCATTTGAAGCTA 660  
Db 601 AGCGTTGATTTTCAATTCATTAAGATGAGTGAATGTTTCAAGACCTCTTCCATTTGAAGCTA 660  
Qy 661 TAAATTTATTTGACCAAGAGAGCCCTGAATGATTAATTAATTAATTAATTAATTAATTAAT 720  
Db 661 TAAATTTATTTGACCAAGAGAGCCCTGAATGATTAATTAATTAATTAATTAATTAATTAAT 720  
Qy 721 CTTCGTGGAAGAGCTTGTGTGAAGAAATGTGTGTGATTAAGTGTGCTATCTGAG 780  
Db 721 CTTCGTGGAAGAGCTTGTGTGAAGAAATGTGTGTGATTAAGTGTGCTATCTGAG 780



Dh 721 CTTCTGTGAAGAGCTTTGTGAAGAAATGTCGTGATTAAGATGTCATCTGAG 780  
Qy 781 TTGGCACTTGTGAGATTACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840  
Db 781 TTGGCACTTGTGAGATTACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840  
Qy 841 GCATCATTTATGAAGACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900  
Db 841 GCATCATTTATGAAGACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900  
Qy 901 TTATTTATGCTTGAATGCTTCACTTAATGACATTTTAAATAGTTATGATACATCT 960  
Db 901 TTATTTATGCTTGAATGCTTCACTTAATGACATTTTAAATAGTTATGATACATCT 960  
Qy 961 GAATGAAAAGCAAGCTAAATATGTTTACAGCAAAAGTGTGATTCACATGTTTTTAA 1020  
Db 961 GAATGAAAAGCAAGCTAAATATGTTTACAGCAAAAGTGTGATTCACATGTTTTTAA 1020  
Qy 1021 ATCTAGCATTTATCATTTTGTCTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
Db 1021 ATCTAGCATTTATCATTTTGTCTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
Qy 1081 AGAATATCTTCTCATATGTCACATCTCTCAACCTATTAATTTGGAATATTTGTGCTT 1140  
Db 1081 AGAATATCTTCTCATATGTCACATCTCTCAACCTATTAATTTGGAATATTTGTGCTT 1140  
Qy 1141 TTTGTTTTTCTCTTATGATAGCAATTTTAAAAAATTAATGCTACCAATCTTTGTAC 1200  
Db 1141 TTTGTTTTTCTCTTATGATAGCAATTTTAAAAAATTAATGCTACCAATCTTTGTAC 1200  
Qy 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTTCCAACTA 1257  
Db 1201 AATTTGTAATGTTAAGAAATTTTATATCTGTTAAATTAATTTTCCAACTA 1257

RESULT 21  
US-10-175-738-365  
; Sequence 365, Application US/10175738  
; Publication No. US20030022294A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C45  
; CURRENT APPLICATION NUMBER: US/10/175, 738  
; PRIORITY FILING DATE: 2002-06-19  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 365  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-175-738-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3,4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGAGAGAGGCGCGGCTGAAGCGCATGATGATGACCTGCGCGCGCTCGAGCGCGG 60  
Db 1 GGAGAGAGGCGCGGCTGAAGCGCATGATGATGACCTGCGCGCGCTCGAGCGCGG 60  
Qy 61 CGAGCGCAGAGCTGACCAAGTTCCTCTCGGCTCTCTCGGCTCAAGCTCCGCGCTG 120

Dh 61 CGAGCGCAGAGCTGACCAAGTTCCTCTCGGCTCTCTCGGCTCAAGCTCCGCGCTG 120  
Qy 121 CCCGCGAGCGCGGAGCATGCGACCCCAAGGCGCGCGCGCTCCCGCGAGCGGCTCCGG 180  
Db 121 CCCGCGAGCGCGGAGCATGCGACCCCAAGGCGCGCGCGCTCCCGCGAGCGGCTCCGG 180  
Qy 181 GCCTCTGTGCTCTCTGTCTGTGACGCTCCGCGCGCTGTGAGCGGCTGTGAGATCCCA 240  
Db 181 GCCTCTGTGCTCTCTGTCTGTGACGCTCCGCGCGCTGTGAGCGGCTGTGAGATCCCA 240  
Qy 241 AGGGAAGCAAAAGCGCAGCTCCGCGAGAGGAGGCTGTGAGCTGTAAATGGAATGT 300  
Db 241 AGGGAAGCAAAAGCGCAGCTCCGCGAGAGGAGGCTGTGAGCTGTAAATGGAATGT 300  
Qy 301 GCTTACAAAGGCGCAGAGAGTGCCTGTGTGAGAGCGGAGCCCTGGGCGCAATGTTATTC 360  
Db 301 GCTTACAAAGGCGCAGAGAGTGCCTGTGTGAGAGCGGAGCCCTGGGCGCAATGTTATTC 360  
Qy 361 CGGCTACCTGGGATCCAGGTCGGGATGGAATTCAGAGAGAGAGGCGGAGATGCTGA 420  
Db 361 CGGCTACCTGGGATCCAGGTCGGGATGGAATTCAGAGAGAGAGGCGGAGATGCTGA 420  
Qy 421 GGGAAAGCTTTGAGAGAGTCTGAGACCCCACTACAGAGCTGTCATGAGATTCATTA 480  
Db 421 GGGAAAGCTTTGAGAGAGTCTGAGACCCCACTACAGAGCTGTCATGAGATTCATTA 480  
Qy 481 ATTATGCAATGATCTTGGGAAAATTTGCGAGTGTACATTTACAAAGATCGTCAATA 540  
Db 481 ATTATGCAATGATCTTGGGAAAATTTGCGAGTGTACATTTACAAAGATCGTCAATA 540  
Qy 541 GTGCTTAAGAGTTTGTCAAGTGTCTCACTCGGTAAATGCAAGAAATGATGCTGTG 600  
Db 541 GTGCTTAAGAGTTTGTCAAGTGTCTCACTCGGTAAATGCAAGAAATGATGCTGTG 600  
Qy 601 AGCGTGTATTTTCAATTCATTAAGAGCTGAATGTTGAGAGCTCTTCCATTTGAAGCTA 660  
Db 601 AGCGTGTATTTTCAATTCATTAAGAGCTGAATGTTGAGAGCTCTTCCATTTGAAGCTA 660  
Qy 661 TAAATTTATTTGACCAAGAGAGCCCTGGAATGATTTCAACATTAATTTATTCATGCACTT 720  
Db 661 TAAATTTATTTGACCAAGAGAGCCCTGGAATGATTTCAACATTAATTTATTCATGCACTT 720  
Qy 721 CTTCTGTGAAGAGCTTGTGAAGAAATGTTGCTGGAATGATGATGTTGCTATCTGGG 780  
Db 721 CTTCTGTGAAGAGCTTGTGAAGAAATGTTGCTGGAATGATGATGTTGCTATCTGGG 780  
Qy 781 TTGGCACTTGTGAGATTACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840  
Db 781 TTGGCACTTGTGAGATTACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840  
Qy 841 GCATCATTTATGAAGACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900  
Db 841 GCATCATTTATGAAGACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900  
Qy 901 TTATTTATGCTTGAATGCTTCACTTAATGACATTTTAAATAGTTATGATACATCT 960  
Db 901 TTATTTATGCTTGAATGCTTCACTTAATGACATTTTAAATAGTTATGATACATCT 960  
Qy 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAAAGTGTGATTCACATGTTTTTAA 1020  
Db 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAAAGTGTGATTCACATGTTTTTAA 1020  
Qy 1021 ATCTAGCATTTATCATTTTGTCTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
Db 1021 ATCTAGCATTTATCATTTTGTCTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
Qy 1081 AGAATATCTTCTCATATGTCACATCTCTCAACCTATTAATTTGGAATATTTGTGCTT 1140  
Db 1081 AGAATATCTTCTCATATGTCACATCTCTCAACCTATTAATTTGGAATATTTGTGCTT 1140  
Qy 1141 TTTGTTTTTCTCTTATGATAGCAATTTTAAAAAATTAATGCTACCAATCTTTGTAC 1200

Db	1141	TTTTGTTTTTCTCTAGTATGACATTTTAAAAAATAAAAAAGTACCAATCTTGTAC	1200
Qy	1201	AAATTGTAATGTGTAAAGATTTTTTTTAAATCTGTAAATAAATATTTCACACA	1257
Db	1201	AAATTGTAATGTGTAAAGATTTTTTTTAAATCTGTAAATAAATATTTCACACA	1257
RESULT 22			
US-10-175-752-365			
; Sequence 365, Application US/10175752			
; Publication No. US20030022295A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin P.			
APPLICANT: Chen, Jian			
APPLICANT: Desnoyers, Luc			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Gurney, Austin L.			
APPLICANT: Pan, James			
APPLICANT: Smith, Victoria			
APPLICANT: Watanabe, Colin K.			
APPLICANT: Wood, William I.			
APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
FILE REFERENCE: P3430R1C60			
CURRENT APPLICATION NUMBER: US/10/175,752			
CURRENT FILING DATE: 2002-06-19			
Prior Application removed - See File Wrapper or Palm			
NUMBER OF SEQ ID NOS: 612			
SEQ ID NO: 365			
LENGTH: 1257			
TYPE: DNA			
ORGANISM: Homo Sapien			
US-10-175-752-365			
Query Match 100.0%; Score 1257; DB 14; Length 1257;			
Best Local Similarity 100.0%; Pred. No. 3.4e-271;			
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GGAGAGAGGCGCGCGGTGAAGGAGCGATTGATGACGCTCGCGCGCTCGAGCGCGG	60
Db	1	GGAGAGAGGCGCGCGGTGAAGGAGCGATTGATGACGCTCGCGCGCTCGAGCGCGG	60
Qy	61	CGGAGCCAGAGCGTGAACCAAGTCTCTCTCGTCTCTCCGCTCCAGCTCCGCGCTG	120
Db	61	CGGAGCCAGAGCGTGAACCAAGTCTCTCTCGTCTCTCCGCTCCAGCTCCGCGCTG	120
Qy	121	CCCGGACGCCGAGAGCATGCGAGCCCGAGGAGCCCGCGCTCCCGCGAGCGCTCCGCG	180
Db	121	CCCGGACGCCGAGAGCATGCGAGCCCGAGGAGCCCGCGCTCCCGCGAGCGCTCCGCG	180
Qy	181	GCTTCCTGCTGCTCTGCTGCTGCTGCAAGCTGCCGCGCGCTGAGCGCCTTGAGATCCCA	240
Db	181	GCTTCCTGCTGCTCTGCTGCTGCTGCAAGCTGCCGCGCGCTGAGCGCCTTGAGATCCCA	240
Qy	241	AGGGGAAGCAAAAGGCGCAGCTCCGCGAGAGGAGTGTGTGACTGTATTAATGGAATGT	300
Db	241	AGGGGAAGCAAAAGGCGCAGCTCCGCGAGAGGAGTGTGTGACTGTATTAATGGAATGT	300
Qy	301	GCTTACAAAGGCGCAGAGAGTGCCTGTGCGAGCGGAGGCCCTGCGGCGCAATGTATTTC	360
Db	301	GCTTACAAAGGCGCAGAGAGTGCCTGTGCGAGCGGAGGCCCTGCGGCGCAATGTATTTC	360
Qy	361	CGGGTACACCTGGGATCCCAAGTGTGGATGGAATTCAAAGAGAAAAGGGGGAATGTGTGA	420
Db	361	CGGGTACACCTGGGATCCCAAGTGTGGATGGAATTCAAAGAGAAAAGGGGGAATGTGTGA	420
Qy	421	GGGAAGCTTTGAGAGTCTTGACACCCAACTCAAGCAAGTGTTCATGTGAGTTCAATGA	480
Db	421	GGGAAGCTTTGAGAGTCTTGACACCCAACTCAAGCAAGTGTTCATGTGAGTTCAATGA	480
Qy	481	ATTATGGCATGATCTTTGGAAAATGGCGAGTGTACATTTACAAAGATCGTTCAATA	540

Db	481	ATTATGAGCATATACCTTGGGAAATATGGAGGTGACATTTCACAAAGATGGCTTCAATA	540
Qy	541	GTGCTCTAAGAGTTTTTGTTCAGTGGCTCACTTCGGCTAAATGCAAGATGCATCTGTC	600
Db	541	GTGCTCTAAGAGTTTTTGTTCAGTGGCTCACTTCGGCTAAATGCAAGATGCATCTGTC	600
Qy	601	ACGGTTGGATTTCACATTCATGAGAGTGTTCAGAGCTTTCCTCCATGAGCTA	660
Db	601	ACGGTTGGATTTCACATTCATGAGAGTGTTCAGAGCTTTCCTCCATGAGCTA	660
Qy	661	TAAITTAATTTGGACCAAGAGAGCCCTGAAATGAATTCACAACTTAATATTCAGCACTT	720
Db	661	TAAITTAATTTGGACCAAGAGAGCCCTGAAATGAATTCACAACTTAATATTCAGCACTT	720
Qy	721	CTTCTGTGGAGAGACTTTGTGAGGAATTTGTGCTGAGTTAGTGGATGTTCTATCTGCG	780
Db	721	CTTCTGTGGAGAGACTTTGTGAGGAATTTGTGCTGAGTTAGTGGATGTTCTATCTGCG	780
Qy	781	TTGGCACTTGTTCAGATTACCCAAAGAGATGCTTCTACGAGATGGAATTCAGTTCTC	840
Db	781	TTGGCACTTGTTCAGATTACCCAAAGAGATGCTTCTACGAGATGGAATTCAGTTCTC	840
Qy	841	GCATCATTATTTGAGAGACTACCAAAATATATGCTTAAATTTTCAATTTGCTACCTTTT	900
Db	841	GCATCATTATTTGAGAGACTACCAAAATATATGCTTAAATTTTCAATTTGCTACCTTTT	900
Qy	901	TTATTATGCCCTTGGATGAGTCACTTAATGACATTTTAATTAAGTTATGATATACATCT	960
Db	901	TTATTATGCCCTTGGATGAGTCACTTAATGACATTTTAATTAAGTTATGATATACATCT	960
Qy	961	GAATGAAAGCAAAAGCTAAATATATGTTTTCACAGACCAAGTGTGATTTTCACATGTTTAA	1020
Db	961	GAATGAAAGCAAAAGCTAAATATATGTTTTCACAGACCAAGTGTGATTTTCACATGTTTAA	1020
Qy	1021	ATCTAGCATATATCATTTTGTCTTCATGACAAAGTGGTTTCAATTTTTTTTAACTGGTT	1080
Db	1021	ATCTAGCATATATCATTTTGTCTTCATGACAAAGTGGTTTCAATTTTTTTTAACTGGTT	1080
Qy	1081	AGAAATACCTTCTCATAGTCACTATCTCTCAACCTATATTTGGAAATTTGTGGGCTC	1140
Db	1081	AGAAATACCTTCTCATAGTCACTATCTCTCAACCTATATTTGGAAATTTGTGGGCTC	1140
Qy	1141	TTTGTTTTTTCTCTTAGTAGCATTTTTTAAAAAATATATAAAGCTACCAATCTTGTAC	1200
Db	1141	TTTGTTTTTTCTCTTAGTAGCATTTTTTAAAAAATATATAAAGCTACCAATCTTGTAC	1200
Qy	1201	AAATTTGTAAGTTAGAAATTTTTTTTATATCTGTTAAATTAATATTTTCACACA	1257
Db	1201	AAATTTGTAAGTTAGAAATTTTTTTTATATCTGTTAAATTAATATTTTCACACA	1257

RESULT 23

US-10-176-482-365

Sequence 365, Application US/10176482

Publication No. US20030022296A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jtan

APPLICANT: Deanoysers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3430R1C70

CURRENT APPLICATION NUMBER: US/10/176,482

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 365  
 ; LENGTH: 1257  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-176-482-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 3,4e-271;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTGCGGCGGCGCTCGAGGCGG 60  
 DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTGCGGCGGCGCTCGAGGCGG 60  
 QY 61 CGAGAGCGCGCGCATGACGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 DB 61 CGAGAGCGCGCGCATGACGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 QY 121 CCGGAGCGCGGAGCGCATGACGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 DB 121 CCGGAGCGCGGAGCGCATGACGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 QY 181 GCCTCTGCTGCT 240  
 DB 181 GCCTCTGCTGCT 240  
 QY 241 AGGAGAGCG 300  
 DB 241 AGGAGAGCG 300  
 QY 301 GCTTAAAGGCG 360  
 DB 301 GCTTAAAGGCG 360  
 QY 361 CGGAGAGCG 420  
 DB 361 CGGAGAGCG 420  
 QY 421 GGGAGAGCG 480  
 DB 421 GGGAGAGCG 480  
 QY 481 ATTATGCGATGATCTTGGGAAATTTGGGAGTGTACATTACAAAGATGCGTTCAATA 540  
 DB 481 ATTATGCGATGATCTTGGGAAATTTGGGAGTGTACATTACAAAGATGCGTTCAATA 540  
 QY 541 GAGCTCTAAGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGT 600  
 DB 541 GAGCTCTAAGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGT 600  
 QY 601 AGGAGAGCG 660  
 DB 601 AGGAGAGCG 660  
 QY 661 TAATTTATTTGGGCGCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
 DB 661 TAATTTATTTGGGCGCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720  
 QY 721 CTTCTGAGAGAGCTTTGTGAGGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGT 780  
 DB 721 CTTCTGAGAGAGCTTTGTGAGGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGT 780  
 QY 781 TTGGGAGCTTTGAGATTAACCAAGGAGATGCTTCTACTGATGGAATTCAGTTCTC 840  
 DB 781 TTGGGAGCTTTGAGATTAACCAAGGAGATGCTTCTACTGATGGAATTCAGTTCTC 840  
 QY 841 GCATCATTTATGGAAGATCAACCAATTAATGCTTTAATTTGATTTGCTCTCTTTT 900  
 DB 841 GCATCATTTATGGAAGATCAACCAATTAATGCTTTAATTTGATTTGCTCTCTTTT 900  
 QY 901 TTATTTAGCTTGTGAATGTTGATTAATGATTTTAAATAGTTTATGATACATCT 960

DB 901 TTATTTAGCTTGTGAATGTTGATTAATGATTTTAAATAGTTTATGATACATCT 960  
 QY 961 GAATGAAAAGCAAGCAATTAATGTTTACAGCCAAAGTGATTTTACACGTTTAA 1020  
 DB 961 GAATGAAAAGCAAGCAATTAATGTTTACAGCCAAAGTGATTTTACACGTTTAA 1020  
 QY 1021 ACTAGCATTTATTCATTTTGTGCTTCAATCAAAAGGTTTCAATTTTATTTAGTTGTT 1080  
 DB 1021 ACTAGCATTTATTCATTTTGTGCTTCAATCAAAAGGTTTCAATTTTATTTAGTTGTT 1080  
 QY 1081 AGAATATCTTCTTCAATGATGATTTCTGCAACCTATATTTGGAATATGTTGCTCT 1140  
 DB 1081 AGAATATCTTCTTCAATGATGATTTCTGCAACCTATATTTGGAATATGTTGCTCT 1140  
 QY 1141 TTTGTTTTTCTTCTTCAATGATGATTTTAAAAAATTAAGTACCAATCTTTGTC 1200  
 DB 1141 TTTGTTTTTCTTCTTCAATGATGATTTTAAAAAATTAAGTACCAATCTTTGTC 1200  
 QY 1201 AATTTGTAATGTTAAGATTTTATTTATGTTTAAATATAATTTATTTCCACA 1257  
 DB 1201 AATTTGTAATGTTAAGATTTTATTTATGTTTAAATATAATTTATTTCCACA 1257

RESULT 24  
 US-10-176-757-365  
 ; Sequence 365, Application US/10176757  
 ; Publication No. US20030022297A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Ausrin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3430R1C86  
 ; CURRENT APPLICATION NUMBER: US/10/176,757  
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 365  
 ; LENGTH: 1257  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-176-757-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
 Best Local Similarity 100.0%; Pred. No. 3,4e-271;  
 Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTGCGGCGGCGCTCGAGGCGG 60  
 DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTGCGGCGGCGCTCGAGGCGG 60  
 QY 61 CGAGAGCGCGCGCATGACGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 DB 61 CGAGAGCGCGCGCATGACGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
 QY 121 CCGGAGCGCGGAGCGCATGACGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 DB 121 CCGGAGCGCGGAGCGCATGACGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 QY 181 GCCTCTGCTGCT 240  
 DB 181 GCCTCTGCTGCT 240



QY 661 TAATTATTGGACCAAGAGCCCTGAATGATTCACAAATTAATTCATCGACT 720  
| | | | |  
Db 661 TAATTATTGGACCAAGAGCCCTGAATGATTCACAAATTAATTCATCGACT 720  
QY 721 CTTCTGTGGAAGACTTTGTGAAGAAATGTTGCTGATTAAGTGTGCTATCTGG 780  
| | | | |  
Db 721 CTTCTGTGGAAGACTTTGTGAAGAAATGTTGCTGATTAAGTGTGCTATCTGG 780  
QY 781 TTGGCACTTGTCAGATTACCCAAAGAGAGCTCTCACTGAGATGGAATTCAGTTTC 840  
| | | | |  
Db 781 TTGGCACTTGTCAGATTACCCAAAGAGAGCTCTCACTGAGATGGAATTCAGTTTC 840  
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAATTTTCATTGCTACCTCTTT 900  
| | | | |  
Db 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAATTTTCATTGCTACCTCTTT 900  
QY 901 TTATTATGCTTGGAAATGCTTCAATTAATGACATTTTAATTAATGTTATGATACAT 960  
| | | | |  
Db 901 TTATTATGCTTGGAAATGCTTCAATTAATGACATTTTAATTAATGTTATGATACAT 960  
QY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
| | | | |  
Db 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
QY 1021 ACTAGCATTAATTCATTTGCTTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
| | | | |  
Db 1021 ACTAGCATTAATTCATTTGCTTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
QY 1081 AGAATACCTTCTTCATAGTCACATCTCTCAACCTTAATTTGGAATATGTTGTGCT 1140  
| | | | |  
Db 1081 AGAATACCTTCTTCATAGTCACATCTCTCAACCTTAATTTGGAATATGTTGTGCT 1140  
QY 1141 TTTGTTTTTCTCTTATGATAGATTTTAAAAAATTAAGCTACCAATCTTTGTAC 1200  
| | | | |  
Db 1141 TTTGTTTTTCTCTTATGATAGATTTTAAAAAATTAAGCTACCAATCTTTGTAC 1200  
QY 1201 AATTGTAAATGTTAAGAAATTTTAAATCTGTTAAATTAATTAATTTCCACA 1257  
| | | | |  
Db 1201 AATTGTAAATGTTAAGAAATTTTAAATCTGTTAAATTAATTAATTTCCACA 1257

## RESULT 26

US-10-180-552-365  
; Sequence 365, Application US/10180552  
; Publication No. US20030022300A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C153  
; CURRENT APPLICATION NUMBER: US/10/180,552  
; CURRENT FILING DATE: 2002-06-25  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 365  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-180-552-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3,4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGGAGTGAAGGCGCATTTGACAGCTGCGGCGGCTCCGAGCGCG 60  
| | | | |  
Db 1 GGAGAGAGCGCGCGGAGTGAAGGCGCATTTGACAGCTGCGGCGGCTCCGAGCGCG 60  
QY 61 CGAGCGCAGACGCTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
| | | | |  
Db 61 CGAGCGCAGACGCTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 121 CCCGCGACCGCGGAGCCATGCGACCCCAAGGCGCCGCGCTCTCTCTCTCTCTCT 180  
| | | | |  
Db 121 CCCGCGACCGCGGAGCCATGCGACCCCAAGGCGCCGCGCTCTCTCTCTCTCTCT 180  
QY 181 GCTCTGCTGCT 240  
| | | | |  
Db 181 GCTCTGCTGCT 240  
QY 241 AGGCGAAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGAGCTGTATTAATGGAAT 300  
| | | | |  
Db 241 AGGCGAAGCAAAAGCGCAGCTCCGCGAGAGGAGTGTGAGCTGTATTAATGGAAT 300  
QY 301 GCTTACAGGCGCAGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
| | | | |  
Db 301 GCTTACAGGCGCAGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
QY 361 CGGTAACACTGCGGATCCCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 420  
| | | | |  
Db 361 CGGTAACACTGCGGATCCCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 420  
QY 421 GGGAAAGCTTTGAGAGTCTCTGAGACCCCACTAGACAGTGTTCATGAGTTCA 480  
| | | | |  
Db 421 GGGAAAGCTTTGAGAGTCTCTGAGACCCCACTAGACAGTGTTCATGAGTTCA 480  
QY 481 AATTATGCAATGATCTTGGGAAAATTTGCGAGTGTACATTACAAAGATGCGTTCA 540  
| | | | |  
Db 481 AATTATGCAATGATCTTGGGAAAATTTGCGAGTGTACATTACAAAGATGCGTTCA 540  
QY 541 GTGCTCTAAGATTTTGTTCATGCTGCTCACTCTGCGTAAATGCAAGAAATGAT 600  
| | | | |  
Db 541 GTGCTCTAAGATTTTGTTCATGCTGCTCACTCTGCGTAAATGCAAGAAATGAT 600  
QY 601 AGCGTTGATTTTCAATTCATGAGAGCTGAATGTTACAGACCTCTTCCCATGGA 660  
| | | | |  
Db 601 AGCGTTGATTTTCAATTCATGAGAGCTGAATGTTACAGACCTCTTCCCATGGA 660  
QY 661 TAATTATTGGACCAAGAGCCCTGAATGATTCACAAATTAATTCATCGACT 720  
| | | | |  
Db 661 TAATTATTGGACCAAGAGCCCTGAATGATTCACAAATTAATTCATCGACT 720  
QY 721 CTTCTGTGGAAGACTTTGTGAAGAAATGTTGCTGATTAAGTGTGCTATCTGG 780  
| | | | |  
Db 721 CTTCTGTGGAAGACTTTGTGAAGAAATGTTGCTGATTAAGTGTGCTATCTGG 780  
QY 781 TTGGCACTTGTCAGATTACCCAAAGAGAGCTCTCACTGAGATGGAATTCAGTTTC 840  
| | | | |  
Db 781 TTGGCACTTGTCAGATTACCCAAAGAGAGCTCTCACTGAGATGGAATTCAGTTTC 840  
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAATTTTCATTGCTACCTCTTT 900  
| | | | |  
Db 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTAATTTTCATTGCTACCTCTTT 900  
QY 901 TTATTATGCTTGGAAATGCTTCAATTAATGACATTTTAATTAATGTTATGATACAT 960  
| | | | |  
Db 901 TTATTATGCTTGGAAATGCTTCAATTAATGACATTTTAATTAATGTTATGATACAT 960  
QY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
| | | | |  
Db 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
QY 1021 ACTAGCATTAATTCATTTGCTTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080  
| | | | |  
Db 1021 ACTAGCATTAATTCATTTGCTTCAATCAAAAGTGTTCATATTTTGTAGTTGTT 1080

QY 1081 AGAATACCTTCTTCATGTCACATTCCTCAACCTATTAATTTGGAAATATGTTGGTCT 1140  
DB 1081 AGAATACCTTCTTCATGTCACATTCCTCAACCTATTAATTTGGAAATATGTTGGTCT 1140  
QY 1141 TTTGTTTTTCTCTAGTATGATATTTTAAATAATATTAAGCTATCCATTTTGTAC 1200  
DB 1141 TTTGTTTTTCTCTAGTATGATATTTTAAATAATATTAAGCTATCCATTTTGTAC 1200  
QY 1201 AATTTGTAATGTTAAGATTTTATATCTGTTAAATTAATTAATTTTCCACA 1257  
DB 1201 AATTTGTAATGTTAAGATTTTATATCTGTTAAATTAATTAATTTTCCACA 1257

RESULT 27  
US-10-180-557-365  
; Sequence 365, Application US/10180557  
; Publication No. US20030022301A1  
GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C147  
; CURRENT FILING DATE: 2002-06-25  
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-180-557-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAGAGCGCGCGGTGAAAGCGCATTTGATGAGCCTGCGCGGCTCGGAGCGCGG 60  
DB 1 GAGAGAGCGCGCGGTGAAAGCGCATTTGATGAGCCTGCGCGGCTCGGAGCGCGG 60  
QY 61 CGAGGCCAGACGCTGACCACTTCTCTCTGCTCTCTCGGCTCGAGCTCGCGGTG 120  
DB 61 CGAGGCCAGACGCTGACCACTTCTCTCTGCTCTCTCGGCTCGAGCTCGCGGTG 120  
QY 121 CCGGCGAGCGGGAAGCATGGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
DB 121 CCGGCGAGCGGGAAGCATGGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
QY 181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 241 AGGAGGAAGCAAAAGCGGAGCTCGGCGAGAGGAGAGTGTGAGCTGTATATGGAATGT 300  
DB 241 AGGAGGAAGCAAAAGCGGAGCTCGGCGAGAGGAGAGTGTGAGCTGTATATGGAATGT 300  
QY 301 GCTTACAGGGCGCGAGAGAGTGTGAGAGCGGAGCGCGCGCGCGCGCGCGCGCGCG 360  
DB 301 GCTTACAGGGCGCGAGAGAGTGTGAGAGCGGAGCGCGCGCGCGCGCGCGCGCGCG 360  
QY 361 CGGAGTACCTGGAGTCCAGAGTGGGATGATTCAGAGAGAGAGAGAGAGAGAGAGTCTGA 420  
DB 361 CGGAGTACCTGGAGTCCAGAGTGGGATGATTCAGAGAGAGAGAGAGAGAGAGAGTCTGA 420

QY 421 GGGAAAGCTTTGAGAGTCTGACACCCCACTAAGAGAGTGTCAAGAGTTCATTGA 480  
DB 421 GGGAAAGCTTTGAGAGTCTGACACCCCACTAAGAGAGTGTCAAGAGTTCATTGA 480  
QY 481 ATTATGCAATAGATCTTGGGAAAATGCGAGGTGATATTAACAAAGTGGTCAATA 540  
DB 481 ATTATGCAATAGATCTTGGGAAAATGCGAGGTGATATTAACAAAGTGGTCAATA 540  
QY 541 GTGCTCTAAGAGTGTGTCAGTGGCTCACTTGGCTTAAATGCGAATGAGATGCTGTC 600  
DB 541 GTGCTCTAAGAGTGTGTCAGTGGCTCACTTGGCTTAAATGCGAATGAGATGCTGTC 600  
QY 601 AGCGTTGGTATTTTCATTCATGAGCTGAATGTCAGAGACCTCTCCCATGGAAGCTA 660  
DB 601 AGCGTTGGTATTTTCATTCATGAGCTGAATGTCAGAGACCTCTCCCATGGAAGCTA 660  
QY 661 TAATTTATTTGACCAAGAGAGCCCTGAAATGATTAACAAATTAATTTATTCGACCTT 720  
DB 661 TAATTTATTTGACCAAGAGAGCCCTGAAATGATTAACAAATTAATTTATTCGACCTT 720  
QY 721 CTTCTGTGGAAGAGCTTTGTGAGAGAAATGGTGTGATTAAGTATGCTATCTGGG 780  
DB 721 CTTCTGTGGAAGAGCTTTGTGAGAGAAATGGTGTGATTAAGTATGCTATCTGGG 780  
QY 781 TTGGCACTTTTCAGATTACCAAAAGAGATGCTTCACTGATGGAATTCAGATTTCTG 840  
DB 781 TTGGCACTTTTCAGATTACCAAAAGAGATGCTTCACTGATGGAATTCAGATTTCTG 840  
QY 841 GCATCATTTATGAAGAACCAAAATTAATGCTTTAATTTTCACTTGTCTACTCTTTT 900  
DB 841 GCATCATTTATGAAGAACCAAAATTAATGCTTTAATTTTCACTTGTCTACTCTTTT 900  
QY 901 TTATATGCTTGAAGAGTTCATTAATGACATTTTAAATGATTAATGATTAATGATCT 960  
DB 901 TTATATGCTTGAAGAGTTCATTAATGACATTTTAAATGATTAATGATTAATGATCT 960  
QY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
DB 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACACTGTTTAA 1020  
QY 1021 ATCTAGCAATTTATTTTGGCTTCAATCAAAAGTGTGATTCACACTGTTTAA 1080  
DB 1021 ATCTAGCAATTTATTTTGGCTTCAATCAAAAGTGTGATTCACACTGTTTAA 1080  
QY 1081 AGAATACCTTCTTCATGTCACATTCCTCAACCTATTAATTTGGAAATATGTTGGTCT 1140  
DB 1081 AGAATACCTTCTTCATGTCACATTCCTCAACCTATTAATTTGGAAATATGTTGGTCT 1140  
QY 1141 TTTGTTTTTCTCTAGTATGATATTTTAAATAATATTAAGCTATCCATTTTGTAC 1200  
DB 1141 TTTGTTTTTCTCTAGTATGATATTTTAAATAATATTAAGCTATCCATTTTGTAC 1200  
QY 1201 AATTTGTAATGTTAAGATTTTATATCTGTTAAATTAATTAATTTTCCACA 1257  
DB 1201 AATTTGTAATGTTAAGATTTTATATCTGTTAAATTAATTAATTTTCCACA 1257

RESULT 28  
US-10-063-502-121  
; Sequence 121, Application US/10063502  
; Publication No. US20030023042A1  
GENERAL INFORMATION:  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,502  
CURRENT FILING DATE: 2002-05-01  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 121  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-063-502-121

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTGCGCGGCTCGAGCGCGG 60  
DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTGCGCGGCTCGAGCGCGG 60  
QY 61 CGAGAGCAGACCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
DB 61 CGAGAGCAGACCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 121 CCCGCGAGCGCGGAGCGCATGCGACCCCGAGGCGCGCGCGCTCCCGCAGCGGCTCCG 180  
DB 121 CCCGCGAGCGCGGAGCGCATGCGACCCCGAGGCGCGCGCGCTCCCGCAGCGGCTCCG 180  
QY 181 GCGCTCTGCTGCT 240  
DB 181 GCGCTCTGCTGCT 240  
QY 241 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
DB 241 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
QY 301 GCTTACAAAGGCGCAGAGAGTCTCTGATCGAGACGCGGAGCGCTCGGAGCGCATTTATTC 360  
DB 301 GCTTACAAAGGCGCAGAGAGTCTCTGATCGAGACGCGGAGCGCTCGGAGCGCATTTATTC 360  
QY 361 CGGCTACACCTGAGATCCAGGCTCGGAGTGAATTCAGAGAGGAGGAGGAGGAGGAGGAG 420  
DB 361 CGGCTACACCTGAGATCCAGGCTCGGAGTGAATTCAGAGAGGAGGAGGAGGAGGAGGAG 420  
QY 421 GGGAGAGCTTTGAGAGAGTCTCTGACACCCAGCTACAGAGAGTCTTATGAGTTCATGGA 480  
DB 421 GGGAGAGCTTTGAGAGAGTCTCTGACACCCAGCTACAGAGAGTCTTATGAGTTCATGGA 480  
QY 481 ATTATGAGCATAGATCTTGGGAGGAGTGTGATTTACAAAGATGCGTTCAGATA 540  
DB 481 ATTATGAGCATAGATCTTGGGAGGAGTGTGATTTACAAAGATGCGTTCAGATA 540  
QY 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGGCTAAATGACAGAAATGATGCTGTTC 600  
DB 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGGCTAAATGACAGAAATGATGCTGTTC 600  
QY 601 AGGCTGTGATTTCAATTCATGAGAGCTGAGATGTTTCAAGAGCTCTTCCCATTTGAAGCTA 660  
DB 601 AGGCTGTGATTTCAATTCATGAGAGCTGAGATGTTTCAAGAGCTCTTCCCATTTGAAGCTA 660  
QY 661 TAATTAATTTGAGCAAGGAGGCTGAATGAATCAATTAATTAATTAATTAATTAATTAAT 720  
DB 661 TAATTAATTTGAGCAAGGAGGCTGAATGAATCAATTAATTAATTAATTAATTAATTAAT 720  
QY 721 GTTCTGTGAGAGACTTTGTGAAGAAATGCTGATGATGATGATGATGATGATGATGATG 780  
DB 721 GTTCTGTGAGAGACTTTGTGAAGAAATGCTGATGATGATGATGATGATGATGATGATG 780  
QY 781 TTGGGACCTTTGATCAATTCACCAAGAGAGATCTTCTACTGATGATGATGATGATGATG 840  
DB 781 TTGGGACCTTTGATCAATTCACCAAGAGAGATCTTCTACTGATGATGATGATGATGATG 840  
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGATGACTCTTTT 900

DB 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGATGACTCTTTT 900  
QY 901 TTATTAATGCTTTGAGATGCTTCAATTAATGATGATGATGATGATGATGATGATGATG 960  
DB 901 TTATTAATGCTTTGAGATGCTTCAATTAATGATGATGATGATGATGATGATGATGATG 960  
QY 961 GAATGAAGAGCAAGCTAATATGTTTACAGACCAAGGATGATTTTCACTGATTTTAA 1020  
DB 961 GAATGAAGAGCAAGCTAATATGTTTACAGACCAAGGATGATTTTCACTGATTTTAA 1020  
QY 1021 ATCTAGCATTTATGATTTTGTCTTCAATCAAAAGGATGATTTTATTTTATGTTGTT 1080  
DB 1021 ATCTAGCATTTATGATTTTGTCTTCAATCAAAAGGATGATTTTATTTTATGTTGTT 1080  
QY 1081 AGAATATCTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
DB 1081 AGAATATCTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
QY 1141 TTGTTTTTTCTTCTAGTATGATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1200  
DB 1141 TTGTTTTTTCTTCTAGTATGATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1200  
QY 1201 AATTTGTAATGTTAAGATTTTATTTTATCTGTTAATTAATTAATTAATTTTCAACA 1257  
DB 1201 AATTTGTAATGTTAAGATTTTATTTTATCTGTTAATTAATTAATTAATTTTCAACA 1257

RESULT 29  
US-10-173-700-365  
Sequence 365, Application US/10173700  
Publication No. US20030027262A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C14  
CURRENT APPLICATION NUMBER: US/10/173,700  
CURRENT FILING DATE: 2002-06-17  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 365  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-173-700-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTGCGCGGCTCGAGCGCGG 60  
DB 1 GGAGAGAGCGCGCGGGTGAAGGCGCATTTGATGACGCTGCGCGGCTCGAGCGCGG 60  
QY 61 CGAGAGCAGACCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
DB 61 CGAGAGCAGACCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 121 CCCGCGAGCGCGGAGCGCATGCGACCCCGAGGCGCGCGCTCCCGCAGCGGCTCCG 180  
DB 121 CCCGCGAGCGCGGAGCGCATGCGACCCCGAGGCGCGCGCTCCCGCAGCGGCTCCG 180









```
QY 1021 ATCTAGCATTTATTCATTTTCTTCATCAATCAAAAGTGGTTCAATATTTTATTTAGTTGTT 1080
Db 1021 ATCTAGCATTTATTCATTTTCTTCATCAATCAAAAGTGGTTCAATATTTTATTTAGTTGTT 1080
QY 1081 AGAATACCTTTCTTCATAGTCACTTTCTTCACCTTAAATTTGGAATATTTTGGTGTCT 1140
Db 1081 AGAATACCTTTCTTCATAGTCACTTTCTTCACCTTAAATTTGGAATATTTGTTGGTGTCT 1140
QY 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAATAAATATTAAGCTACCAATCTTTGTAC 1200
Db 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAATAAATATTAAGCTACCAATCTTTGTAC 1200
QY 1201 AATTGTAAATGTAAAGATTTTATTAATCTGTAAATTAATAATTTATTTCCACA 1257
Db 1201 AATTGTAAATGTAAAGATTTTATTAATCTGTAAATTAATAATTTATTTCCACA 1257

RESULT 32
US-10-174-582-365
; Sequence 365, Application US/10174582
; Publication No. US20030027265A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C36
; CURRENT APPLICATION NUMBER: US/10/174,582
; PRIORITY FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-174-582-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGAGGCGCGCGGGTGAAGGCGCATTTGATGAGCCTTGCGGCGGCTCGGAGCGCGG 60
Db 1 GGAAGAGGCGCGCGGGTGAAGGCGCATTTGATGAGCCTTGCGGCGGCTCGGAGCGCGG 60
QY 61 CGAGAGCGAGCGCTGACACGTTCTCTCTCGGCTCTCTCGGCTCTCGACGCTCGGCGGTG 120
Db 61 CGAGAGCGAGCGCTGACACGTTCTCTCTCGGCTCTCTCGGCTCTCGACGCTCGGCGGTG 120
QY 121 CCGGCGAGCGCGGAGCCATGCGACCCCGAGGCGCCCGCGCTCCCGAGCGGCTCGCGG 180
Db 121 CCGGCGAGCGCGGAGCCATGCGACCCCGAGGCGCCCGCGCTCCCGAGCGGCTCGCGG 180
QY 181 GCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 GCGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 AGGGGAAGCAAAAGCGCAGCTCGCGAGAGGAGGTGTGTAATGTAATGTAATGTAATGTA 300
Db 241 AGGGGAAGCAAAAGCGCAGCTCGCGAGAGGAGGTGTGTAATGTAATGTAATGTAATGTA 300
QY 301 GCTTACAGGCGCGAGCAAGAGTGTGCTGAGAGCGGAGGCGCTGCGGCGCAATGTTATTC 360
Db 301 GCTTACAGGCGCGAGCAAGAGTGTGCTGAGAGCGGAGGCGCTGCGGCGCAATGTTATTC 360
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QY 361 CGGGTACACCTGGGATTCACAGTGGGATGGATTTCAAGAGAAAGGGGAATGTCTGA 420
Db 361 CGGGTACACCTGGGATTCACAGTGGGATGGATTTCAAGAGAAAGGGGAATGTCTGA 420
QY 421 GGGAAAGCTTTGAGAGTCTGAGACCCCACTCAAGAGTGTTCATGAGGTTCAATGA 480
Db 421 GGGAAAGCTTTGAGAGTCTGAGACCCCACTCAAGAGTGTTCATGAGGTTCAATGA 480
QY 481 ATTATGCAATGATCTTGGGAAAATGGGAGTGTATCAATTAACAAGATCGTTCAATA 540
Db 481 ATTATGCAATGATCTTGGGAAAATGGGAGTGTATCAATTAACAAGATCGTTCAATA 540
QY 541 GTGCTCTAAGAGTTTGTTCAGTGTCTCACTTGGGCTTAAATGAGAAATGATGCTGTC 600
Db 541 GTGCTCTAAGAGTTTGTTCAGTGTCTCACTTGGGCTTAAATGAGAAATGATGCTGTC 600
QY 601 AGCGTTGATTTTCATTCATGAGCTGATGATGTCAGACCTCTCCCATTTGAAGCTA 660
Db 601 AGCGTTGATTTTCATTCATGAGCTGATGATGTCAGACCTCTCCCATTTGAAGCTA 660
QY 661 TAATTTATTTGAGCCAGAGAGCCCTGAAATGAATTCACAAATTAATATTCATGCACTT 720
Db 661 TAATTTATTTGAGCCAGAGAGCCCTGAAATGAATTCACAAATTAATATTCATGCACTT 720
QY 721 CTTCGTGGAAGAGCTTTGTGAAGAAATGGTGTGATGATGATGATGATGATGATGATG 780
Db 721 CTTCGTGGAAGAGCTTTGTGAAGAAATGGTGTGATGATGATGATGATGATGATGATG 780
QY 781 TTGGCACTTGTTCAGATTTCCCAAGAGAGATGCTTCTAGTGTGATGATGATGATGATG 840
Db 781 TTGGCACTTGTTCAGATTTCCCAAGAGAGATGCTTCTAGTGTGATGATGATGATGATG 840
QY 841 GCATCATTTATGAGAACTCCAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTT 900
Db 841 GCATCATTTATGAGAACTCCAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTT 900
QY 901 TTATTTAGCCTTGGAAATGTTCACTTAATGATCAATTTAATGATTTATGATGATGATG 960
Db 901 TTATTTAGCCTTGGAAATGTTCACTTAATGATCAATTTAATGATTTATGATGATGATG 960
QY 961 GAATGAAAAGCAAGCTAATATGTTTACAGACCAAGGTGATTTCACTGTTTTTAA 1020
Db 961 GAATGAAAAGCAAGCTAATATGTTTACAGACCAAGGTGATTTCACTGTTTTTAA 1020
QY 1021 ATCTAGCATTTATTCATTTTCTTCATCAATCAAAAGTGGTTCAATATTTTATTTAGTTG 1080
Db 1021 ATCTAGCATTTATTCATTTTCTTCATCAATCAAAAGTGGTTCAATATTTTATTTAGTTG 1080
QY 1081 AGAATACCTTTCTTCATAGTCACTTTCTTCACCTTAAATTTGGAATATTTTGGTGTCT 1140
Db 1081 AGAATACCTTTCTTCATAGTCACTTTCTTCACCTTAAATTTGGAATATTTTGGTGTCT 1140
QY 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAATAAATATTAAGCTACCAATCTTTGTAC 1200
Db 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAATAAATATTAAGCTACCAATCTTTGTAC 1200
QY 1201 AATTGTAAATGTAAAGATTTTATTAATCTGTAAATTAATAATTTATTTCCACA 1257
Db 1201 AATTGTAAATGTAAAGATTTTATTAATCTGTAAATTAATAATTTATTTCCACA 1257

RESULT 33
US-10-174-588-365
; Sequence 365, Application US/10174588
; Publication No. US20030027266A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
```



Dp	61	CGAGGCGAAGCGTGAACCAAGTTCCTCTCTCGGTCTCTCTCCGCTCCAGCTCCGGCTG	120
Qy	121	CCCGGAGGCGGGAGCCATTGCGAACCAGGGCCCCGCGCTCCCGGACGGCTCGCG	180
Dp	121	CCGGGAGCGGGAGCCATGCGAACCAGGGCCCCGCGCTCCCGGACGGCTCGCG	180
Qy	181	GCGTCTGCTGCTCTGCTGCTGAGCTGCGCGGCGGCTGAGAGGCGCTCGAATGCCA	240
Dp	181	GCTCTGTGCTCTCTGCTGCTGAGCTGCGCGGCGGCTGAGAGGCGCTCGAATGCCA	240
Qy	241	AGGGGAAGCAAAAGGCGGAGCTCCGGCAAGGAGGAGTGATGACCTGTATATGAAATGT	300
Dp	241	AGGGGAAGCAAAAGGCGGAGCTCCGGCAAGGAGGAGTGATGACCTGTATATGAAATGT	300
Qy	301	GCTTACAAGGGCCAGGAGAGTGCCTGCTGTGAGACGGGAGCCCTGGGGCCAAATGTTATC	360
Dp	301	GCTTACAAGGGCCAGGAGAGTGCCTGCTGTGAGACGGGAGCCCTGGGGCCAAATGTTATC	360
Qy	361	CGGGTACACCTGGGATCCAGGTCGGGATGGAATTCAAAGAGAAAAGGGGAATGTCGA	420
Dp	361	CGGGTACACCTGGGATCCAGGTCGGGATGGAATTCAAAGAGAAAAGGGGAATGTCGA	420
Qy	421	GGGAAGGCTTTGAGAGTCTCGGACACCCAACTACAAGAGTGTTCATGAGTTCATTGA	480
Dp	421	GGGAAGGCTTTGAGAGTCTCGGACACCCAACTACAAGAGTGTTCATGAGTTCATTGA	480
Qy	481	ATTATGCGATAGATCTTGGGAAAATTCGGAGTGTACATTTACAAGATGCGTTCAAAAT	540
Dp	481	ATTATGCGATAGATCTTGGGAAAATTCGGAGTGTACATTTACAAGATGCGTTCAAAAT	540
Qy	541	GTGCTTAAGAGTGTGTGTTCACTGCGTCACTTGCGCTAAATGCAAAAATGCATGCTGC	600
Dp	541	GTGCTTAAGAGTGTGTGTTCACTGCGTCACTTGCGCTAAATGCAAAAATGCATGCTGC	600
Qy	601	ACGCTGTGATTTCACTTCAATGAGGCTGAATGTCAGAGCCCTCCCATTTGAAGCTA	660
Dp	601	ACGCTGTGATTTCACTTCAATGAGGCTGAATGTCAGAGCCCTCCCATTTGAAGCTA	660
Qy	661	TAAATTTTGGACCAAGAGCCCTGAATGAATTCAAATTAATTTCAATGCACTT	720
Dp	661	TAAATTTTGGACCAAGAGCCCTGAATGAATTCAAATTAATTTCAATGCACTT	720
Qy	721	CTTCTGTGAGAGACTTGTGGAAGAAATGGGCTGGATTAATGAGATGTTGCTAATCTGGG	780
Dp	721	CTTCTGTGAGAGACTTGTGGAAGAAATGGGCTGGATTAATGAGATGTTGCTAATCTGGG	780
Qy	781	TTGGCACTTGTCAGATTACCCAAAAGAGATGCTTCACTGAGATGCAATGCACTTCTC	840
Dp	781	TTGGCACTTGTCAGATTACCCAAAAGAGATGCTTCACTGAGATGCAATGCACTTCTC	840
Qy	841	GCATCATTTATGAAAGACTACCAAAATAATGCTTTAATTTCACTTGGCTACCTCTTTT	900
Dp	841	GCATCATTTATGAAAGACTACCAAAATAATGCTTTAATTTCACTTGGCTACCTCTTTT	900
Qy	901	TTATATGCTTGGAATGCTTCACTTAAATGACATTTTAAATAGTTATGATPACCT	960
Dp	901	TTATATGCTTGGAATGCTTCACTTAAATGACATTTTAAATAGTTATGATPACCT	960
Qy	961	GATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGATGATTCACACTGTTTTTA	1020
Dp	961	GATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGATGATTCACACTGTTTTTA	1020
Qy	1021	ATCTGACATTTATCAATTTTGCCTCAATCAAAAGTGTTCAATTTTTTTTAAATGTTG	1080
Dp	1021	ATCTGACATTTATCAATTTTGCCTCAATCAAAAGTGTTCAATTTTTTTTAAATGTTG	1080
Qy	1081	AGATATCTTCTTCATAGTCACTTCTCAACCTAATATTTGGAATATGTTGTGTGCTC	1140
Dp	1081	AGATATCTTCTTCATAGTCACTTCTCAACCTAATATTTGGAATATGTTGTGTGCTC	1140
Qy	1141	TTGTGTTTTCTCTAGTATAGCAATTTTAAAAAATATAAAGCTACCAATCTTTGAC	1200
Dp	1141	TTGTGTTTTCTCTAGTATAGCAATTTTAAAAAATATAAAGCTACCAATCTTTGAC	1200

QY	1201	AATTGTAAGTAAAGAAATTTTCTTAAATCTGTTAAATAAAATTAATTCACA	1257
Db	1201	AATTGTAAGTAAAGAAATTTTCTTAAATCTGTTAAATAAAATTAATTCACA	1257
RESULT 35			
US-10-175-740-365			
/ Sequence 365, Application US/10175740			
/ Publication No. US20030027268A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin P.			
APPLICANT: Chen, Jian			
APPLICANT: Desnoyers, Luc			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Gurney, Austin L.			
APPLICANT: Pan, James			
APPLICANT: Smith, Victoria			
APPLICANT: Watanabe, Colin K.			
APPLICANT: Wood, William I.			
APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
TITLE OF INVENTION: ACIDS ENCODING THE SAME			
FILE REFERENCE: P3430R1C61			
CURRENT APPLICATION NUMBER: US/10/175,740			
PRIOR FILING DATE: 2002-06-18			
PRIOR APPLICATION removed - See File Wrapper or Palm			
NUMBER OF SEQ ID NOS: 612			
SEQ ID NO 365			
/ LENGTH: 1257			
/ TYPE: DNA			
/ ORGANISM: Homo Sapien			
US-10-175-740-365			
Query Match 100.0%; Score 1257; DB 14; Length 1257;			
Beat Local Similarity 100.0%; Pred. No. 3,4e-271;			
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GGAGAGAGCGCGCGGTGAAAGGCGCATTTGATCAGACCTCCGCGGCTCCGAGCGGG	60
Db	1	GGAGAGAGGCGCGCGGTGAAAGGCGCATTTGATCAGACCTCCGAGCGGG	60
QY	61	CGAGGCGAAGCGCTGACACGTTCTCTCTCGGTCTCTCCGCGCTCCAGACTCCGCGCTG	120
Db	61	CGAGGCGAAGCGCTGACACGTTCTCTCTCGGTCTCTCCGCGCTCCAGACTCCGCGCTG	120
QY	121	CCGCGAGCGCGGAGCGCATGCGACCCCAAGGCGCCCGCGCTCCCGCAGCGGCTCCGCG	180
Db	121	CCGCGAGCGCGGAGCGCATGCGACCCCAAGGCGCCCGCGCTCCCGCAGCGGCTCCGCG	180
QY	181	GCCTCTGCTGCTCCGCTGCTGCTGACGCGCCCGCGCGTGCAGCGGCTCTGAGATCCCA	240
Db	181	GCCTCTGCTGCTCCGCTGCTGCTGACGCGCCCGCGCGTGCAGCGGCTCTGAGATCCCA	240
QY	241	AGGCGAAGCAAAAGGCGAGCTCCGCGAGAGGAGGTGTGACCTGTAAATGGAATGT	300
Db	241	AGGCGAAGCAAAAGGCGAGCTCCGCGAGAGGAGGTGTGACCTGTAAATGGAATGT	300
QY	301	GCCTTAAAGGCGCAGACAGAGATGCTGTGAGACGGGAGCCCTGGGCGCAATGTTATTC	360
Db	301	GCCTTAAAGGCGCAGACAGAGATGCTGTGAGAGCGGAGCCCTGGGCGCAATGTTATTC	360
QY	361	CGGGTACACTTGAGATCCAGAGTCCGAGATGATTTCAAAGAGAAAGGGGGAATGTCTGA	420
Db	361	CGGGTACACTTGAGATCCAGAGTCCGAGATGATTTCAAAGAGAAAGGGGGAATGTCTGA	420
QY	421	GGGAAAGCTTTGAGAGATCTTGACACCCAACTTCAAGAGAGTGTTCATGAGATTCAATGA	480
Db	421	GGGAAAGCTTTGAGAGATCTTGACACCCAACTTCAAGAGAGTGTTCATGAGATTCAATGA	480
QY	481	AATTAGCATAGATTTTGGGAAATTCGAGAGTGTCAATTTCAAAGATGCGTCAATTA	540



1	PRIOR APPLICATION NUMBER: 60/082566
2	PRIOR FILING DATE: 1998-04-21
3	PRIOR APPLICATION NUMBER: 60/082566
4	PRIOR FILING DATE: 1998-04-21
5	PRIOR APPLICATION NUMBER: 60/082704
6	PRIOR FILING DATE: 1998-04-22
7	PRIOR APPLICATION NUMBER: 60/082797
8	PRIOR FILING DATE: 1998-04-22
9	PRIOR APPLICATION NUMBER: 60/083322
10	PRIOR FILING DATE: 1998-04-28
11	PRIOR APPLICATION NUMBER: 60/083495
12	PRIOR FILING DATE: 1998-04-29
13	PRIOR APPLICATION NUMBER: 60/083496
14	PRIOR FILING DATE: 1998-04-29
15	PRIOR APPLICATION NUMBER: 60/083499
16	PRIOR FILING DATE: 1998-04-29
17	PRIOR APPLICATION NUMBER: 60/083558
18	PRIOR FILING DATE: 1998-04-29
19	PRIOR APPLICATION NUMBER: 60/084366
20	PRIOR FILING DATE: 1998-05-05
21	PRIOR APPLICATION NUMBER: 60/084414
22	PRIOR FILING DATE: 1998-05-06
23	PRIOR APPLICATION NUMBER: 60/084639
24	PRIOR FILING DATE: 1998-05-07
25	PRIOR APPLICATION NUMBER: 60/084640
26	PRIOR FILING DATE: 1998-05-07
27	PRIOR APPLICATION NUMBER: 60/084643
28	PRIOR FILING DATE: 1998-05-07
29	PRIOR APPLICATION NUMBER: 60/085573
30	PRIOR FILING DATE: 1998-05-15
31	PRIOR APPLICATION NUMBER: 60/085579
32	PRIOR FILING DATE: 1998-05-15
33	PRIOR APPLICATION NUMBER: 60/085580
34	PRIOR FILING DATE: 1998-05-15
35	PRIOR APPLICATION NUMBER: 60/085582
36	PRIOR FILING DATE: 1998-05-15
37	PRIOR APPLICATION NUMBER: 60/085700
38	PRIOR FILING DATE: 1998-05-15
39	PRIOR APPLICATION NUMBER: 60/086023
40	PRIOR FILING DATE: 1998-05-18
41	PRIOR APPLICATION NUMBER: 60/086392
42	PRIOR FILING DATE: 1998-05-22
43	PRIOR APPLICATION NUMBER: 60/086486
44	PRIOR FILING DATE: 1998-05-22
45	PRIOR APPLICATION NUMBER: 60/087098
46	PRIOR FILING DATE: 1998-05-28
47	PRIOR APPLICATION NUMBER: 60/087208
48	PRIOR FILING DATE: 1998-05-28
49	PRIOR APPLICATION NUMBER: 60/087609
50	PRIOR FILING DATE: 1998-06-02
51	PRIOR APPLICATION NUMBER: 60/087759
52	PRIOR FILING DATE: 1998-06-02
53	PRIOR APPLICATION NUMBER: 60/087827
54	PRIOR FILING DATE: 1998-06-03
55	PRIOR APPLICATION NUMBER: 60/088025
56	PRIOR FILING DATE: 1998-06-04
57	PRIOR APPLICATION NUMBER: 60/088028
58	PRIOR FILING DATE: 1998-06-04
59	PRIOR APPLICATION NUMBER: 60/088029
60	PRIOR FILING DATE: 1998-06-04
61	PRIOR APPLICATION NUMBER: 60/088033
62	PRIOR FILING DATE: 1998-06-04
63	PRIOR APPLICATION NUMBER: 60/088167
64	PRIOR FILING DATE: 1998-06-05
65	PRIOR APPLICATION NUMBER: 60/088202
66	PRIOR FILING DATE: 1998-06-05
67	PRIOR APPLICATION NUMBER: 60/088212
68	PRIOR FILING DATE: 1998-06-05
69	PRIOR APPLICATION NUMBER: 60/088217
70	PRIOR FILING DATE: 1998-06-05
71	PRIOR APPLICATION NUMBER: 60/088326
72	PRIOR FILING DATE: 1998-06-04
73	PRIOR APPLICATION NUMBER: 60/088655

1	PRIOR FILING DATE: 1996-06-09
2	PRIOR APPLICATION NUMBER: 60/0086722
3	PRIOR FILING DATE: 1999-06-10
4	PRIOR APPLICATION NUMBER: 60/086733
5	PRIOR FILING DATE: 1996-06-10
6	PRIOR APPLICATION NUMBER: 60/086744
7	PRIOR FILING DATE: 1999-06-10
8	PRIOR APPLICATION NUMBER: 60/008611
9	PRIOR FILING DATE: 1999-06-10
10	PRIOR APPLICATION NUMBER: 60/008622
11	PRIOR FILING DATE: 1999-06-10
12	PRIOR APPLICATION NUMBER: 60/008622
13	PRIOR FILING DATE: 1999-06-10
14	PRIOR APPLICATION NUMBER: 60/008622
15	PRIOR FILING DATE: 1999-06-10
16	PRIOR APPLICATION NUMBER: 60/008610
17	PRIOR FILING DATE: 1999-06-11
18	PRIOR APPLICATION NUMBER: 60/008661
19	PRIOR FILING DATE: 1999-06-11
20	PRIOR APPLICATION NUMBER: 60/008666
21	PRIOR FILING DATE: 1999-06-11
22	PRIOR APPLICATION NUMBER: 60/008676
23	PRIOR FILING DATE: 1998-06-11
24	PRIOR APPLICATION NUMBER: 60/008909
25	PRIOR FILING DATE: 1996-06-12
26	PRIOR APPLICATION NUMBER: 60/009105
27	PRIOR FILING DATE: 1998-06-12
28	PRIOR APPLICATION NUMBER: 60/009512
29	PRIOR FILING DATE: 1998-06-16
30	PRIOR APPLICATION NUMBER: 60/009514
31	PRIOR FILING DATE: 1998-06-16
32	PRIOR APPLICATION NUMBER: 60/009538
33	PRIOR FILING DATE: 1998-06-17
34	PRIOR APPLICATION NUMBER: 60/009599
35	PRIOR FILING DATE: 1998-06-17
36	PRIOR APPLICATION NUMBER: 60/009653

Query Match	100.0%;	Score 1257;	DB 14;	Length 1257;
Best Local Similarity	100.0%;	Pred. No. 3.4e-271;		
Matches 1257; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	GGAGAGGGGGCCCGGGTAAAGAGCCATTTATGACGCTCGGGGGGCTCGAGGCGCG	60
Db	1	GGAGAGGGGGCCCGGGTAAAGAGCCATTTATGAGCCTGGGGGGCTCGAGGCGCG	60
QY	61	CGAGCCAGACGCTGACCAAGTTCCTCTCTCGGTCTCCTCGACCTCAGCTCCGCGCTG	120
Db	61	CGAGCCAGACGCTGACCAAGTTCCTCTCTCGGTCTCCTCGACCTCAGCTCCGCGCTG	120
QY	121	CCGGCAGCCCGGAGGCCATGCGACCCCAAGGACCCCGCGCTCCCGCAGCGGCTCCGC	180
Db	121	CCGGCAGCCCGGAGGCCATGCGACCCCAAGGACCCCGCGCTCCCGCAGCGGCTCCGC	180
QY	181	GCCCTCCGCTGCTCTGCTGCTGCGACGCTCCCGCGCGCTCCAGAGGCTCTGAGATCCCA	240
Db	181	GCCCTCCGCTGCTCTGCTGCTGCGACGCTCCCGCGCGCTCCAGAGGCTCTGAGATCCCA	240
QY	241	AGGGAGAGCAAAAGGCGCAGCTCCGCGAGAGGAGGTGTGACCTGTATATGAAATG	300
Db	241	AGGGAGAGCAAAAGGCGCAGCTCCGCGAGAGGAGGTGTGACCTGTATATGAAATG	300
QY	301	GCTTACAAAGGCGACAGAGATGCTCGAGCGGAGACCTTGGGGCCAAATGTTATTC	360
Db	301	GCTTACAAAGGCGACAGAGATGCTCGAGCGGAGACCTTGGGGCCAAATGTTATTC	360
QY	361	CGGGTACACCTGGGATCCCAAGTCGGAGTTCGATTCAAAGAGAAAGGGGAAATGCTGA	420
Db	361	CGGGTACACCTGGGATCCCAAGTCGGAGTTCGATTCAAAGAGAAAGGGGAAATGCTGA	420
QY	421	GGGAAAGCTTTGAGAGTCTTGAGACCCAACTACAGACAGTGTTCATGAGTTCAATGA	480
Db	421	GGGAAAGCTTTGAGAGTCTTGAGACCCAACTACAGACAGTGTTCATGAGTTCAATGA	480
QY	481	ATTATGGCATAGTCTTGGGAAATTCGCGAGTGTACATTTACAAAGATCGTTCAATA	540
Db	481	ATTATGGCATAGTCTTGGGAAATTCGCGAGTGTACATTTACAAAGATCGTTCAATA	540

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Db      481 ATTATGCAATAGATCTTGGGAAATTCGGAGTGTACATTTACAAAGATCGTTCAAA 540
Qy      541 GTCCTTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCAAAATGCAATGCTGTC 600
Db      541 GTGCTCAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCAAAATGCAATGCTGTC 600
Qy      601 AGCGTGTATTTACATTCATGAGAGCTGATGTTGAGAGCTCTTCCCATGGAAGCTA 660
Db      601 AGCGTGTATTTACATTCATGAGAGCTGATGTTGAGAGCTCTTCCCATGGAAGCTA 660
Qy      661 TAAATTAATTTGACCAAGAAAGCCCTGAAATGAATTCACATTAATTAATTCATGCACTT 720
Db      661 TAAATTAATTTGACCAAGAAAGCCCTGAAATGAATTCACATTAATTAATTCATGCACTT 720
Qy      721 CTTCCTGGAAGAGCTTTGTGAAGAAATGCTGCTGATTAAGTATGTTGCTATCTGGG 780
Db      721 CTTCCTGGAAGAGCTTTGTGAAGAAATGCTGCTGATTAAGTATGTTGCTATCTGGG 780
Qy      781 TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840
Db      781 TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840
Qy      841 GCATCATTAATTAAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900
Db      841 GCATCATTAATTAAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900
Qy      901 TTATTAATGCTTGAATGCTTCACTTAATGACATTTTAATTAAGTTATGATATCATCT 960
Db      901 TTATTAATGCTTGAATGCTTCACTTAATGACATTTTAATTAAGTTATGATATCATCT 960
Qy      961 GAATGAAAAGCAAGCTAATTAATGTTTACAGACCAAGGTGATTCACACTGTTTTTA 1020
Db      961 GAATGAAAAGCAAGCTAATTAATGTTTACAGACCAAGGTGATTCACACTGTTTTTA 1020
Qy      1021 ATCTAGCATTAATTCATTTTGTCTTCAATCAAAAGGTGTTCAATTAATTTTATGTTGTT 1080
Db      1021 ATCTAGCATTAATTCATTTTGTCTTCAATCAAAAGGTGTTCAATTAATTTTATGTTGTT 1080
Qy      1081 AGAATCTTCTTCATGATGACATTCCTCAACCTAATTAATTTGGAATATGTTGCTCT 1140
Db      1081 AGAATCTTCTTCATGATGACATTCCTCAACCTAATTAATTTGGAATATGTTGCTCT 1140
Qy      1141 TTGTTTCTCTCTAGTATGACATTTTAAATAAATTAAGCTCAATCTTTGTAC 1200
Db      1141 TTGTTTCTCTCTAGTATGACATTTTAAATAAATTAAGCTCAATCTTTGTAC 1200
Qy      1201 AATTGTAAATGTTAAGAAATTTTATATCTGTTAATTAATTAATTAATTTTCCAACTA 1257
Db      1201 AATTGTAAATGTTAAGAAATTTTATATCTGTTAATTAATTAATTAATTTTCCAACTA 1257

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RESULT 37
US-10-176-488-365
; Sequence 365, Application US/10176488
; Publication No. US20030027271A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C119
; CURRENT APPLICATION NUMBER: US/10/176,488
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm

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; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-488-365

Query Match      100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGAGAGAGCGCGCGGGTGAAGCGCATTTGATGCAAGCTGCGCGGCTCGAGCGCG 60
Db      1  GGAGAGAGCGCGCGGGTGAAGCGCATTTGATGCAAGCTGCGCGGCTCGAGCGCG 60
Qy      61  CGAGGCCAAGCGCTGACACAGCTTCTCTCTGCTCTCTCTGCTCTCTGCTCTCTGCT 120
Db      61  CGAGGCCAAGCGCTGACACAGCTTCTCTCTGCTCTCTCTGCTCTCTGCTCTCTGCT 120
Qy      121  CCGGCAAGCGGGAGCATGCAAGCCCAAGGAGCGCGCTCCCGGAGCGGCTCGG 180
Db      121  CCGGCAAGCGGGAGCATGCAAGCCCAAGGAGCGCGCTCCCGGAGCGGCTCGG 180
Qy      181  GCCTCCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db      181  GCCTCCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy      241  AGGGGAAGCAAAAGCGCGAGCTCCGGCAGAGGAGGTGCTGACCTGTATTAATGCAATGT 300
Db      241  AGGGGAAGCAAAAGCGCGAGCTCCGGCAGAGGAGGTGCTGACCTGTATTAATGCAATGT 300
Qy      301  GCTTAAAGGCGCAGAGAGAGTGCCTGTCGAGAGCGGAGCCCTGGGCGCAATGTTATTC 360
Db      301  GCTTAAAGGCGCAGAGAGAGTGCCTGTCGAGAGCGGAGCCCTGGGCGCAATGTTATTC 360
Qy      361  CGGGTACACCTGAGATCCCAAGGTGCGGATGATTCACAAAGAGAAAGGGGGAATGCTGA 420
Db      361  CGGGTACACCTGAGATCCCAAGGTGCGGATGATTCACAAAGAGAAAGGGGGAATGCTGA 420
Qy      421  GGGAAAGCTTTGAGAGAGTCTTGACACCCCACTACAGAGTGTTCATGAGTTCAATGA 480
Db      421  GGGAAAGCTTTGAGAGAGTCTTGACACCCCACTACAGAGTGTTCATGAGTTCAATGA 480
Qy      481  ATTATGCAATAGATCTTGGGAAATTTGGGAGGTGATCATTTTCAAAAGATGCGTTCAATA 540
Db      481  ATTATGCAATAGATCTTGGGAAATTTGGGAGGTGATCATTTTCAAAAGATGCGTTCAATA 540
Qy      541  GTGCTTAAGAGTTTGTTCAGTGGCTCACTTCGGCTAATTAATGCAAGAAATGATGCTGTC 600
Db      541  GTGCTTAAGAGTTTGTTCAGTGGCTCACTTCGGCTAATTAATGCAAGAAATGATGCTGTC 600
Qy      601  AGCGTGTATTTACATTCATGAGAGCTGATGTTGAGAGCTCTTCCCATGGAAGCTA 660
Db      601  AGCGTGTATTTACATTCATGAGAGCTGATGTTGAGAGCTCTTCCCATGGAAGCTA 660
Qy      661  TAAATTAATTTGACCAAGAAAGCCCTGAAATGAATTCACATTAATTAATTCATGCACTT 720
Db      661  TAAATTAATTTGACCAAGAAAGCCCTGAAATGAATTCACATTAATTAATTCATGCACTT 720
Qy      721  CTTCCTGGAAGAGCTTTGTGAAGAAATGCTGCTGATTAAGTATGTTGCTATCTGGG 780
Db      721  CTTCCTGGAAGAGCTTTGTGAAGAAATGCTGCTGATTAAGTATGTTGCTATCTGGG 780
Qy      781  TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840
Db      781  TTGGCACTTGTTCAGATTAACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840
Qy      841  GCATCATTAATTAAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900
Db      841  GCATCATTAATTAAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900
Qy      901  TTATTAATGCTTGAATGCTTCACTTAATGACATTTTAATTAAGTTATGATATCATCT 960

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Db 901 TTATTATGCTTGGATGGTTCATTAAATGACATTTTAAATAGTTATGTATACATCT 960  
Qy 961 GAATGAAAGCAAGCTAAATNGTTTACAGACCAAGTGTATTTTCACTGTCTTTTAA 1020  
Db 961 GAATGAAAGCAAGCTAAATNGTTTACAGACCAAGTGTATTTTCACTGTCTTTTAA 1020  
Qy 1021 ATCTAGCATTAATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTGTAGTGT 1080  
Db 1021 ATCTAGCATTAATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTGTAGTGT 1080  
Qy 1081 AGAATACCTTCTTCAATGTCACATTTCTTCAACCTTAAATTTGGAAATTTGTGTCT 1140  
Db 1081 AGAATACCTTCTTCAATGTCACATTTCTTCAACCTTAAATTTGGAAATTTGTGTCT 1140  
Qy 1141 TTTGTTTTTCTTCTAGTATGATTTTAAATTAATTAAGTACCAATCTTTGTAC 1200  
Db 1141 TTTGTTTTTCTTCTAGTATGATTTTAAATTAATTAAGTACCAATCTTTGTAC 1200  
Qy 1201 AATTTGTAATGTAAAGATTTTAAATATCTGTTAAATTAATTTTCCACA 1257  
Db 1201 AATTTGTAATGTAAAGATTTTAAATATCTGTTAAATTAATTTTCCACA 1257

RESULT 38  
US-10-176-492-365  
; Sequence 365, Application US/10176492  
; Publication No. US20030027272A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C107  
; CURRENT APPLICATION NUMBER: US/10/176,492  
; PRIORITY FILING DATE: 2002-06-21  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 365  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-176-492-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAGAGCGCGCGGTGAAGAGCGCATTTGAGAGCTGCGCGCGCTCGAGAGCGCG 60  
Db 1 GGAAGAGAGCGCGCGGTGAAGAGCGCATTTGAGAGCTGCGCGCGCTCGAGAGCGCG 60  
Qy 61 CGAGAGCGAGCGGTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Db 61 CGAGAGCGAGCGGTGACCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
Qy 121 CCCGAGCGCGGAGCGCATGAGACCCGAGGCGCGCGCTCTCTCTCTCTCTCTCTCTCT 180  
Db 121 CCCGAGCGCGGAGCGCATGAGACCCGAGGCGCGCGCTCTCTCTCTCTCTCTCTCTCT 180  
Qy 181 GCT 240  
Db 181 GCT 240  
Qy 241 AGGGAAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGAGCTGTATATGGAATGT 300

Db 241 AGGGAAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGAGCTGTATATGGAATGT 300  
Qy 301 GCTTACAAAGGCGAGAGAGTGTCTGTGAGAGCGAGCGCTTGAATTC 360  
Db 301 GCTTACAAAGGCGAGAGAGTGTCTGTGAGAGCGAGCGCTTGAATTC 360  
Qy 361 CGGTAACCTTGGATGCCAGTGGATGATTCAAAGAGAAAGGGGAATGTCTGA 420  
Db 361 CGGTAACCTTGGATGCCAGTGGATGATTCAAAGAGAAAGGGGAATGTCTGA 420  
Qy 421 GGAAGAGCTTTGAGAGTCTGACACCACTACAGAGTGTTCATGAGTTCATGA 480  
Db 421 GGAAGAGCTTTGAGAGTCTGACACCACTACAGAGTGTTCATGAGTTCATGA 480  
Qy 481 ATTATGCAATGATCTTGGGAAATTTGGAGTGTATCAATTAAGATCGTTCAATA 540  
Db 481 ATTATGCAATGATCTTGGGAAATTTGGAGTGTATCAATTAAGATCGTTCAATA 540  
Qy 541 GTGCTTAAGAGTGTGTGAGTGTCTGACCTTGGCTTAAATGCAAAATGCAATG 600  
Db 541 GTGCTTAAGAGTGTGTGAGTGTCTGACCTTGGCTTAAATGCAAAATGCAATG 600  
Qy 601 AGCGTTGATTTGACATTCATGAGCTGATGATTTGACAGACCTTCCCATGGAAGTA 660  
Db 601 AGCGTTGATTTGACATTCATGAGCTGATGATTTGACAGACCTTCCCATGGAAGTA 660  
Qy 661 TAATTTATTTGGACCAAGAAAGCCCTGAATGAATTCACAAATTAATTCATGCACTT 720  
Db 661 TAATTTATTTGGACCAAGAAAGCCCTGAATGAATTCACAAATTAATTCATGCACTT 720  
Qy 721 CTCTGTGGAAGAGCTTTGTAAGAAATTTGTGTGATTAAGTATGATGATGATGATG 780  
Db 721 CTCTGTGGAAGAGCTTTGTAAGAAATTTGTGTGATTAAGTATGATGATGATGATG 780  
Qy 781 TTGGCACTTGTGATTAATCCAAAGAGATGCTTCTACGTGATGATGATGATGATG 840  
Db 781 TTGGCACTTGTGATTAATCCAAAGAGATGCTTCTACGTGATGATGATGATGATG 840  
Qy 841 GCATCATTAATGAAACATCAAAATTAATGCTTAAATTTTCACTTCTCTCTCTCTCT 900  
Db 841 GCATCATTAATGAAACATCAAAATTAATGCTTAAATTTTCACTTCTCTCTCTCTCT 900  
Qy 901 TTATTATGCTTGAAGTGTCACTTAATGATGATTTAAATAGTTATGTATACATCT 960  
Db 901 TTATTATGCTTGAAGTGTCACTTAATGATGATTTAAATAGTTATGTATACATCT 960  
Qy 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACATGTTTTTAA 1020  
Db 961 GAATGAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTCACATGTTTTTAA 1020  
Qy 1021 ATCTAGCATTAATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTGTAGTGT 1080  
Db 1021 ATCTAGCATTAATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTGTAGTGT 1080  
Qy 1081 AGAATACCTTCTTCAATGTCACATTTCTTCAACCTTAAATTTGGAAATTTGTGTCT 1140  
Db 1081 AGAATACCTTCTTCAATGTCACATTTCTTCAACCTTAAATTTGGAAATTTGTGTCT 1140  
Qy 1141 TTTGTTTTTCTTCTAGTATGATTTTAAATTAATTAAGTACCAATCTTTGTAC 1200  
Db 1141 TTTGTTTTTCTTCTAGTATGATTTTAAATTAATTAAGTACCAATCTTTGTAC 1200  
Qy 1201 AATTTGTAATGTAAAGATTTTAAATATCTGTTAAATTAATTTTCCACA 1257  
Db 1201 AATTTGTAATGTAAAGATTTTAAATATCTGTTAAATTAATTTTCCACA 1257

RESULT 39  
US-10-176-747-365  
; Sequence 365, Application US/10176747  
; Publication No. US20030027273A1  
; GENERAL INFORMATION:



APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C92  
CURRENT FILING DATE: 2002-06-20  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 365  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-176-747-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGGCGCGGGGTGAAAGCGCATTTGATGACGCTCGCGCGGCTCGAGGCGCG 60  
DB 1 GGAGAGAGGCGCGGGGTGAAAGCGCATTTGATGACGCTCGCGCGGCTCGAGGCGCG 60

QY 61 CGAGAGCCAGACGCTGACACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
DB 61 CGAGAGCCAGACGCTGACACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120

QY 121 CCGGAGAGCGCGGGAGCGATGCGACCCGAGGCGCGCGCGCTCGCGAGCGGCTCGCGG 180  
DB 121 CCGGAGAGCGCGGGAGCGATGCGACCCGAGGCGCGCGCGCTCGCGAGCGGCTCGCGG 180

QY 181 GCCT 240  
DB 181 GCCT 240

QY 241 AGGGAGAGCAAGAGAGCGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
DB 241 AGGGAGAGCAAGAGAGCGGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

QY 301 GCTTACAGAGGCGAGAGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360  
DB 301 GCTTACAGAGGCGAGAGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360

QY 361 CGGGTACACCTGGGATCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
DB 361 CGGGTACACCTGGGATCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420

QY 421 GGGAGAGCTTTGAGAGTCT 480  
DB 421 GGGAGAGCTTTGAGAGTCT 480

QY 481 ATTATGAGCATAGATCTTTGGAGAAATGCGAGATGATATTAAGAGATCGTTCAATA 540  
DB 481 ATTATGAGCATAGATCTTTGGAGAAATGCGAGATGATATTAAGAGATCGTTCAATA 540

QY 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGAGAAATGAGATGCTGTC 600  
DB 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGAGAAATGAGATGCTGTC 600

QY 601 AGCGTGTGATTTTTCACATTTGAAGAGCTGATGTTTGAAGAGCTCTCTCTCTCTCTCT 660  
DB 601 AGCGTGTGATTTTTCACATTTGAAGAGCTGATGTTTGAAGAGCTCTCTCTCTCTCTCT 660

QY 661 TAATTATTTTGAACCAAGAGAGCGCTGAATGAATTAACAATTAATATTCATGCACTT 720

DB 661 TAATTATTTTGAACCAAGAGAGCGCTGAATGAATTAACAATTAATATTCATGCACTT 720

QY 721 CTTCTGTGAGAGACTTTGTGAGAGATTTGGTGTGATTTGATGATGTTGATCTGGG 780  
DB 721 CTTCTGTGAGAGACTTTGTGAGAGATTTGGTGTGATTTGATGATGTTGATCTGGG 780

QY 781 TTGGCACTTTGACATTAACCAAGAGAGATCTTCTACTGATGATGATGATGATGATGAT 840  
DB 781 TTGGCACTTTGACATTAACCAAGAGAGATCTTCTACTGATGATGATGATGATGATGAT 840

QY 841 GCATCATTTATTAAGAGACTACCAAAATTAATGCTTAATTTTCAATTTGCTACCTCTTTT 900  
DB 841 GCATCATTTATTAAGAGACTACCAAAATTAATGCTTAATTTTCAATTTGCTACCTCTTTT 900

QY 901 TTATTAATGCTTTGAGATGTTCACTTAATGACATTTTAAATGATTAATGATTAATCT 960  
DB 901 TTATTAATGCTTTGAGATGTTCACTTAATGACATTTTAAATGATTAATGATTAATCT 960

QY 961 GAATGAGAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTCACTGATTTTAA 1020  
DB 961 GAATGAGAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTCACTGATTTTAA 1020

QY 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATTTTATTTTATTTGTT 1080  
DB 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATTTTATTTTATTTGTT 1080

QY 1081 AGAATATCTTTCTTCAATGACATTTCTCTCAACCTTAATTTGGAATATGTTGTGCT 1140  
DB 1081 AGAATATCTTTCTTCAATGACATTTCTCTCAACCTTAATTTGGAATATGTTGTGCT 1140

QY 1141 TTTGTTTTTCTCTAGTATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 1200  
DB 1141 TTTGTTTTTCTCTAGTATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 1200

QY 1201 AATTTGTAATGTTAAAGATTTTAAATGATGTTAAATTAATTAATTAATTTTCAACA 1257  
DB 1201 AATTTGTAATGTTAAAGATTTTAAATGATGTTAAATTAATTAATTAATTTTCAACA 1257

RESULT 40  
US-10-176-750-365  
; Sequence 365, Application US/10176750  
; Publication No. US20030027274A1

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C103  
CURRENT FILING DATE: 2002-06-21  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 365  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-176-750-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGAAGAGGCGCGGGGTGAAAAGCGCATTTGATGACGCTCGCGCGGCGCTCGAGAGCGCG 60  
1 GGAAGAGGCGCGGGGTGAAAAGCGCATTTGATGACGCTCGCGCGGCGCTCGAGAGCGCG 60  
61 CGAGCGCAACGCTGACACAGTTCTCTCTCGGTCCTCTCGGCTTCAGCTCCGCGCTG 120  
61 CGAGCGCAACGCTGACACAGTTCTCTCTCGGTCCTCTCGGCTTCAGCTCCGCGCTG 120  
121 CCCGCGAGCGGGAGCGATGCGACCCCGAGGGGCCCGCGCTCCCGCGAGCGGCTCGCG 180  
121 CCCGCGAGCGGGAGCGATGCGACCCCGAGGGGCCCGCGCTCCCGCGAGCGGCTCGCG 180  
181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
241 AGGGGAGGAAAAGGCGGAGCTTCGCGCAAGGAGAGGTGGTGAACCTGTATATGAAATG 300  
241 AGGGGAGGAAAAGGCGGAGCTTCGCGCAAGGAGAGGTGGTGAACCTGTATATGAAATG 300  
301 GCTTACAAAGGCGCAGAGAGTGCCTGCTGAGACGCGAGCCCTGGGCGCAATGTATTTC 360  
301 GCTTACAAAGGCGCAGAGAGTGCCTGCTGAGACGCGAGCCCTGGGCGCAATGTATTTC 360  
361 CGGGTACACCTTGGGATCCCAAGTCCGAGTGAATTCGAAAGAGAAAAGGGGGAATGTCTGA 420  
361 CGGGTACACCTTGGGATCCCAAGTCCGAGTGAATTCGAAAGAGAAAAGGGGGAATGTCTGA 420  
421 GGGAAAGCTTTGAGGAGCTCTGAGACCCGACATCAAGAGAGTTCATGAGATCTTTA 480  
421 GGGAAAGCTTTGAGGAGCTCTGAGACCCGACATCAAGAGAGTTCATGAGATCTTTA 480  
481 ATTATGCAATAGATCTTGGGAAAATTGCGAGTGTATCTTTA CAAAGATGCTTCAATA 540  
481 ATTATGCAATAGATCTTGGGAAAATTGCGAGTGTATCTTTA CAAAGATGCTTCAATA 540  
541 GTGCTCTAAGAGTTTGTTCAGTGGCTCCTTGGCTTAAATGCAAGAAATGCAATGCTGTC 600  
541 GTGCTCTAAGAGTTTGTTCAGTGGCTCCTTGGCTTAAATGCAAGAAATGCAATGCTGTC 600  
601 AGCGTGTGATTTTCAATTCATGAGAGTGAAGTTCAGAGCTCTGCTCCCATTTGAAGCTA 660  
601 AGCGTGTGATTTTCAATTCATGAGAGTGAAGTTCAGAGCTCTGCTCCCATTTGAAGCTA 660  
661 TAAATTTATTTGAGCAAGAGAGCCCTGAATGAATTCACATTAATATTCACACTT 720  
661 TAAATTTATTTGAGCAAGAGAGCCCTGAATGAATTCACATTAATATTCACACTT 720  
721 CTTCGTGAGAGGACTTTGTGAGAGAAATGCTGCTGATTTAGTGAATGCTTATCTGGG 780  
721 CTTCGTGAGAGGACTTTGTGAGAGAAATGCTGCTGATTTAGTGAATGCTTATCTGGG 780  
781 TTGGCACTTGTTCAGATTACCCAAAAGAGAGATGCTTCTACATGAGATTCAGTTTCTC 840  
781 TTGGCACTTGTTCAGATTACCCAAAAGAGAGATGCTTCTACATGAGATTCAGTTTCTC 840  
841 GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCATTGCTACCTCTTTT 900  
841 GCATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCATTGCTACCTCTTTT 900  
901 TTATTTATGCTTGGAAATGTTCACTTAATGCACTTTTAAATTAATTTATGATCACT 960  
901 TTATTTATGCTTGGAAATGTTCACTTAATGCACTTTTAAATTAATTTATGATCACT 960  
961 GAATGAAAAGCAAGCTAATATGTTTACAGCAAGAGTGTGATTTCACTGTTTTTAA 1020  
961 GAATGAAAAGCAAGCTAATATGTTTACAGCAAGAGTGTGATTTCACTGTTTTTAA 1020  
1021 ATCTAGCAATTTATCTTTGCTTCAATCAAAAGTGTTCATTAATTTTATGTTGTT 1080  
1021 ATCTAGCAATTTATCTTTGCTTCAATCAAAAGTGTTCATTAATTTTATGTTGTT 1080  
1081 AGAATACCTTTCTTATGTCACATTCCTCAACCTATTAATTTGGAATATGTGTGCT 1140

1081 AGAATACCTTTCTTATGTCACATTCCTCAACCTATTAATTTGGAATATGTGTGCT 1140  
1141 TTTGTTTTTCTTATGATAGCATTTTAAATTAATTAAGCTACCAATCTTTGTAC 1200  
1141 TTTGTTTTTCTTATGATAGCATTTTAAATTAATTAAGCTACCAATCTTTGTAC 1200  
1201 AATTTGTAATGCTTAAGAAATTTTATATCTGTTAAATTAATTTATTTCCACA 1257  
1201 AATTTGTAATGCTTAAGAAATTTTATATCTGTTAAATTAATTTATTTCCACA 1257

## RESULT 41

US-10-176-985-365  
Sequence 365, Application US/10176985  
Publication No. US2003002727A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C99  
CURRENT APPLICATION NUMBER: US/10/176,985  
CURRENT FILING DATE: 2002-06-21  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 365  
LENGTH: 1257  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-176-985-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3,4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 GGAAGAGGCGCGGGGTGAAAAGCGCATTTGATGACGCTCGCGCGGCGCTCGAGAGCGCG 60  
1 GGAAGAGGCGCGGGGTGAAAAGCGCATTTGATGACGCTCGCGCGGCGCTCGAGAGCGCG 60  
61 CGAGCGCAACGCTGACACAGTTCTCTCTCGGTCCTCTCGGCTTCAGCTCCGCGCTG 120  
61 CGAGCGCAACGCTGACACAGTTCTCTCTCGGTCCTCTCGGCTTCAGCTCCGCGCTG 120  
121 CCCGCGAGCGGGAGCGATGCGACCCCGAGGGGCCCGCGCTCCCGCGAGCGGCTCGCG 180  
121 CCCGCGAGCGGGAGCGATGCGACCCCGAGGGGCCCGCGCTCCCGCGAGCGGCTCGCG 180  
181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
181 GCTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
241 AGGGGAGGAAAAGGCGGAGCTTCGCGCAAGGAGAGGTGGTGAACCTGTATATGAAATG 300  
241 AGGGGAGGAAAAGGCGGAGCTTCGCGCAAGGAGAGGTGGTGAACCTGTATATGAAATG 300  
301 GCTTACAAAGGCGCAGAGAGTGCCTGCTGAGACGCGAGCCCTGGGCGCAATGTATTTC 360  
301 GCTTACAAAGGCGCAGAGAGTGCCTGCTGAGACGCGAGCCCTGGGCGCAATGTATTTC 360  
361 CGGGTACACCTTGGGATCCCAAGTCCGAGTGAATTCGAAAGAGAAAAGGGGGAATGTCTGA 420  
361 CGGGTACACCTTGGGATCCCAAGTCCGAGTGAATTCGAAAGAGAAAAGGGGGAATGTCTGA 420



QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACTCTTTT 900  
DB 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACTCTTTT 900  
QY 901 TTAATATGCTTGGATGGTTCCTTAATGACATTTTAAATAGTTTATGATATCATCT 960  
DB 901 TTAATATGCTTGGATGGTTCCTTAATGACATTTTAAATAGTTTATGATATCATCT 960  
QY 961 GAATGAAAAGCAAGCTAATATGTTTACAGACCAAGTGTATTCACAGCTTTTAA 1020  
DB 961 GAATGAAAAGCAAGCTAATATGTTTACAGACCAAGTGTATTCACAGCTTTTAA 1020  
QY 1021 ATCTAGCATTTATTCATTTGCTTCAATCAAAAGTGTTCATATTTTATTTAGTTGTT 1080  
DB 1021 ATCTAGCATTTATTCATTTGCTTCAATCAAAAGTGTTCATATTTTATTTAGTTGTT 1080  
QY 1081 AGAATACCTTTCTTCATAGTCACTTCCTCAACCTTAATTTGGAATATTTGTGTCT 1140  
DB 1081 AGAATACCTTTCTTCATAGTCACTTCCTCAACCTTAATTTGGAATATTTGTGTCT 1140  
QY 1141 TTTGTTTTTCTCTTAGTATAGCATTTTAAAAAATATATAAGTACCAATCTTTGATC 1200  
DB 1141 TTTGTTTTTCTCTTAGTATAGCATTTTAAAAAATATATAAGTACCAATCTTTGATC 1200  
QY 1201 AATTGTAAATGTTAAGAAATTTTATATCTGTTAAATTAATTTATTTTCAACA 1257  
DB 1201 AATTGTAAATGTTAAGAAATTTTATATCTGTTAAATTAATTTATTTTCAACA 1257

## RESULT 43

US-10-176-992-365

Sequence 365, Application US/10176992

Publication No. US20030027279A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Deanovs, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C100

CURRENT APPLICATION NUMBER: US/10/176,992

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 365

LENGTH: 1257

TYPE: DNA

ORGANISM: Homo Sapien

US-10-176-992-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3,4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGAGGCGCGCGGTGAAAGGCGATTTATGAGCTTGCGGCGCGCTCGAGAGCGG 60  
DB 1 GGAAGAGGCGCGCGGTGAAAGGCGATTTATGAGCTTGCGGCGCGCTCGAGAGCGG 60  
QY 61 CGAGAGCGAGCGCTGACCACTTCTCTCGGTCTCTCGGCTCTCGAGCTCGCGGCTG 120  
DB 61 CGAGAGCGAGCGCTGACCACTTCTCTCGGTCTCTCGGCTCTCGAGCTCGCGGCTG 120  
QY 121 CCGGCGAGCGGAGCGCATGCGACCCCGAGGCGCGCGCTCCCGAGCGGCTCGCGG 180  
DB 121 CCGGCGAGCGGAGCGCATGCGACCCCGAGGCGCGCGCTCCCGAGCGGCTCGCGG 180

QY 181 GCTCTCTGCTGCTCTGCTGCTGCACTGCCCCCGCGCTGAGCGCTTGAAGTCCCA 240  
DB 181 GCTCTCTGCTGCTCTGCTGCTGCACTGCCCCCGCGCTGAGCGCTTGAAGTCCCA 240  
QY 241 AGGGAAGCAAAAGCGAGCTCGCGAGAGGAGGTGTGTGACCTGTATTAATGGAATGT 300  
DB 241 AGGGAAGCAAAAGCGAGCTCGCGAGAGGAGGTGTGTGACCTGTATTAATGGAATGT 300  
QY 301 GCTTCAAGGGCCAGACGAGTGCCTGTGAGACGAGAGCGCTCGGCGCAATGTTATTC 360  
DB 301 GCTTCAAGGGCCAGACGAGTGCCTGTGAGACGAGAGCGCTCGGCGCAATGTTATTC 360  
QY 361 CGGATACCTGGGATCCAGGTGGGATGATTCAAAGAGAAAGGGGGAATGTCTGA 420  
DB 361 CGGATACCTGGGATCCAGGTGGGATGATTCAAAGAGAAAGGGGGAATGTCTGA 420  
QY 421 GGGAAAGCTTTGAGGAGTCTGAGACCCCACTCAAGACAGTGTTCATGAGTTCAATGA 480  
DB 421 GGGAAAGCTTTGAGGAGTCTGAGACCCCACTCAAGACAGTGTTCATGAGTTCAATGA 480  
QY 481 ATTATGCGATGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATCGTTCAATA 540  
DB 481 ATTATGCGATGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATCGTTCAATA 540  
QY 541 GTGCTTAAAGATTTGTTGAGTGTGCTCACTTGGGCTTAAATGCAAAATGCAATGCTGTC 600  
DB 541 GTGCTTAAAGATTTGTTGAGTGTGCTCACTTGGGCTTAAATGCAAAATGCAATGCTGTC 600  
QY 601 AGCGTGTATTTACATTCATGAGCTGAAATGTTTCAAGACCTCTTCCCATTTAGAGCTA 660  
DB 601 AGCGTGTATTTACATTCATGAGCTGAAATGTTTCAAGACCTCTTCCCATTTAGAGCTA 660  
QY 661 TAAATTAATTTGAGCAAGAAAGCCCTGAATGAAATTCAAATTAATTTATTCAGCACTT 720  
DB 661 TAAATTAATTTGAGCAAGAAAGCCCTGAATGAAATTCAAATTAATTTATTCAGCACTT 720  
QY 721 CTTCTGTGGAAGGACTTTGTAAGAAATTTGCTGTGATAGTGAATGTTGCTATCTGAG 780  
DB 721 CTTCTGTGGAAGGACTTTGTAAGAAATTTGCTGTGATAGTGAATGTTGCTATCTGAG 780  
QY 781 TTGGCACTTTGTCAGATTTACCCAAAGAGATGCTTCTACTGAGTGAATTCAGTTCTC 840  
DB 781 TTGGCACTTTGTCAGATTTACCCAAAGAGATGCTTCTACTGAGTGAATTCAGTTCTC 840  
QY 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTT 900  
DB 841 GCATCATTTATGAGAACTACCAAAATTAATGCTTTAATTTTCAATTTGCTACTCTTTT 900  
QY 901 TTAATATGCTTGGATGGTTCCTTAATGACATTTTAAATAGTTTATGATATCATCT 960  
DB 901 TTAATATGCTTGGATGGTTCCTTAATGACATTTTAAATAGTTTATGATATCATCT 960  
QY 961 GAATGAAAAGCAAGCTAATATGTTTACAGACCAAGTGTATTCACAGCTTTTAA 1020  
DB 961 GAATGAAAAGCAAGCTAATATGTTTACAGACCAAGTGTATTCACAGCTTTTAA 1020  
QY 1021 ATCTAGCATTTATTCATTTGCTTCAATCAAAAGTGTTCATATTTTATTTAGTTGTT 1080  
DB 1021 ATCTAGCATTTATTCATTTGCTTCAATCAAAAGTGTTCATATTTTATTTAGTTGTT 1080  
QY 1081 AGAATACCTTTCTTCATAGTCACTTCCTCAACCTTAATTTGGAATATTTGTGTCT 1140  
DB 1081 AGAATACCTTTCTTCATAGTCACTTCCTCAACCTTAATTTGGAATATTTGTGTCT 1140  
QY 1141 TTTGTTTTTCTCTTAGTATAGCATTTTAAAAAATATATAAGTACCAATCTTTGATC 1200  
DB 1141 TTTGTTTTTCTCTTAGTATAGCATTTTAAAAAATATATAAGTACCAATCTTTGATC 1200  
QY 1201 AATTGTAAATGTTAAGAAATTTTATATCTGTTAAATTAATTTATTTTCAACA 1257  
DB 1201 AATTGTAAATGTTAAGAAATTTTATATCTGTTAAATTAATTTATTTTCAACA 1257

```
RESULT 44
US-10-176-993-365
; Sequence 365, Application US/10176993
; Publication No. US20030027280A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C89
; CURRENT APPLICATION NUMBER: US/10/176,993
; PRIOR FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-993-365

Query Match      100.0%; Score 1257; DB 14; Length 1257;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAGAGCGCGCGGTGAAGCGCATTTGATGACGCTCGGCGCGCTCGGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGTGAAGCGCATTTGATGACGCTCGGCGCGCTCGGAGCGCG 60
QY 61 CGGAGCGCAAGCGCTGACGACGCTTCTCTCGGCTCTCTCGGCTCTCGGCTCTCGGCTCT 120
DB 61 CGGAGCGCAAGCGCTGACGACGCTTCTCTCGGCTCTCTCGGCTCTCTCGGCTCTCGGCTCT 120
QY 121 CCGGAGCGCGGAGCGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CCGGAGCGCGGAGCGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 AGGAGGAGCAAAAGCGCGAGCTCCGCGAGAGGAGGTGTGACCTGTATATGAAATGT 300
DB 241 AGGAGGAGCAAAAGCGCGAGCTCCGCGAGAGGAGGTGTGACCTGTATATGAAATGT 300
QY 301 GCTTACAGGGGCGAGAGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GCTTACAGGGGCGAGAGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CGGAGTACCTGCGGATCCAGGCTCGGAGTGTGATTTCAAGAGGAAAGGGGGAATGTCTGA 420
DB 361 CGGAGTACCTGCGGATCCAGGCTCGGAGTGTGATTTCAAGAGGAAAGGGGGAATGTCTGA 420
QY 421 GGGAAAGCTTTGAGAGTCTCTGACACCCAACTACAGAGCTGTTCATGAGTTCAATGA 480
DB 421 GGGAAAGCTTTGAGAGTCTCTGACACCCAACTACAGAGCTGTTCATGAGTTCAATGA 480
QY 481 ATTATGAGCATATGCTTTGGGAAATGCGAGGTGATCATTTAAGAGATGCGTTCAAAAT 540
DB 481 ATTATGAGCATATGCTTTGGGAAATGCGAGGTGATCATTTAAGAGATGCGTTCAAAAT 540
QY 541 GTGCTCTAAGAGTTTGTTCAGTGTGCTCACTTCGCGCTAAATGACAGAAATGATGCTGTC 600
DB 541 GTGCTCTAAGAGTTTGTTCAGTGTGCTCACTTCGCGCTAAATGACAGAAATGATGCTGTC 600
```

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QY 601 AGCGTTGGATTTCACATTCATGAGCTGAATGTTTCAGAGACCTCTCCATTTGAAGCTA 660
DB 601 AGCGTTGGATTTCACATTCATGAGCTGAATGTTTCAGAGACCTCTCCATTTGAAGCTA 660
QY 661 TAAATTTATTTGAGCAAGAGAGCCCTGAATGATTCACATTAATATTCATTCGCACTT 720
DB 661 TAAATTTATTTGAGCAAGAGAGCCCTGAATGATTCACATTAATATTCATTCGCACTT 720
QY 721 CTTCGTGAGAGACCTTTGTGAGAGAAATTTGCTGAGATTAATGATGATGCTATCTGGG 780
DB 721 CTTCGTGAGAGACCTTTGTGAGAGAAATTTGCTGAGATTAATGATGATGCTATCTGGG 780
QY 781 TTGGGACCTTTGACATTAACCAAAAGAGAGCTTCACTGAGATGATTCAGTTCTTC 840
DB 781 TTGGGACCTTTGACATTAACCAAAAGAGAGCTTCACTGAGATGATTCAGTTCTTC 840
QY 841 GCATCATTTATGAGAGACCTCAAAATTAATGCTTAAATTTTCATTTGCTACCTCTTTT 900
DB 841 GCATCATTTATGAGAGACCTCAAAATTAATGCTTAAATTTTCATTTGCTACCTCTTTT 900
QY 901 TTATTAATGCTTGAATGCTTCACTTAATGACATTTTAATTAATGATTAATGATCATCT 960
DB 901 TTATTAATGCTTGAATGCTTCACTTAATGACATTTTAATTAATGATTAATGATCATCT 960
QY 961 GAATGAAAGCAAGCTAATATGTTTACAGACCAAGGATGATTCACAGCTTTTAA 1020
DB 961 GAATGAAAGCAAGCTAATATGTTTACAGACCAAGGATGATTCACAGCTTTTAA 1020
QY 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGGCTTCAATTTTATTTAGTTGCTT 1080
DB 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGGCTTCAATTTTATTTAGTTGCTT 1080
QY 1081 AGAATATCTTTCTTCAATGACATTTCTCAACCTTAATTTGGAATATGTTGTGCTCT 1140
DB 1081 AGAATATCTTTCTTCAATGACATTTCTCAACCTTAATTTGGAATATGTTGTGCTCT 1140
QY 1141 TTTGTTTTTCTCTAGTATACATTTTAAATAATTAAGTACCAATCTTTGTAC 1200
DB 1141 TTTGTTTTTCTCTAGTATACATTTTAAATAATTAAGTACCAATCTTTGTAC 1200
QY 1201 AATTTGTAATGTTAAGATTTTATTTATCTGTTAATTAATTAATTTATTTCCACA 1257
DB 1201 AATTTGTAATGTTAAGATTTTATTTATCTGTTAATTAATTAATTTATTTCCACA 1257

RESULT 45
US-10-184-658-365
; Sequence 365, Application US/10184658
; Publication No. US20030027281A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C228
; CURRENT APPLICATION NUMBER: US/10/184,658
; PRIOR FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
```

US-10-184-658-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGAGAGAGCGCGCGGTGAAAAGCGCATTGATGACGCTCGCGCGGCTCGAGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGTGAAAAGCGCATTGATGACGCTCGCGCGGCTCGAGAGCGCG 60
QY 61 CGGAGCGAGCGCTGACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGGAGCGAGCGCTGACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCGGCGAGCGCGGAGCGCATGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CCGGCGAGCGCGGAGCGCATGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGCGAGCGAAAGCGCGAGCTCCGCGAGAGGAGTGCTGAGACCTGTATTAATGAAAT 300
DB 241 AGGCGAGCGAAAGCGCGAGCTCCGCGAGAGGAGTGCTGAGACCTGTATTAATGAAAT 300
QY 301 GCTTACAAAGGCGCAGAGAGTGCTGTGAGACGCGAGCGCGCGCGCGCGCGCGCGCG 360
DB 301 GCTTACAAAGGCGCAGAGAGTGCTGTGAGACGCGAGCGCGCGCGCGCGCGCGCGCG 360
QY 361 CGGAGTACCTTGGATCCCAAGCTCGGAGTGAATTCAAAGAGAGAGAGAGAGAGAG 420
DB 361 CGGAGTACCTTGGATCCCAAGCTCGGAGTGAATTCAAAGAGAGAGAGAGAGAGAG 420
QY 421 GGGAAAGCTTTGAGAGAGTCTGAGACCGCACTAAGAGAGTGCTGAGAGAGAGAGAG 480
DB 421 GGGAAAGCTTTGAGAGAGTCTGAGACCGCACTAAGAGAGTGCTGAGAGAGAGAGAG 480
QY 481 ATTATGAGATGATCTTGGAGAAATTCGCGAGTGATCATTTTCAAGAGAGAGAGAG 540
DB 481 ATTATGAGATGATCTTGGAGAAATTCGCGAGTGATCATTTTCAAGAGAGAGAGAG 540
QY 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCGAGAGAGAGAGAG 600
DB 541 GTGCTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAATGCGAGAGAGAGAGAG 600
QY 601 AGCGTGTATTTTCACTTCAATGAGAGTGAATGTTCCAGAGAGAGAGAGAGAGAG 660
DB 601 AGCGTGTATTTTCACTTCAATGAGAGTGAATGTTCCAGAGAGAGAGAGAGAGAG 660
QY 661 TAAATTTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 TAAATTTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 CTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 CTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TTGGCACTTGTTCAGATTAACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TTGGCACTTGTTCAGATTAACCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 GCATCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GCATCATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 TTATTTAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 TTATTTAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
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QY 1021 ATCTAGCATTAATTCATTTTGGCTTCAATCAAAAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 ATCTAGCATTAATTCATTTTGGCTTCAATCAAAAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 AGAATACCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
DB 1081 AGAATACCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1141 TTTGTTTTTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 1141 TTTGTTTTTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 AATTTGAAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1257
DB 1201 AATTTGAAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1257
```

RESULT 46  
US-10-176-991-365

```
; Sequence 365, Application US/10176991
; Publication No. US20030027324A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C122
; CURRENT APPLICATION NUMBER: US/10/176, 991
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 365
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-991-365
```

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GGAGAGAGCGCGCGGTGAAAAGCGCATTGATGACGCTCGCGCGGCTCGAGAGCGCG 60
DB 1 GGAGAGAGCGCGCGGTGAAAAGCGCATTGATGACGCTCGCGCGGCTCGAGAGCGCG 60
QY 61 CGGAGCGAGCGCTGACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 61 CGGAGCGAGCGCTGACCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCGGCGAGCGCGGAGCGCATGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CCGGCGAGCGCGGAGCGCATGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGCGAGCGAAAGCGCGAGCTCCGCGAGAGGAGTGCTGAGACCTGTATTAATGAAAT 300
DB 241 AGGCGAGCGAAAGCGCGAGCTCCGCGAGAGGAGTGCTGAGACCTGTATTAATGAAAT 300
QY 301 GCTTACAAAGGCGCAGAGAGTGCTGTGAGACGCGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 GCTTACAAAGGCGCAGAGAGTGCTGTGAGACGCGAGAGAGAGAGAGAGAGAGAGAG 360
```

Db 301 GCTTACAGGCGCAGAGAGTGCCTGCTGAGACGAGCCCTGGGCGCAATGTTATTC 360  
Qy 361 CGGGTACACCTGGGATCCAGGTCGGGATGATTTCAAGAGAGAAAGGGGGAATGTCGA 420  
Db 361 CGGGTACACCTGGGATCCAGGTCGGGATGATTTCAAGAGAGAAAGGGGGAATGTCGA 420  
Qy 421 GGGAAAGCTTTGAGAGTCTTGACACCCCACTACAGCAGTGTTCAGAGTTCATTA 480  
Db 421 GGGAAAGCTTTGAGAGTCTTGACACCCCACTACAGCAGTGTTCAGAGTTCATTA 480  
Qy 481 ATTATGCGATAGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCGTTCAATA 540  
Db 481 ATTATGCGATAGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCGTTCAATA 540  
Qy 541 GTGCTTAAAGATTTTGTTCAGAGTGTCTCTGCTTAAATGCAAAATGATGCTGTTC 600  
Db 541 GTGCTTAAAGATTTTGTTCAGAGTGTCTCTGCTTAAATGCAAAATGATGCTGTTC 600  
Qy 601 AGCGTGTATTTTCAATTCATGAGTGAATGTTCAAGACCTCTTCCATTTGAAGTGA 660  
Db 601 AGCGTGTATTTTCAATTCATGAGTGAATGTTCAAGACCTCTTCCATTTGAAGTGA 660  
Qy 661 TAAATTTATTTGACCAAGAGAGCCCTGAAATGAAATTCACATTAATTCATGCACTT 720  
Db 661 TAAATTTATTTGACCAAGAGAGCCCTGAAATGAAATTCACATTAATTCATGCACTT 720  
Qy 721 CTTCCTGGAAGAGCTTTGTGAAGAAATGCTGTGATTAAGTGAATGTTGCTATCTGG 780  
Db 721 CTTCCTGGAAGAGCTTTGTGAAGAAATGCTGTGATTAAGTGAATGTTGCTATCTGG 780  
Qy 781 TTGGCACTTGTTCAGATTTACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840  
Db 781 TTGGCACTTGTTCAGATTTACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTC 840  
Qy 841 GCATCATTTATTTGAAGAACTACCAAAATGAAATGCTTTAATTTTCAATTTGCTTCTT 900  
Db 841 GCATCATTTATTTGAAGAACTACCAAAATGAAATGCTTTAATTTTCAATTTGCTTCTT 900  
Qy 901 TTTATTTGCTTGGAAATGTTCTTCAATTAATGACATTTTAAATGATTAATGATTAATCT 960  
Db 901 TTTATTTGCTTGGAAATGTTCTTCAATTAATGACATTTTAAATGATTAATGATTAATCT 960  
Qy 961 GAATGAAAGCAAGCAATTAATGTTTACAGACCAAGTGTGATTTTCACTGTTTAA 1020  
Db 961 GAATGAAAGCAAGCAATTAATGTTTACAGACCAAGTGTGATTTTCACTGTTTAA 1020  
Qy 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATTAATTTTAAATGTTG 1080  
Db 1021 ATCTAGCATTTATTCATTTTGTCTTCAATCAAAAGTGTTCATTAATTTTAAATGTTG 1080  
Qy 1081 AGAATACCTTCTTCATGATGACATTTCTCAACCTTAATTTGGAATATTTGTTGCTCT 1140  
Db 1081 AGAATACCTTCTTCATGATGACATTTCTCAACCTTAATTTGGAATATTTGTTGCTCT 1140  
Qy 1141 TTTGTTTTTCTCTGATGATGACATTTTAAATAATTAATTAAGCTACCAATCTTTGATC 1200  
Db 1141 TTTGTTTTTCTCTGATGATGACATTTTAAATAATTAATTAAGCTACCAATCTTTGATC 1200  
Qy 1201 AATTTGTAATGTTAAGAAATTTTAAATGTTTAAATTAATTAATTTTCAACA 1257  
Db 1201 AATTTGTAATGTTAAGAAATTTTAAATGTTTAAATTAATTAATTTTCAACA 1257

RESULT 47

US-10-063-549-121  
; Sequence 121, Application US/10063549  
; Publication No. US20030027986A1

; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Geritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,549  
; PRIORITY FILING DATE: 2002-05-02  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 121  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-063-549-121

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAAGAGGCGCGCGGCTGAAGGCGCATTTGATGACGCTGGGCGGCGCTCGAGGCGGG 60  
Db 1 GGAAGAGGCGCGCGGCTGAAGGCGCATTTGATGACGCTGGGCGGCGCTCGAGGCGGG 60  
Qy 61 CGAGGCAAGCGCTGACACGTTCTCTGCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTG 120  
Db 61 CGAGGCAAGCGCTGACACGTTCTCTGCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTG 120  
Qy 121 CCCGGAGCGCGGAGCGATCGACCCAGAGGCGCGCGCTCTCCGCGAGCGGCTCTCGG 180  
Db 121 CCCGGAGCGCGGAGCGATCGACCCAGAGGCGCGCGCTCTCCGCGAGCGGCTCTCGG 180  
Qy 181 GCTCTCTGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 240  
Db 181 GCTCTCTGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 240  
Qy 241 AGGGAAGCAAAAGGCGAGCTCCGCGAGAGGAGTGTGAGACCTGTAAATGAAATGT 300  
Db 241 AGGGAAGCAAAAGGCGAGCTCCGCGAGAGGAGTGTGAGACCTGTAAATGAAATGT 300  
Qy 301 GCTTACAGGCGCAGAGAGTGTCTGTGAGACGAGAGCCCTGGGCGCAATGTTATTC 360  
Db 301 GCTTACAGGCGCAGAGAGTGTCTGTGAGACGAGAGCCCTGGGCGCAATGTTATTC 360  
Qy 361 CGGGTACACCTGGGATCCAGGTCGGGATGATTTCAAGAGAGAAAGGGGGAATGTCGA 420  
Db 361 CGGGTACACCTGGGATCCAGGTCGGGATGATTTCAAGAGAGAAAGGGGGAATGTCGA 420  
Qy 421 GGGAAAGCTTTGAGAGTCTTGACACCCCACTACAGCAGTGTTCAGAGTTCATTA 480  
Db 421 GGGAAAGCTTTGAGAGTCTTGACACCCCACTACAGCAGTGTTCAGAGTTCATTA 480  
Qy 481 ATTATGCGATAGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCGTTCAATA 540  
Db 481 ATTATGCGATAGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCGTTCAATA 540  
Qy 541 GTGCTTAAAGATTTTGTTCAGAGTGTCTCTGCTTAAATGCAAAATGATGCTGTTC 600  
Db 541 GTGCTTAAAGATTTTGTTCAGAGTGTCTCTGCTTAAATGCAAAATGATGCTGTTC 600  
Qy 601 AGCGTGTATTTTCAATTCATGAGTGAATGTTCAAGACCTCTTCCATTTGAAGTGA 660  
Db 601 AGCGTGTATTTTCAATTCATGAGTGAATGTTCAAGACCTCTTCCATTTGAAGTGA 660  
Qy 661 TAAATTTATTTGACCAAGAGAGCCCTGAAATGAAATTCACATTAATTCATGCACTT 720  
Db 661 TAAATTTATTTGACCAAGAGAGCCCTGAAATGAAATTCACATTAATTCATGCACTT 720  
Qy 721 CTTCCTGGAAGAGCTTTGTGAAGAAATGCTGTGATTAAGTGAATGTTGCTATCTGG 780  
Db 721 CTTCCTGGAAGAGCTTTGTGAAGAAATGCTGTGATTAAGTGAATGTTGCTATCTGG 780



QY 781 TTGGCACTTGTTCAGATTACCCAAAAGAGATGCTTCACTGATGGAATTGAGTTCTC 840  
DB 781 TTGGCACTTGTTCAGATTACCCAAAAGAGATGCTTCTACTGATGGAATTGAGTTCTC 840  
QY 841 GCATCATTTATTTGAAGAACTACCAAAATATATGCTTTAATTTTCATTGCTACTCTTTT 900  
DB 841 GCATCATTTATTTGAAGAACTACCAAAATATATGCTTTAATTTTCATTGCTACTCTTTT 900  
QY 901 TTATTAATGCTTTGAGATGCTTCACTTAATATGACATTTTAATATGATTAATGATCATCT 960  
DB 901 TTATTAATGCTTTGAGATGCTTCACTTAATATGACATTTTAATATGATTAATGATCATCT 960  
QY 961 GAATGAAAAGCAAAAGCTTAATATGTTTACAGACCAAGTGATTTACACTGTTTTTA 1020  
DB 961 GAATGAAAAGCAAAAGCTTAATATGTTTACAGACCAAGTGATTTACACTGTTTTTA 1020  
QY 1021 ATCTAGCATTTATTCATTTTCTTCAATCAAAAGTGTTCATTTTATTTTATTTTATTTT 1080  
DB 1021 ATCTAGCATTTATTCATTTTCTTCAATCAAAAGTGTTCATTTTATTTTATTTTATTTT 1080  
QY 1081 AGAATACTTCTTCTTCACTGATCTCTCAACCTTAATTTGAAATATTTGATGCTCT 1140  
DB 1081 AGAATACTTCTTCTTCACTGATCTCTCAACCTTAATTTGAAATATTTGATGCTCT 1140  
QY 1141 TTGTTTTTCTCTTATGATGATTTTAAATATTAATTAATTAATTTTATTTTATTTT 1200  
DB 1141 TTGTTTTTCTCTTATGATGATTTTAAATATTAATTAATTTTATTTTATTTTATTTT 1200  
QY 1201 AATTGTAATGTTAAGATTTTATTTATCTGTTAAATTAATTTATTTTATTTTATTTT 1257  
DB 1201 AATTGTAATGTTAAGATTTTATTTATCTGTTAAATTAATTTATTTTATTTTATTTT 1257

## RESULT 48

US-10-173-695-365  
; Sequence 365, Application US/10173695  
; Publication No. US20030032101A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C3  
; CURRENT FILING DATE: 2002-06-17  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 365  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-173-695-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGAGGCGCGCGGTGAAGGCGCATGTATGAGCTTGCGGCGCTCGAGAGCGG 60  
DB 1 GGAAGAGGCGCGCGGTGAAGGCGCATGTATGAGCTTGCGGCGCTCGAGAGCGG 60  
QY 61 CGAGAGCAGAGCGCTGACCAAGTTCTCTCGGCTCGCTCGGCTCGAGAGCGGCTG 120  
DB 61 CGAGAGCAGAGCGCTGACCAAGTTCTCTCGGCTCGCTCGGCTCGAGAGCGGCTG 120

QY 121 CCCGAGCCGAGAGCCATGCGACCCAGGGCCCCGCGCTCCCGCAGCGGCTCCGCG 180  
DB 121 CCCGAGCCGAGAGCCATGCGACCCAGGGCCCCGCGCTCCCGCAGCGGCTCCGCG 180  
QY 181 GCTCTCTGCTCTGCTGCTGAGCTGCCCGCGCGGTGAGGCTCTGAGATCCCA 240  
DB 181 GCTCTCTGCTCTGCTGCTGAGCTGCCCGCGCGGTGAGGCTCTGAGATCCCA 240  
QY 241 AGGGAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGAGACTGATTAATGGAATGT 300  
DB 241 AGGGAGCAAAAGCGAGCTCCGCGAGAGGAGGTGTGAGACTGATTAATGGAATGT 300  
QY 301 GCTTCAAGGGCCAGAGAGTGCCTGCTCGAGAGCGGAGCCCTGGGGCCAAATTTATTC 360  
DB 301 GCTTCAAGGGCCAGAGAGTGCCTGCTCGAGAGCGGAGCCCTGGGGCCAAATTTATTC 360  
QY 361 CGGTTACACTGGGATCCCAAGTGGATGATTCAAAGGAGAAAGGGGGAATGTCTGA 420  
DB 361 CGGTTACACTGGGATCCCAAGTGGATGATTCAAAGGAGAAAGGGGGAATGTCTGA 420  
QY 421 GGGAAAGCTTTGAGGAGCTGAGACCCCACTACCAAGCATGTTCAATGAGTTTATTA 480  
DB 421 GGGAAAGCTTTGAGGAGCTGAGACCCCACTACCAAGCATGTTCAATGAGTTTATTA 480  
QY 481 ATTATGCGATGATCTTGGGAAAATTTGGGAGTGTATCTTACAAAGATGCTTCAATA 540  
DB 481 ATTATGCGATGATCTTGGGAAAATTTGGGAGTGTATCTTACAAAGATGCTTCAATA 540  
QY 541 GTGCTCTAAGATTTTGTTCAGTGTCTCACTTGGGCTTAAATGCAAAATGCAATGCTGTC 600  
DB 541 GTGCTCTAAGATTTTGTTCAGTGTCTCACTTGGGCTTAAATGCAAAATGCAATGCTGTC 600  
QY 601 AGCGTTGATTTTCAATCAATGAGAGTGAATGTGAGAGCCCTCCCATGGAAGCTA 660  
DB 601 AGCGTTGATTTTCAATCAATGAGAGTGAATGTGAGAGCCCTCCCATGGAAGCTA 660  
QY 661 TAAATTTATTTGAGCAAGAGAGCCCTGAAATGCAATTAATTAATTTTATTTTATTTT 720  
DB 661 TAAATTTATTTGAGCAAGAGAGCCCTGAAATGCAATTAATTAATTTTATTTTATTTT 720  
QY 721 CTCTGTGGAAGACTTTGTGAAGAAATTTGTGTGATTAATGAGATTTGATCTGCTG 780  
DB 721 CTCTGTGGAAGACTTTGTGTGAAGAAATTTGTGTGATTAATGAGATTTGATCTGCTG 780  
QY 781 TTGGCACTTGTTCAGATTACCCAAAAGAGATGCTTCACTGATGGAATTGAGTTCTC 840  
DB 781 TTGGCACTTGTTCAGATTACCCAAAAGAGATGCTTCACTGATGGAATTGAGTTCTC 840  
QY 841 GCATCATTTATTTGAAGAACTACCAAAATATATGCTTTAATTTTATTTTATTTTATTTT 900  
DB 841 GCATCATTTATTTGAAGAACTACCAAAATATATGCTTTAATTTTATTTTATTTTATTTT 900  
QY 901 TTATTAATGCTTTGAGATGCTTCACTTAATATGACATTTTAATATGATTAATGATCATCT 960  
DB 901 TTATTAATGCTTTGAGATGCTTCACTTAATATGACATTTTAATATGATTAATGATCATCT 960  
QY 961 GAATGAAAAGCAAAAGCTTAATATGTTTACAGACCAAGTGATTTACACTGTTTTTA 1020  
DB 961 GAATGAAAAGCAAAAGCTTAATATGTTTACAGACCAAGTGATTTACACTGTTTTTA 1020  
QY 1021 ATCTAGCATTTATTCATTTTCTTCAATCAAAAGTGTTCATTTTATTTTATTTTATTTT 1080  
DB 1021 ATCTAGCATTTATTCATTTTCTTCAATCAAAAGTGTTCATTTTATTTTATTTTATTTT 1080  
QY 1081 AGAATACTTCTTCTTCACTGATCTCTCAACCTTAATTTGAAATATTTGATGCTCT 1140  
DB 1081 AGAATACTTCTTCTTCACTGATCTCTCAACCTTAATTTGAAATATTTGATGCTCT 1140  
QY 1141 TTGTTTTTCTCTTATGATGATTTTAAATATTAATTAATTTTATTTTATTTTATTTT 1200  
DB 1141 TTGTTTTTCTCTTATGATGATTTTAAATATTAATTAATTTTATTTTATTTTATTTT 1200



Query Match	100.0%	Score 1257	DB 14	Length 1257
Best Local Similarity	100.0%	Pred. No. 3.4e-271		
Matches 1257	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	GGAGAGAGCGCGCGGGTGAAGAGCGCATTTGATGCAAGCCTGCGCGAGCCTCGAGCGCGG	60	
Db	1	GGAGAGAGCGCGCGGGTGAAGAGCGCATTTGATGCAAGCCTGCGCGAGCCTCGAGCGCGG	60	
QY	61	CGGAGCCGAGAGGCTGACCAAGTTCTCTTCCTGAGTCTCTCGGCTCCAGCTCCGCGCTG	120	
Db	61	CGGAGCCGAGAGGCTGACCAAGTTCTCTTCCTGAGTCTCTCGGCTCCAGCTCCGCGCTG	120	
QY	121	CCCGGACGCGGGAGCCATGCGACCCCAAGGGGCGCGCGCGCTCCCGGAGCGGCTCCGCG	180	
Db	121	CCCGGACGCGGGAGCCATGCGACCCCAAGGGGCGCGCGCGCTCCCGGAGCGGCTCCGCG	180	
QY	181	GCTTCCTGCTCTCTGCTGTGTGACGTGCGCGCGCTGAGCGCTCTGAGATCCCCA	240	
Db	181	GCTTCCTGCTCTCTGCTGTGTGACGTGCGCGCGCTGAGCGCTCTGAGATCCCCA	240	
QY	241	AGGGAGACAAAAGCGCAGCTCCGGCAGAGGGAGGTGTGACCTGTATTAATGGAATGT	300	
Db	241	AGGGAGACAAAAGCGCAGCTCCGGCAGAGGGAGGTGTGACCTGTATTAATGGAATGT	300	
QY	301	GCTTACAAGGGCCACGAGAGTGCTGTGTCAGAGAGGGAGCCCTGTGGGCCAATGTTATTTC	360	
Db	301	GCTTACAAGGGCCACGAGAGTGCTGTGTCAGAGAGGGAGCCCTGTGGGCCAATGTTATTTC	360	
QY	361	CGGGTACACCTGGGATCCCAAGTCCGGATGGATTTCAAGAGAAAGGGGGAATGTCTGA	420	
Db	361	CGGGTACACCTGGGATCCCAAGTCCGGATGGATTTCAAGAGAAAGGGGGAATGTCTGA	420	
QY	421	GGGAAAGCTTTGAGAGATCTTGACACCCCAACTACAGCAGTTCATGAGATTCATTGA	480	
Db	421	GGGAAAGCTTTGAGAGATCTTGACACCCCAACTACAGCAGTTCATGAGATTCATTGA	480	
QY	481	ATTATGGATATGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCTTCAATA	540	
Db	481	ATTATGGATATGATCTTGGGAAATTTGGGAGTGTACATTTACAAAGATGCTTCAATA	540	

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RESULT 50
US-10-173-705-365
: Sequence 365, Application US/10173705
: Publication No. US20030032103A1
: GENERAL INFORMATION:
:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Deenoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3430R1C18
: CURRENT FILING DATE: 2002-06-17
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 612
:

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; SEQ ID NO 365  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-173-705-365

Query Match 100.0%; Score 1257; DB 14; Length 1257;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 1257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GGAAGAGAGCCGCGCGGTGAAGAGCGCATTTGACAGCTTGGCGGCGCTCGAGAGCGCG 60
DB 1 GGAAGAGAGCCGCGCGGTGAAGAGCGCATTTGACAGCTTGGCGGCGCTCGAGAGCGCG 60
QY CGAGAGCGAGCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB CGAGAGCGAGCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 121 CCCGCGAGCCGCGGAGCCATGCGAGCCCGAGGCGCCGCGCGCTCTCCGCGAGCGCTCGCG 180
DB 121 CCCGCGAGCCGCGGAGCCATGCGAGCCCGAGGCGCCGCGCGCTCTCCGCGAGCGCTCGCG 180
QY 181 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 AGGGAAGCAAAAGCGCAGCTCCGCGAGAGGAGGTGGTGGACCTGTATTAATGGAATGT 300
DB 241 AGGGAAGCAAAAGCGCAGCTCCGCGAGAGGAGGTGGTGGACCTGTATTAATGGAATGT 300
QY 301 GCTTCAAGAGGCGCAGAGAGTCTGTGTGAGACGAGAGCCCTGGGCGCAATGTTATTC 360
DB 301 GCTTCAAGAGGCGCAGAGAGTCTGTGTGAGACGAGAGCCCTGGGCGCAATGTTATTC 360
QY 361 CGGGAACACCTGGGATCCCAAGTCCGAGATGATTCAMAGAGAGAGAGGAGATGCTCTGA 420
DB 361 CGGGAACACCTGGGATCCCAAGTCCGAGATGATTCAMAGAGAGAGAGGAGATGCTCTGA 420
QY 421 GGGAAAGCTTTGAGAGAGTCTTGAACACCACTACAGAGAGTTCATGAGATTCATGA 480
DB 421 GGGAAAGCTTTGAGAGAGTCTTGAACACCACTACAGAGAGTTCATGAGATTCATGA 480
QY 481 ATTATGAGATGATTTGGGAAATTTGCGAGTGTACATTTACAAAGATGCGTCAATA 540
DB 481 ATTATGAGATGATTTGGGAAATTTGCGAGTGTACATTTACAAAGATGCGTCAATA 540
QY 541 GTGCTTAAGAGTTTGTTCAAGTGTCTCTCTCGGTAAATGCAAAATGCAATGCTCTTC 600
DB 541 GTGCTTAAGAGTTTGTTCAAGTGTCTCTCTCGGTAAATGCAAAATGCAATGCTCTTC 600
QY 601 AGCGTTGATTTTCAATTCATGAGAGTGTGAGAGCTTCAAGAGCTTCTCCCATTTGAAGCTA 660
DB 601 AGCGTTGATTTTCAATTCATGAGAGTGTGAGAGCTTCTCCCATTTGAAGCTA 660
QY 661 TAAATTTATTTGACCAAGAGAGCCCTGAATGAATTCACAAATTAATTAATTCATTCGCACT 720
DB 661 TAAATTTATTTGACCAAGAGAGCCCTGAATGAATTCACAAATTAATTAATTCATTCGCACT 720
QY 721 CTTCTGTGAGAGAGCTTTGTGTGAAGAGATTGTGTGAGATTAGTGTGTGTGTGTGTGTGT 780
DB 721 CTTCTGTGAGAGAGCTTTGTGTGAAGAGATTGTGTGAGATTAGTGTGTGTGTGTGTGTGT 780
QY 781 TTGGCACTGTTCAATTAACCAAAAGAGATGCTCTTACTGATGGAATTCAGTTCTTC 840
DB 781 TTGGCACTGTTCAATTAACCAAAAGAGATGCTCTTACTGATGGAATTCAGTTCTTC 840
QY 841 GCATCATTTATGAAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900
DB 841 GCATCATTTATGAAGAACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCTTTT 900
QY 901 TTATTTATGCTTTGAGATGTTCACTTAATGAATTCATTTTAATTAATTAATTAATTAAT 960
DB 901 TTATTTATGCTTTGAGATGTTCACTTAATGAATTCATTTTAATTAATTAATTAATTAAT 960
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QY 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTGACACTGTTTTTAA 1020
DB 961 GAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTGACACTGTTTTTAA 1020
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DB 1021 ATCTAGCAATTTATTCATTTTGGCTTCAATCAAAAAGTGTTCATATTTTTTTTAACTTGT 1080
QY 1081 AGAATACCTTCTCATAGTCAATTCCTCAACCTATTAATTTGGAATTTGTGTGTCT 1140
DB 1081 AGAATACCTTCTCATAGTCAATTCCTCAACCTATTAATTTGGAATTTGTGTGTCT 1140
QY 1141 TTTGTTTTTCTCTTAGTATGCAATTTTAAAAAATTAAGCTACCAATCTTTGTAC 1200
DB 1141 TTTGTTTTTCTCTTAGTATGCAATTTTAAAAAATTAAGCTACCAATCTTTGTAC 1200
QY 1201 AATTGTAATGTTAAGAAATTTTTTTTATCTGTAAATTAATTAATTAATTTTCCACA 1257
DB 1201 AATTGTAATGTTAAGAAATTTTTTTTATCTGTAAATTAATTAATTAATTTTCCACA 1257
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Search completed: December 25, 2004, 02:12:42  
Job time : 743 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 22:01:19 ; Search time 4401 Seconds

(without alignments)  
10407.803 Million cell updates/sec

Title: US-10-063-734-121

Perfect score: 1257

Sequence: 1 ggaagagagcgcgcgcggtga.....aataaaattatccaca 1257

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_est4: \*  
5: gb\_est5: \*  
6: gb\_est6: \*  
7: gb\_est7: \*  
8: gb\_est8: \*  
9: gb\_est9: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252.2	99.6	1288	3	BC021025 Homo sapi
2	1202.2	95.6	1207	3	CR605392 full-length
3	1184.2	94.2	1189	3	CR596030
4	1106.2	88.0	1111	3	CR612318 full-length
5	1098.2	87.4	1103	3	CR594803 full-length
6	999	79.5	1098	1	AL532456
7	951.6	75.7	1102	1	AL575307
8	941	74.9	1064	1	AL564395
9	914.2	72.7	1100	1	AL551834
10	861.6	68.5	986	5	BM560093
11	842.2	67.0	1073	5	BM560093
12	842.2	67.0	1132	4	BM560093
13	815.2	64.9	903	4	BM560093
14	811.2	64.5	827	1	AL544722
15	739.4	58.8	851	1	BM560093
16	727.2	57.9	732	9	AY399084
17	716.4	56.8	732	9	AY399084
18	714.4	56.8	732	9	AY399084
19	705.2	56.1	1037	3	BM5915926
20	705.2	56.1	710	3	CR592899
21	700.4	55.7	747	6	CA415410
22	695.6	55.3	796	5	BQ008675
23	693.2	55.1	734	5	BX114800
24	691	55.0	723	6	CA431413

25	690	54.9	724	5	BQ009009
26	685.8	54.6	706	7	CN394776
27	682.2	54.3	710	6	CA413294
28	682	54.3	702	5	BQ010155
29	681.4	54.2	683	2	BE607413
30	681.4	54.2	683	2	BE607414
31	679.6	54.1	836	1	AL570753
32	679.6	54.1	709	1	AL553798
33	679	54.0	730	5	BUT29033
34	678.2	54.0	1099	4	BM155288
35	678.2	53.5	986	5	BQ648112
36	672.4	53.5	707	5	BX386416
37	672.2	53.5	902	5	BQ424201
38	658.2	52.4	1161	3	AK003674
39	655.4	52.1	723	5	BQ005403
40	651.6	51.8	1168	3	AK076498
41	649.8	51.7	671	5	BQ624465
42	641.8	51.1	688	2	BE896915
43	641	50.6	688	2	BX386415
44	636.4	50.4	654	5	BM524261
45	633.8	50.4	654	5	AL553771
46	628.2	50.0	676	1	AL553771
47	608.8	48.4	798	6	CB959810
48	606.2	48.2	1023	4	BG421228
49	597	47.5	849	6	CB201936
50	581.4	46.3	610	5	BQ013605
51	577	45.9	814	6	CB991371
52	573.6	45.6	738	9	AY399086
53	569.6	45.3	617	5	BQ574527
54	567.8	45.2	571	7	CN394775
55	567.4	45.1	582	2	AM071610
56	565.8	45.0	582	1	AA584310
57	561.4	44.7	567	6	CA868366
58	552	43.9	556	1	AT162109
59	548.2	43.6	599	2	BF691507
60	547	43.5	579	1	AT174374
61	532.8	42.4	549	1	AT1085616
62	531.8	42.3	790	4	BE550475
63	523.4	41.6	583	2	AM994682
64	516.6	41.1	583	2	AM994682
65	514.8	41.0	512	4	BM63039
66	512	40.7	512	4	BM687835
67	504.4	40.1	511	1	AT122726
68	503	40.0	511	4	BM701829
69	502.2	40.0	507	1	AT109642
70	499.4	39.7	504	2	AM316960
71	495	39.4	521	6	CA414544
72	486.8	38.7	518	6	CB9898290
73	486.8	38.7	518	6	CB9898290
74	486	38.7	504	1	AT120963
75	485.4	38.6	492	2	BF000103
76	481.8	38.3	485	1	AA482398
77	480.8	38.2	506	7	CN394773
78	474.6	37.8	482	2	BE551643
79	468	37.2	513	2	BF432104
80	465	37.0	467	2	BE550264
81	464.2	36.9	593	7	CQ696082
82	461	36.7	466	1	AT135984
83	459.2	36.5	464	1	AA482544
84	457	36.4	463	1	AT179443
85	456.8	36.3	644	7	CQ681284
86	453	36.0	453	2	BE215566
87	450.6	35.8	590	6	CF180990
88	448	35.6	455	2	AM518948
89	446.4	35.5	463	1	AA406425
90	445.4	35.4	476	1	AT1760411
91	444	35.3	472	1	AT1391517
92	439.4	35.0	473	2	AM084890
93	436	34.7	436	1	AA410434
94	435.6	34.7	1159	5	BU155889
95	435	34.6	435	1	AT1081084
96	434	34.5	435	2	AM236626
97	434	34.5	448	1	AT656907

BQ009009	UI-H-EIO-
CN394776	UI-H-EZO-
CA413294	UI-H-EDO-
BQ010155	UI-H-EDO-
BE607413	coloneSTO
BE607414	coloneSTO
BE607415	coloneSTO
AL570753	AL570753
AL553798	AL553798
AL553798	AL553798
BU729033	UI-E-COL-
BM155288	AGENCOURT
BQ648112	AGENCOURT
BX386416	AGENCOURT
BQ424201	AGENCOURT
AK003674	Mus muscu
BQ005403	UI-H-E11-
AK076498	Mus muscu
BU624465	UI-H-FG1-
BE387335	601276538
BE896915	601439437
BX386415	BX386415
BM524261	UI-H-FG1-
AL553771	AL553771
CB959810	AGENCOURT
BG421228	602451719
CB201936	AGENCOURT
BQ013605	UI-1-BC1P
CB991371	AGENCOURT
AY399086	Mus muscu
BQ574527	UI-H-E21-
CN394775	170005325
AM071610	wt94D06.x
AA584310	nm79G01..8
CA868366	1r78A06.x
AT162109	w153908.x
BF691507	602247681
AT174374	w953G03.x
AT1085616	0243C04.x
BE550475	602895273
BE550475	7a27A08.x
AM994682	RCL-BN003
BM63039	AGENCOURT
BM687835	TMT015_Hu
AT122726	tf29E06.x
BM701829	UI-E-CQ1-
AT109642	wf31G08.x
AM316960	XX10D09.x
CA414544	UI-H-EZO-
CB9898290	AGENCOURT
CB9898290	AGENCOURT
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AA482398	2r34A06.x
CN394773	170006001
BE551643	h296C03.x
BF432104	nab88512.x
BE550264	7a21A03.x
CQ696082	DO11-93m2
AT135984	qy34h03.x
AA482544	2r34A06..8
AT179443	lc66h12..x
CQ681284	DO11-127n
BE215566	hu26d01.x
CF180990	817779_MA
AM518948	ha47A02.x
AA406425	2v12C11..f
AT1760411	w151A10..x
AT1391517	cg15606.x
AM084890	cc64h04.x
AA410434	2v12C11..8
BU155889	AGENCOURT
AT1081084	0262A08..x
AM236626	xm48G03.x
AT656907	lt54G03.x

C 98	434.	34.5	449	2	AM276370	AM276370	xr11h05.x
C 99	431	34.3	436	1	A1380885	A1380885	tg17d07.x
C 100	430.8	34.3	638	7	CO696320	CO696320	DG11-96p2

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	1288 bp	mRNA	linear	HTC 04-AUG-2004
BC021025		Homo sapiens collagen triple helix repeat containing 1, clone IMAGE:5617332.				mRNA (CDNA
ACCESSION		BC021025				
VERSION		BC021025.1				
KEYWORDS		GI:18045042				
SOURCE		Htc.				
ORGANISM		Homo sapiens (human)				

REFERENCE  
AUTHORS  
1 (bases 1 to 1288)  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R. D., Collins, F. S., Wagner, L., Shemen, C. M., Schuler, G. D. Altschul, S. F., Zeeberg, B., Buecok, K. H., Schaefer, C. F., Blat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Scaletton, M., Soares, M. B., Bonaldo, M. P., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toetiyaki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mulhaly, S. J., Bosak, S. A., McSwan, P. J., McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S. C., Garcia, A. M., Gay, L. J., Halik, S. W., Villalón, D. K., Muzny, D. M., Sodergren, E. U., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriques, A., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Sherchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzyzanski, M. I., Skelske, J., Smalls, D. E., Scherch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

*Proc. Natl. Acad. Sci. U.S.A.* 99 (26), 16899-16903 (2002)

12477932

REFERENCE 2 (pages 1 to 1288)  
AUTHORS Director MGC project.  
TITLE Direct Submission  
JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
COMMENT Contact: MGC help desk

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: ATCC/DCTD/BTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbiology.org>  
contact: [amadamsystemsbiology.org](mailto:amadamsystemsbiology.org)  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 24 Row: i Column: 7  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 19923988  
This clone has the following problem: no cloning site / microdeletion.

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FEATURES
source      Location/Qualifiers
1..1288     /organism="Homo sapiens"
/mol_type="mRNA"
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Db		966	GAAATGAAGAAGCAAGCTAAATATGTGTTACAGACCMAAGTGATTTCCACACTGTTTTTAA	1025
Qy		1021	ATCTAGCATTTATTCATTTTGGCTTCAATCAAAAAGGTTTCAATATTTTTTTTAGTGGTT	1080
Db		1026	ATCTAGCATTTATTCATTTTGGCTTCAATCAAAAAGGTTTCAATATTTTTTTTAGTGGTT	1085
Qy		1081	AGAAATACCTTCCTGATAGTGCACATTCCTCAACCTATAATTGGAAATATGTGGNGTCT	1140
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Db		1206	AATTTGTAAAGTTAAGCAATTTTTTTTATATCTGTTAATAATAAATTTTCCAACA	1262
RESULT 2				
LOCUS	CR605392			
DEFINITION	full-length cDNA clone CSOD1037YD19 of Placenta Cot 25-normalized	1207 bp	mRNA	linear HTC 21-JUL-2004
ACCESSION	CR605392.1			
KEYWORDS	HTC; CNSLT_cDNA.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	L.I.W.B., Gruber,C., Jessee,J. and Polayes,D.			
TITLE	Li,W.-length cDNA libraries and normalization			
JOURNAL	Unpublished			
REMARK	Contact : Feng Liang Email : fliang@life.rockefeller.edu http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue 2 (bases 1 to 1207) Genoscope.			
REFERENCE	Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage ; BP 191 91006 Evry cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr			
AUTHORS	- Web : www.genoscope.cns.fr			
TITLE	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.			
JOURNAL	Location/Qualifiers			
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Best Local Similarity	99.8%;	Pred. No. 2.4e-247;		
Matches 1204;	Conservative	0;	Mismatches 3;	Indels 0;
			Gaps 0;	
Qy	45	CGGCTCTGAGACGCGCGGAGCAACACCTGACACAGTTCTCTCTCGGTCTCCTCGC	104	
Db	1	CGGCTCTGAGACGCGCGGAGCAACACCTGACACAGTTCTCTCTCGGTCTCCTCGC	60	
Qy	105	CTCACAGTCCGCGCTGCCCGGACGCGGAGCATGCAACCCAGAGCCCCCGCGCTCC	164	

Db	61	CTCAGCTCCGCGCTGCCCGGACCCGGAGCCATGGACCCCAAGGACCCTCGCGCTCC	120
Qy	165	CCGACGGCGCTCCGCGGCTCTCTGCTGCTCTCTGCTGAGCTGCCGCGCTGCAGC	224
Db	121	CCGACGGCGCTCCGCGGCTCTCTGCTGCTCTCTGCTGAGCTGCCGCGCTGCAGC	180
Qy	225	GCCCTGAGATCCCGACGGGGAAAGCAAAAGCCGACTCCGGCAGAGAGGTGTGTAC	284
Db	181	GCCCTGAGATCCCGACGGGGAAAGCAAAAGCCGACTCCGGCAGAGAGGTGTGTAC	240
Qy	285	CTGTATATGGAATGTGCTTACAAGGGCCACAGAGAGTGCCTGGTCCAGA	344
Db	241	CTGTATATGGAATGTGCTTACAAGGGCCACAGAGAGTGCCTGGTCCAGA	300
Qy	345	GGGGCCAAATGTTATCCGGGTACACTGGGATCCAGGTCCGAGTGGATTCAAAGGAA	404
Db	301	GGGGCCAAATGTTATCCGGGTACACTGGGATCCAGGTCCGAGTGGATTCAAAGGAA	360
Qy	405	AAGGGGGAATGTCTGAGGGAAGCTTTGAGAGTCTCTGACACCCACTACAGACGT	464
Db	361	AAGGGGGAATGTCTGAGGGAAGCTTTGAGAGTCTCTGACACCCACTACAGACGT	420
Qy	465	TCATGGAATCATTGAATTTATGCAATGCAATGTTGGGAAAATTTGGGAGTGTACATTACA	524
Db	421	TCATGGAATCATTGAATTTATGCAATGCAATGTTGGGAAAATTTGGGAGTGTACATTACA	480
Qy	525	AAGATGGCTTCAAAATAGTGTCTTAAGAGTTTGTTCAGTGGCTCACTTCGGCTAAAAATGC	584
Db	481	AAGATGGCTTCAAAATAGTGTCTTAAGAGTTTGTTCAGTGGCTCACTTCGGCTAAAAATGC	540
Qy	585	AGAAATGATGCTGTACAGCTTGGTATTTCAATTCAATGAGCTGAATGTTCCAGACCT	644
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Qy	645	CTTCCCATTTGAAGTATTAATTTTGGACCAAGAGAGCCCTGAATGAATTCACAACTT	704
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Qy	705	AATATTCATCGCACTTCTCTGTGAAGAGCTTTGTGAAGAAATTTGTGTGATTTAGTG	764
Db	661	AATATTCATCGCACTTCTCTGTGTGAAGAGCTTTGTGAAGAAATTTGTGTGATTTAGTG	720
Qy	765	GATGTGTCTATCTGGGTGGGCACTTGTTCAGATTTACCCAAAAGAGATGCTTCTACTGGA	824
Db	721	GATGTGTCTATCTGGGTGGGCACTTGTTCAGATTTACCCAAAAGAGATGCTTCTACTGGA	780
Qy	825	TGGAATTCAGTTTCTCGCATTCATTAATGAAGAACTACCAAAATTAATGCTTATTTTCA	884
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Qy	885	TTTGTCACTCTTTTATTTATATGCTTGGAAATGGTTCACCTTAATGACATTTTAAATTA	944
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Qy	945	GTTATATGATACATCTGAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGCTGAT	1004
Db	901	GTTATATGATACATCTGAATGAAAAGCAAGCTAAATATGTTTACAGACCAAGCTGAT	960
Qy	1005	TTTACACTGTTTTTAAATCTAGCAATTAATCTTTTGTCTCAATCAAAAAGTGTTCATA	1064
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Db 1141 CTACCAATCTTTGACAAATTTGTAAATTTTATATCTGTTAAATMAA 1200  
QY 1245 ATTATTT 1251  
Db 1201 ATTATTT 1207

RESULT 3  
CR596030  
LOCUS full-length cDNA clone CS0D1061YA20 of Placenta Cot 25-normalized  
DEFINITION 1189 bp mRNA linear HTC 21-JUL-2004  
ACCESSION CR596030  
VERSION CR596030.1 GI:50476837  
KEYWORDS HTC; CNSLT cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 1189)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact: Feng Liang Email: fliang@life.techn.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1189)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail: seque@genoscope.cns.fr  
JOURNAL - Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen  
FEATURES  
source location/Qualifiers  
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Best Local Similarity 99.7% Pred. No. 1.7e-243;  
Matches 1186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 CGGCTCGGAGCGCGGCGGAGCCAGACGCTGACACGCTTCTCTCTCTCTCTCCG 60  
QY 105 CTCAGCTCGGCGCTGCGCGGAGCGCGGAGCCAGACGCTTCTCTCTCTCTCTCCG 164  
Db 61 CTCAGCTCGGCGCTGCGCGGAGCGCGGAGCCAGACGCTTCTCTCTCTCTCTCCG 120  
QY 165 CCGAGCGGCTCGCGGCT 224  
Db 121 CCGAGCGGCTCGCGGCT 180  
QY 225 GCCTCTGAGATCCCAAGGAGGAGCAAAAGCGAGCTCGGCGAGAGGAGTGTGAC 284  
Db 181 GCCTCTGAGATCCCAAGGAGGAGCAAAAGCGAGCTCGGCGAGAGGAGTGTGAC 240  
QY 285 CTGATATGGAAGTGTCTTCAAGGCGCACAGAGTCTGTCTGAGAGCGGAGCCCT 344  
Db 241 CTGATATGGAAGTGTCTTCAAGGCGCACAGAGTCTGTCTGAGAGCGGAGCCCT 300  
QY 345 GGGGCCAATGTTATTCGGGTACACTGTGATCCAGGTGGAGTGTGATCAAGGAGAA 404  
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Db 301 GGGGCCAATGCAATCCGGGTACACTGTGATCCAGGTGGAGTGTGATCAAGGAGAA 360  
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QY 465 TCATGAGTTCATGAAATTTATGATAGATCTTGGGAAAATTTGGGAGTGTATCTTACA 524  
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Db 601 CTTCATTTGAAGCTATATTTATTTGAGACCAAGAGCCCTGAAATGAAATTCACAAATT 660  
QY 705 AATATTCATGCCACTTCTCTGTTGAGAGACTTTGAGAGAAATGGTGTGATTAATG 764  
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QY 885 TTGCTACCTCTTTTATTTATTTAGCCCTGGAATGTTCACTTAATGACATTTTAATTA 944  
Db 841 TTGCTACCTCTTTTATTTATTTAGCCCTGGAATGTTCACTTAATGACATTTTAATTA 900  
QY 945 GTTATGATATCATCTGATGAAAGCAAGCAAGTAAATATTTATACAGACCAAGTGTGAT 1004  
Db 901 GTTATGATATCATCTGATGAAAGCAAGCAAGTAAATATTTATACAGACCAAGTGTGAT 960  
QY 1005 TTCACTGTTTAAATTTAGCATTAATTTGCTTCAATCAAAAGTGTTCATTA 1064  
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QY 1065 TTTTATTTAGTGTGAAATTAATCTTCTCATAGTCAATCTCTCACTTAATTTGG 1124  
Db 1021 TTTTATTTAGTGTGAAATTAATCTTCTCATAGTCAATCTCTCACTTAATTTGG 1080  
QY 1125 AATATGTTGAGCTTTTGTGTTTCTCTTATATAGCATTTTAAATAATATTAAG 1184  
Db 1081 AATATGTTGAGCTTTTGTGTTTCTCTTATATAGCATTTTAAATAATATTAAG 1140  
QY 1185 CTACCAATCTTTGACAAATTTGTAAATGTTAAGAAATTTTATATCT 1233  
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RESULT 4  
CR612318  
LOCUS full-length cDNA clone CS0D014YN20 of Fetal liver of Homo sapiens (human).  
DEFINITION 1111 bp mRNA linear HTC 21-JUL-2004  
ACCESSION CR612318  
VERSION CR612318.1 GI:50493125  
KEYWORDS HTC; CNSLT cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 1111)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1111)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : segr@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES  
source  
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/clone="CSODM014YN20"  
/issue\_type="Fetal liver"  
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ORIGIN

Query Match 88.0%; Score 1106.2; DB 3; Length 1111;  
Best Local Similarity 99.7%; Pred. No. 9.5e-227;  
Matches 1108; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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61 GCTGACGCTGCCGCGCGCGCTGAGGCGCTTGTAGATCCCAAGGAGCAAAAGGCGCA 120

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320 AGTGCGCTGTCAGAGCGGAGCGCTGGGCGCAATGTTATCCGGGTACACCTGGATCCC 379  
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380 AGGTGCGGATGATTCAAAGAGAGAAAGGGGGAATGTCAGAGGAAAGCTTTGAGGAGTC 439  
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500 GAAATTTGGCGAGTGTATCAATTTCAAAAGATGCGTCAAAATAGTCTTAAGATTTGTT 559  
361 GAAATTTGGCGAGTGTATCAATTTCAAAAGATGCGTCAAAATAGTCTTAAGATTTGTT 420

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620 CATGAGAGTGTATGTCAGAGTCTTCCCATTTGAAGCTATTAATTTATTTGAGCAAG 679  
481 CATGAGAGTGTATGTCAGAGTCTTCCCATTTGAAGCTATTAATTTATTTGAGCAAG 540

680 AACCCCTGAATGAATTCACAAATTAATTAATTCATTCGACATCTTCTGTGAGAGCATTTG 739  
541 AACCCCTGAATGAATTCACAAATTAATTAATTCATTCGACATCTTCTGTGAGAGCATTTG 600

740 TGAAGGAATTTGCTGTGATTAAGTGTATGATGCTATCTGGGTTGCACTTTGTCAGATTA 799  
601 TGAAGGAATTTGCTGTGATTAAGTGTATGATGCTATCTGGGTTGCACTTTGTCAGATTA 660

800 CCCAAAGAGATGCTTCTACTGATGAAATTCAGTTTCTCGCATCATTAATGAAGAACT 859  
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860 ACCAAATTAATGCTTAAATTTTCAATTTGCTACTCTTTTAAATTAATGCTTGAATGC 919  
721 ACCAAATTAATGCTTAAATTTTCAATTTGCTACTCTTTTAAATTAATGCTTGAATGC 780

920 TTCACCTTAATTAATGCTTAAATTTTCAATTTGCTACTCTTTTAAATTAATGCTTGA 979  
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1040 GCTTCATCAAAAGTGTTCAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 1099  
901 GCTTCATCAAAAGTGTTCAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 960

1100 CACATTTCTCAACCTATTAATTTGGAATTTGTGTGCTTTTGTGTTTCTCTTACTA 1159  
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1160 TAGCATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1219  
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1220 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1250  
1081 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1111

RESULT 5  
CR594803  
LOCUS  
DEFINITION full-length cDNA clone CSODI022YF04 of Placenta Cot 25-normalized  
of Homo sapiens (human).  
CR594803  
ACCESSION  
VERSION CR594803.1 GI:50475610  
KEYWORDS HTC; CNSLT; cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1103)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : segr@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES  
source  
1. 1103  
/organism="Homo sapiens"  
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/plasmid="pCMVSPORT\_6"

ORIGIN







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Db	240	AGGTGCGGATGGAATTCAGAGAGAAAGGGGAAAGTCTGAGGGAAACCTTTGAGATC	299
Qy	440	CTGACACCCCAACTACAGACAGTGTTCATGAGTTCATTGAAATATGACATAGACTTGG	499
Db	300	CTGACACCCCAACTACAGACAGTGTTCATGAGTTCATTGAAATATGACATAGACTTGG	359
Qy	500	GAAATTTGCGGAGTGTACATTTACAAAGATGCGTTCAATATGCTCTAAGAGTTTGT	559
Db	360	GAAATTTGCGGAGTGTACATTTACAAAGATGCGTTCAATATGCTCTAAGAGTTTGT	419
Qy	560	CAGTGGCTCACTTGGCTAAATATGACAAATGACATGCTGACGCTTGATATTCACAT	619
Db	420	CAGTGGCTCACTTGGCTAAATATGACAAATGACATGCTGACGCTTGATATTCACAT	479
Qy	620	CAATGAGCTGAATGTTCAGACCTCTTCCATTGAGCTATTAATTTATTTGACCAAG	679
Db	480	CAATGAGCTGAATATGTTCAAGACCTCTTCCATTGAGCTATTAATTTATTTGACCAAG	539
Qy	680	AAGCCCTGAATGATTCACAACATTAATATTCATGACACTTCTTGAGGAAGACTTGG	739
Db	540	AAGCCCTGAATGATTCACAACATTAATATTCATGACACTTCTTGAGGAAGACTTGG	599
Qy	740	TGAAGAAATTTGTTGCTGAGATTAGTGAATGTTGCTATCTGGGTTGGCACTTGTCAATTA	799
Db	600	TGAAGAAATTTGTTGCTGAGATTAGTGAATGTTGCTATCTGGGTTGGCACTTGTCAATTA	659
Qy	800	CCCAAAAAGGAATGCTTCTACTGATGGAATTCAGTCTTCGCATCATTTATGGAAGACT	859
Db	660	CCCAAAAAGGAATGCTTCTACTGATGGAATTCAGTCTTCGCATCATTTATGGAAGACT	719
Qy	860	ACCAAAATTAATGCTTTAATTTCTATTGCTACCTCTTTTATTTATGACCTTGGATGG	919
Db	720	ACCAAAATTAATGCTTTAATTTCTATTGCTACCTCTTTTATTTATGACCTTGGATGG	779
Qy	920	TTCACTTAATGACATTTTAAATAAGTTATGATATACATCTGAATGAAGAAGCAAGCTTA	979
Db	780	TTCACTTAATTAAGACATTTTAAATAAGTTATGATATACATCTGAATGAAGAAGCAAGCTTA	839
Qy	980	ATATGTTTACAGACCAAGGTGATTTCAACCTGTTTTTAAATCAGACATTAATCAATTT	1039
Db	840	ATATGTTTACAGACCAAGGTGATTTCAACCTGTTTTTAAATCAGACATTAATCAATTT	899
Qy	1040	GCTTCAATCAAAAGTGTTCATATATTTTATTTAGTGGTTAGAAATCACTTCTTCATAGT	1099
Db	900	GCTTCAATCAAAAGTGTTCATATATTTTATTTAGTGGTTAGAAATCACTTCTTCATAGT	959
Qy	1100	CACATTCCTCAACCTATTAATTTGGAATATGTTGTGTGCTTTTGTCTTCTTAATA	1159
Db	960	CACATTCCTCAACCTATTAATTTGGAATATGTTGTGTGCTTTTGTCTTCTTAATA	1019
Qy	1160	TAGCATTTTAAATAAATAATATAAGCTACCAATCTTTGTACAAATTTGTAATGTTAAGA	1219
Db	1017	TAGCATTTTAAATAAATAATATAAGCTACCAATCTTTGTACAAATTTGTAATGTTAAGT	1073
Qy	1220	TTTTTTTTTAATCTGTTAAT	1240
Db	1074	TTTTTTTTTTTTTAAATAAT	1094

RESULT 7	AL575307/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
	AL575307	1102 bp	mRNA	linear	EST 06-APR-2004			
	AL575307		Homo sapiens PLACENTA COT 25-NORMALIZED	Homo sapiens cDNA				
	clone CS001061Ya20	3-PRIME, mRNA sequence.						
	AL575307							
	AL575307.3	GI:46248266						
	EST.							
	Homo sapiens (human)							
	Homo sapiens							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							

REFERENCE	1 (bases 1 to 1102)
AUTHORS	Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On Feb 16, 2001 this sequence version replaced gi:31313615.

REFERENCE  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 1102)  
AUTHORS  
Li, W. B., Gruber, C., Jesssee, J. and Polayes, D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished (2001)  
COMMENT  
On Feb 16, 2001 this sequence version replaced gi:31313615.  
Contact: Genoscope - Centre National de Sequencage  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqret@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
4941.f  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna/s=CS0DI061BA10NP1&c=4941.f>.

ORIGIN

Query Match	75.7%:	Score 951.6;	DB 1;	Length 1102;
Match Local Similarity	95.7%:	Pred. No. 1.5e-193;		
Matches 992;	Conservative 4;	Mismatch 38;	Indels 3;	Gaps 2;
QY	199	TGCTGCAGCTGCCCCGCGCCGTGAGCGCCTCTGAGATCCCCAGAGGGAGCAAAAGCGC	258	
Db	1036	TTCTGYMSTGCASATGCCCGGCGCTGTGGCGCCTTATGATATCCCAAGGAGCAAAAGCGC	977	
QY	259	AGCTCCGGCAGAGGAGAGTGTGGAACCTGTTATGGAATGTGCTTACAAAGGCCAGAG	318	
Db	976	AGCTCCGGCAGAGGAGAGTGTGT-GACCTGTATATGGAATGTGCTTACAAAGGCCAGAG	918	
QY	319	GAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCATGTGTATTCCGGAGTACACTGGAGTCC	378	
Db	917	GAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCATATGGCATTTCCGGGTAACCTGGAGTCC	858	
QY	379	CAGGTCCGGATGATTCAAAGAGAAAAAGGGGAGATGCTGAGGAAAACCTTGAAGAGT	438	
Db	857	CAGGTCCGGATGATTCAAAGAGAAAAAGGGGGAATGCTGAGGAAAACCTTGAAGAGT	798	
QY	439	CCTGGACACCAATTACAGAGAGTTCATGGAATTCATGAAATTATGGCATATAGTCTTG	498	
Db	797	CCTGGACACCAACTTACAGAGAGTTCATGGAATTCATGAAATTATGGCATATAGTCTTG	738	
QY	499	GGAATAATTCGGAGTGTACATTTTCAAAAGATGCGTTCAATATAGTCTTAAGATTTGT	558	
Db	737	GGAATAATTCGGAGTGTACATTTTCAAAAGATGCGTTCAATATAGTCTTAAGATTTGT	678	
QY	559	TCAGTGGCTCACTTCGGCTAAATATGCAAAATGCAATGCAATGCTGTCAAGCTTGTATTTGCAT	618	
Db	677	TCAGTGGCTCACTTCGGCTAAATATGCAAAATGCAATGCAATGCTGTCAAGCTTGTATTTGCAT	618	
QY	619	TCATATGAGCTGAATGTTTCAGGAACCTCTTCCCATTTGAAGCTATATATTTTGGACCAAG	678	
Db	617	TCATATGAGCTGAATGTTTCAGGAACCTCTTCCCATTTGAAGCTATATATTTTGGACCAAG	558	
QY	679	GAAGCCCTGAAATGAATTCACAACTTAATATTCATGCACTTCTCTGTGAAAGCACTTT	738	
Db	557	GAAGCCCTGAAATGAATTCACAACTTAATATTCATGCACTTCTCTGTGAAAGCACTTT	498	
QY	739	GTVGAGGAATTTGCTGTGATTAAGATGTTGCTATCTGGGTGGCACTTGTTCAGATT	798	



Db	LOCUS	RESULT 9	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	AL551834	1168	AGTGGTTTCATATTTTTCAGTTAGTTCATATCTTTCATATGACATTTCTCA	1100 bp	mRNA	linear	EST 30-MAR-2004					
Db	AL551834	1112	ACCTAATAATTTGGAATATGTTGGTCTTTGTTTCTTTAGTATAGCATTTTAA	1100 bp	mRNA	linear	EST 30-MAR-2004					
Db	AL551834	108	ACCTAATAATTTGGAATATGTTGGTCTTTGTTTCTTTAGTATAGCATTTTAA	1100 bp	mRNA	linear	EST 30-MAR-2004					
Db	AL551834	1172	AAAAATATAAAGCTACCAATCTTTGTATCATTTGTATAATGTTAAGAT	1100 bp	mRNA	linear	EST 30-MAR-2004					
Db	AL551834	48	AAAAATATAAAGCTACCAATCTTTGTACAA-TWGTAAAKGTTAAGAT	1100 bp	mRNA	linear	EST 30-MAR-2004					
Db	AL551834	105	CTCCAGCTCCGCGCGCCGCGGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCG	1100 bp	mRNA	linear	EST 30-MAR-2004					
Db	AL551834	61	CTCCAGCTCCGCGCGCCGCGGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCG	1100 bp	mRNA	linear	EST 30-MAR-2004					
Db	AL551834	165	CCGAGCGGCTCCGCGCGCCGCGGAGCCGAGCCGAGCCGAGCCGAGCCGAG	1100 bp	mRNA	linear	EST 30-MAR-2004					
Db	AL551834	121	CCGAGCGGCTCCGCGCGCCGCGGAGCCGAGCCGAGCCGAGCCGAGCCGAG	1100 bp	mRNA	linear	EST 30-MAR-2004					
Db	AL551834	225	GCCTTGAAGATCCCAAGGGGAGCAAAAGCCGAGCTCCGAGAGGAGGTGGAC	1100 bp	mRNA	linear	EST 30-MAR-2004					

Db	181	GCCTCTGAGATGCCCAAGGGGAAGCAAAAGCCGCA-CTCCGGCAGAGGAGGTGTGAC	239
Qy	285	CTGTATATATGGAATGTGCTTACAAAGGCCACGACGAATGCTTGGTCCAGACGGGAGCCCT	344
Db	240	CTGTATATATGGAATGTGCTTACAAAGGCCACGACGAATGCTTGGTCCAGACGGGAGCCCT	299
Qy	345	GGGGCCAAATTTATTCGGGGTACACCTGGGATGCCAGTGGGGATGGATTCAAGAGGAA	404
Db	300	GGGGCCAAATGCAATCCGGGGTACACCTGGGATGCCAGTGGGGATGGATTCAAGAGGAA	359
Qy	405	AAGGGGGAATGTGAGGGAAGGCTTTGAGAGAGTCTCGACACCCAATAAGACAGTGT	464
Db	360	AAGGGGGAATGTGAGGGAAGGCTTTGAGAGAGTCTCGACACCCAATAAGACAGTGT	419
Qy	465	TCATGAGATTCATTGAATTAATGCGATAGATCTTGGGAAAATTCGGGAGTGTACTTTACA	524
Db	420	TCATGAGATTCATTGAATTAATGCGATAGATCTTGGGAAAATTCGGGAGTGTACTTTACA	479
Qy	525	AAGATGGCTTCAATPATGCTCTTAAGATTTTGTTCAGTGGCTCACCTTGGCTTAATATGC	584
Db	480	AAGATGGCTTCAATPATGCTCTTAAGATTTTGTTCAGTGGCTCACCTTGGCTTAATATATGC	539
Qy	585	AGAAATGATGCTGTGACGGCTGGTATTTTCACATTCATGAGAGTGTTCAGACACT	644
Db	540	AGAAATGATGCTGTGACGGCTGGTATTTTCACATTCATGAGAGTGTTCAGACACT	599
Qy	645	CTTCCCATTTGAAAGCTAATTTATTTTGGACCAAGGAAGCCCTGAAATGAATTCACAATT	704
Db	600	CTTCCCATTTGAAAGCTAATTTATTTTGGACCAAGGAAGCCCTGAAATGAATTCACAATT	659
Qy	705	AATATTCATGCACTTCTTCTGTGGAAGGACTTTGTGAAGAAATGGTGTCTGATTTAGTG	764
Db	660	AATATTCATGCACTTCTTCTGTGGAAGGACTTTGTGAAGAAATGGTGTCTGATTTAGTG	719
Qy	765	GATGTTCGTAATCTGGTGTGGCACTGTTTCAGATTATCCAAAGAGAGATGCTTCTACTGGA	824
Db	720	GATGTTCGTAATCTGGTGTGGCACTGTTTCAGATTATCCAAAGAGAGATGCTTCTACTGGA	779
Qy	825	TGGAATTCAGTTTCTCGCATCATATTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCA	884
Db	780	TGGAATTCAGTTTCTCGCATCATATTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCA	839
Qy	885	TTTGCTTACCTCTTTTATTTATTTATGCTTGGAAATGTTTCACTTAAATGACATTTTAAATTA	944
Db	840	TTTGCTTACCTCTTTTATTTATTTATGCTTGGAAATGTTTCACTTAAATGACATTTTAAATTA	899
Qy	945	GTTTATGTAATACATCTGAATGGAAGGAAGCAAGCTAATATGTTTTCAGAGCCAAAGTGAT	1004
Db	900	GTTTATGTAATACATCTTAAATGGAAGG-AGCTAATAATATGTTTTCAGAGCMAA--GTGTG	955
Qy	1005	TTTCACACGTTTAAATCTAGCAATTAATTCATTTTGGCTTCATCAAAAGTGTTTCATA	1064
Db	956	ATTTCMCCTGTTTAAATCTAGCAATTAATTCATTTGCTY----AATCAAGTGTTCATATT	1011
Qy	1065	TTTTTTTTTAACTGGTTA	1081
Db	1012	TTTTTAACTGGTAGATA	1028
RESULT 10			
EX387691			
LOCUS	986 bp	linear	EST 29-APR-2004
DEFINITION	BX387691 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA		
ACCESSION	BX387691		
VERSION	BX387691.2		
KEYWORDS	GI:46875049		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 986)		
REFERENCE	L.I. W.B., Gruber,C., Jeejee,J. and Polayes,D.		





QY 412 AATGCTGAGGAAAGCTTTGAGAGTCTGAGACCCCAACTCAAGACAGTTCATGGA 471  
 DB 361 AATGCTGAGGAAAGCTTTGAGAGTCTGAGACCCCAACTCAAGACAGTTCATGGA 420  
 QY 472 GTTCAATGGAATATGCAATGATCTTTGGGAAAATTCGGAGTGTACATTTACAAAGATGC 531  
 DB 421 GTTCAATGGAATATGCAATGATCTTTGGGAAAATTCGGAGTGTACATTTACAAAGATGC 480  
 QY 532 GTTCAATGGAATGCTCTGAGAGTCTTTGTCAGTGTGCTCAGTGGGCTTAAATGCAAGAAAG 591  
 DB 481 GTTCAATGGAATGCTCTGAGAGTCTTTGTCAGTGTGCTCAGTGGGCTTAAATGCAAGAAAG 540  
 QY 552 CATGCTGTGACGCTGTGATATTTCACTCAATGAGCTGAATGTTCAGACCTCTTCCCA 651  
 DB 541 CATGCTGTGACGCTGTGATATTTCACTCAATGAGCTGAATGTTCAGACCTCTTCCCA 600  
 QY 652 TTGAGCTATATATTTATTTGGACCAAGAAAGCCCTGAAATGAAATTTCAATTAATATTC 711  
 DB 601 TTGAGCTATATATTTATTTGGACCAAGAAAGCCCTGAAATGAAATTTCAATTAATATTC 660  
 QY 712 ATGCACTCTCTCTGTGAGAGCTTTGTAAGAAATGTGTGCTGATTAAGATGTTG 771  
 DB 661 ATGCACTCTCTCTGTGAGAGCTTTGTAAGAAATGTGTGCTGATTAAGATGTTG 720  
 QY 772 CTATCTGGG-TTGGCACTTTGTTCAATTAACCAAAAAGAGTGTCTTCACTGGATGGAAT 830  
 DB 721 CTATCTGGGTTTGGCACTTTGTTCAATTAACCAAAAAGAGTGTCTTCACTGGATGGAAT 780  
 QY 831 TCAGTTTCTGGCATATTTATGAGAACTACCAAAATTAATGCTTAAATTTTCAATTTGCT 890  
 DB 781 TCAGTTTCTGGCATATTTATGAGAACTACCAAAATTAATGCTTAAATTTTCAATTTGCT 840  
 QY 891 ACCT-CTTTTTTATTAATGCTTGGAAAT-GGTTCACTTAAATGACATTTTAAATAATGTT 948  
 DB 841 ACCTCTTTTTTATTAATGAGCCCTGGAGATGGGTTCACTTAAAGACATTTTAAATAATGTT 900  
 QY 949 ATGATATATCTGATGAGAAAGCAAGCTTA 979  
 DB 901 TATGAAATATCTCGGAATGAAAAAGGCAAA 931

RESULT 13  
 LOCUS B1763295 903 bp mRNA linear EST 25-SEP-2001  
 DEFINITION 603047656P1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5188069 5',  
 mRNA sequence.  
 ACCESSION B1763295  
 VERSION B1763295.1 GI:15754873  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 903)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLNL1469 row: 0 column: 14  
 High quality sequence stop: 875.

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 /db\_xref="taxon:9606"

ORIGIN  
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 Best Local Similarity 96.4%; Pred.No. 2.8e-164;  
 Matches 855; Conservative 0; Mismatches 29; Indels 3; Gaps 2;  
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 /clone\_id="NIH\_MGC\_116"  
 /note="Organ: pooled colon, kidney, stomach; Vector:  
 pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 3 clones, age 26 yo male, 49 yo  
 female, 71 yo male colon; 46 yo male kidney, and pool of 2  
 stomachs, 62 yo male and 70 yo female. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.4 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 023. Note: this is a NIH\_MGC Library."

QY 362 GGTACACCTGGATCCAGTCCGATGATTTAAAGGAAAGGGGATGTCTGAG 421  
 DB 1 GGTACACCTGGATCCAGTCCGATGATTTAAAGGAAAGGGGATGTCTGAG 60  
 QY 422 GAAAAGCTTTGAGAGTCTGAGACCCCACTACAGCAGTTCATGAGTTCATGGA 481  
 DB 61 GAAAAGCTTTGAGAGTCTGAGACCCCACTACAGCAGTTCATGAGTTCATGGA 120  
 QY 482 TTATGCAATATCTTGGAAAATTTGGAGTGTACATTTACAAAGATGCTCAATAG 541  
 DB 121 TTATGCAATATCTTGGAAAATTTGGAGTGTACATTTACAAAGATGCTCAATAG 180  
 QY 542 TGCCTAAGAGTCTTTGTCAGTGTGCTCACTTGGCTTAAATGCAAGAAATGCAATGCTGTCA 601  
 DB 181 TGCCTAAGAGTCTTTGTCAGTGTGCTCACTTGGCTTAAATGCAAGAAATGCAATGCTGTCA 240  
 QY 602 GCGTGTGATTTCACTCAATGAGCTGATGTTCAGACCTCTTCCCATGGAAGCTAT 661  
 DB 241 GCGTGTGATTTCACTCAATGAGCTGATGTTCAGACCTCTTCCCATGGAAGCTAT 300  
 QY 662 AATTTATTTGGAACCAAGAAAGCCCTGAATGAAATTCACAAATTAATTAATTCATGCACTTC 721  
 DB 301 AATTTATTTGGAACCAAGAAAGCCCTGAATGAAATTCACAAATTAATTAATTCATGCACTTC 360  
 QY 722 TTCTGTGGAAGACCTTTGTAAGAAATGTGTGCTGATTAAGTGAAGTGTGATCTGGGT 781  
 DB 361 TTCTGTGGAAGACCTTTGTAAGAAATGTGTGCTGATTAAGTGAAGTGTGATCTGGGT 420  
 QY 782 TGGCACTTGTTCAGATTAACCAAGAGATGCTTCACTGATGATGATTCAGTTCCTG 841  
 DB 421 TGGCACTTGTTCAGATTAACCAAGAGATGCTTCACTGATGATGATTCAGTTCCTG 480  
 QY 842 CATCATTAATGGAAGACTTACCAAAATTAATGCTTAAATTTTCAATTTGCTACCTCTTTT 901  
 DB 481 CATCATTAATGGAAGACTTACCAAAATTAATGCTTAAATTTTCAATTTGCTACCTCTTTT 540  
 QY 902 TATATGCTTGAATGCTTCACTTAATGACATTTTAAATAGTTTATGATTAATCATG 961  
 DB 541 TATATGCTTGAATGCTTCACTTAATGACATTTTAAATAGTTTATGATTAATCATG 600  
 QY 962 AATGAAAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTCACACTGTTTTTAA 1021  
 DB 601 AATGAAAAGCAAGCTTAATATGTTTACAGACCAAGTGTGATTCACACTGTTTTTAA 660  
 QY 1022 TCTAGCATTTTCAATTTGCTTAAATCAAAAGTGTTCATTA-TTTTTTTAAAGTGT 1080  
 DB 661 TCTAGCATTTTCAATTTGCTTAAATCAAAAGTGTTCATTA-TTTTTTTAAAGTGT 720  
 QY 1081 AGAATCTTCTCATAGTCACTTCTCAACTAATTTGGAATATGTTGAGTCT 1140  
 DB 721 AGAATCTTCTCATAGTCACTTCTCTCAACTAATTTTGAATATGTTGAGTCT 780  
 QY 1141 TTTGTTTTTCTCTAGTATAGCATTTTAAAAAATATTAAGCTACCAATCTTTGTAC 1200

Dd	781	TTAG--TTATCTCTTAGTATGCAATTTTAAATAAATTAAAGTACCACATCTTCGCAC	838
Oy	1201	AATTTGTAAATGTTAAGAAATTTTTTAAATCTGTTAAATAAAAATT	1247
Dd	839	AATTTGTATGTTAAGAATTTTTTAAATATCTGTTAATAAATTAATTT	885
RESULT 14			
AL544722			
LOCUS	827 bp	mRNA	linear EST 25-MAR-2004
DEFINITION	AL544722 Homo sapiens PLACENTA COT 25-NORMALIZED	Homo sapiens CDNA	
VERSION	clone CSOD1022YF04 5-PRIME, mRNA sequence.		
KEYWORDS	AL544722.3 GI:45745219		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 827)		
JOURNAL	L.I.W.B., Gruber,C., Jeesee,J. and Polayes,D.		
COMMENT	Full-length cDNA libraries and normalization Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:3126563. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4941.f For more information about this cluster, see <a href="http://www.genoscope.cns.fr/cdna?ts=CSOD1022DCO2QP1&amp;c=4941.f">http://www.genoscope.cns.fr/cdna?ts=CSOD1022DCO2QP1&amp;c=4941.f</a> .		
FEATURES			
Source	Location/Qualifiers		
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	/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
ORIGIN			
Query Match	64.5%	Score 811.2; DB 1; Length 827;	
Best Local Similarity	99.5%	Pred. No. 2e-163;	
Matches	824; Conservative	0; Mismatches 3; Indels 1; Gaps 1;	
Oy	69	GACGCTGACCAAGTTCTCTCTCGGTCTCTCCGCTTCAGACTGCCGGCAGC	128
Dd	1	GATGCTGACCAAGTTCTCTCTCGGTCTCTCCGCTTCAGACTGCCGGCAGC	60
Oy	129	CCGGGAGCGATGCGAACCCCAAGGCCCCCGCTTCCTCCGACAGGGCTCCGGGCTCTG	188
Dd	61	CCGGGAGCGATGCGAACCCCAAGGCCCCCGCTTCCTCCGACAGGGCTCCGGGCTCTG	120
Oy	189	CTGCTCTCTGCTGCTGACGTGCGCGCGCGCGCTGACGCGCTGGAATCCCAAGGGAG	248
Dd	121	CTGCTCTCTGCTGCTGACGTGCGCGCGCGCGCTGGAATCCCAAGGGAG	180
Oy	249	CAAAAGCGCAGCTCCGACAGAGGAGGTGTGA(CTGTATATGATGTGCTTACA	308
Dd	181	CAAAAGCGCAG-TCGGCAGAGGAGGTGTGTGA(CTGTATATGATGTGCTTACA	239
Oy	309	GGGCGAGAGAGTGCTGTGTGAGAGCGGAGCCTGGGCGCAATGTTATTCGGGATCA	368

Db	Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	240	GGGCGACAGAGAGTGCCTGGTCCAGACGGGAGCCCTG366GCAATGGCATTCGCGGTACA	299							
Qy	369	CTGGGATCCCAAGTCCGGATGGATTTAAAGAGAGAAAAGGCGAAATGTCTGAGGAAAAGC	428							
Db	300	CTGGGATCCCAAGTCCGGATGGATTTAAAGAGAGAAAAGGCGAAATGTCTGAGGAAAAGC	359							
Qy	429	TTTGGAGAGTCTGGGACCACTACACAGAGGTTTCATGAGGTTCAATTAATATGAC	488							
Db	360	TTTGGAGAGTCTGGGACCACTACACAGAGGTTTCATGAGGTTCAATTAATATGAC	419							
Qy	489	ATAGATCTTGGGAAAATTTGGCGAGTGTACATTTACAAAAGATGCGTTCAAAATAGTCTCA	548							
Db	420	ATAGATCTTGGGAAAATTTGGCGAGTGTACATTTACAAAAGATGCGTTCAAAATAGTCTCA	479							
Qy	549	AGAGTTTGTTCAGTGGCTCACTTCGCGTAAATGCGAAATGCACTGCTGACGCTTGG	608							
Db	480	AGAGTTTGTTCAGTGGCTCACTTCGCGTAAATGCGAAATGCACTGCTGACGCTTGG	539							
Qy	609	TATTTCACTTCAATGAGCTGAATGTTTCAGAGCTCTTCCCATTTGAAGCATATATAT	668							
Db	540	TATTTCACTTCAATGAGCTGAATGTTTCAGAGCTCTTCCCATTTGAAGCATATATAT	599							
Qy	669	TTGGACCAAGAGAGCCCTGAAATGAATTTCAACATTAATTTCAATGCACTTCTTGTG	728							
Db	600	TTGGACCAAGAGAGCCCTGAAATGAATTTCAACATTAATTTCAATGCACTTCTTGTG	659							
Qy	729	GAAGACTTTGTGAGGAATTTGTGCTGATTTAGTGAGATTTGCTATCTGGGTTGGCACT	788							
Db	660	GAAGACTTTGTGAGGAATTTGTGCTGATTTAGTGAGATTTGCTATCTGGGTTGGCACT	719							
Qy	789	TGTTCAATTAACCAAAAGAGATGCTTTCACTGAGATGGAATTCAGTTTCTCGATCAT	848							
Db	720	TGTTCAATTAACCAAAAGAGATGCTTTCACTGAGATGGAATTCAGTTTCTCGATCAT	779							
Qy	849	ATTGAAGACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCT	896							
Db	780	ATTGAAGACTACCAAAATTAATGCTTTAATTTTCATTTGCTACCTCT	827							
RESULT 15										
LOCUS	BO425266	851 bp	mRNA	linear	EST 23-MAY-2002					
DEFINITION	AGENCOURT_7912803 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6150166									
ACCESSION	BO425266									
VERSION	BO425266.1	GI:21120581								
KEYWORDS	EST.									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.									
AUTHORS	1 (bases 1 to 851)									
TITLE	NIH-MGC http://mgs.nci.nih.gov/.									
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)									
COMMENT	Unpublished (1999)									
	Contact: Robert Strausberg, Ph.D.									
	Email: cgaabs-remail.nih.gov									
	Tissue Procurement: ATCC/DCTP/DMP									
	CDNA Library Preparation: Life Technologies, Inc.									
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)									
	DNA Sequencing by: Agencourt Bioscience Corporation									
	Clone distribution: MGC clone distribution information can be									
	found through the I.M.A.G.E. Consortium/LNLN at:									
	http://image.llnl.gov									
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	Location/Qualifiers									
	1..851									
FEATURES	/organism="Homo sapiens"									



/lab\_host="DH10B (phage-resistant)"  
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/note="Organ: skin; Vector: PCMV-SPORT6; Site: 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2 kb. Library constructed by Life  
Technologies."

## ORIGIN

Query Match 58.8%; Score 739.4; DB 5; Length 851;  
Best Local Similarity 99.1%; Pred. No. 5.2e-148;  
Matches 754; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 6 GAGGGCGCGGGTGAAGGCGCATGATGACGCTCCGGCGGCTTGAGCGCGGAG 65  
DB 36 GAGGGCGCGGGTGAAGGCGCATGATGACGCTCCGGCGGCTTGAGCGCGGAG 95  
QY 66 CCAGACGCTGACCAAGTCTCTCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 125  
DB 96 CCAGACGCTGACCAAGTCTCTCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 155  
QY 126 CAGCGGAGGAGCCGAGCCGAGGAGCCGCGGCTCCGCGAGCGGCTCCGCGGCT 185  
DB 156 CAGCGGAGGAGCCGAGCCGAGGAGCCGCGGCTCCGCGAGCGGCTCCGCGGCT 215  
QY 186 CTGCTGCTCTGCTGCTGAGCTGCGCGGCTGAGCGGCTTGAGTCCGCAAGG 245  
DB 216 CTGCTGCTCTGCTGCTGAGCTGCGCGGCTGAGCGGCTTGAGTCCGCAAGG 275  
QY 246 AAGCAAAAGGCGCAGCTCCGCGAGAGAGAGTGTGAGCCTGTATATGAATGCTTA 305  
DB 276 AAGCAAAAGGCGCAGCTCCGCGAGAGAGAGTGTGAGCCTGTATATGAATGCTTA 335  
QY 306 CAGGCGCAGCAGAGTGCCTGCTGAGACGAGAGCCTGGGCGCAATGTATTCGGGT 365  
DB 336 CAGGCGCAGCAGAGTGCCTGCTGAGACGAGAGCCTGGGCGCAATGTATTCGGGT 395  
QY 366 ACACCTGGGATCCAGAGTCCGAGTGAATTCAAAGAGAAAGGGGAAATGCTTGGGAA 425  
DB 396 ACACCTGGGATCCAGAGTCCGAGTGAATTCAAAGAGAAAGGGGAAATGCTTGGGAA 455  
QY 426 AGCTTTGAGAGTCTTGAGCAACCACTACAGAGTGTTCATGAGTTCATTAATAT 485  
DB 456 AGCTTTGAGAGTCTTGAGCAACCACTACAGAGTGTTCATGAGTTCATTAATAT 515  
QY 486 GGCATGATCTTTGGAAATTCGAGAGTGTACATTTACAAAGATCGTTCAATATGCT 545  
DB 516 GGCATGATCTTTGGAAATTCGAGAGTGTACATTTACAAAGATCGTTCAATATGCT 575  
QY 546 CTAAGAGTTTGTTCAGTGGCTCACTCGGCTAAATGAGAAATGAGTGTGAGGCT 605  
DB 576 CTAAGAGTTTGTTCAGTGGCTCACTCGGCTAAATGAGAAATGAGTGTGAGGCT 635  
QY 606 TGTATTTACATTCATGAGCTGAATGTTTCAAGACCTCTCCATGAGCTATTAAT 665  
DB 636 TGTATTTACATTCATGAGCTGAATGTTTCAAGACCTCTCCATGAGCTATTAAT 695  
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DB 696 TATTTGACCAAGAGAGCTTGAATGAATTAATTAATTAATTAATTAATTAAT 755  
QY 726 GTGAGAGAGCTTTGTG--AAGAAATGTGCTGATTAAGTG 765  
DB 756 GTGAGAGAGCTTTGTGAGAAAGAAATTTGTGCTGATTAATTTG 796

RESULT 16  
AY399084  
LOCUS  
DEFINITION Homo sapiens CTRH1 gene, VIRUTAL TRANSCRIPT, partial sequence,  
AY399084  
ACCESSION  
VERSION  
KEYWORDS  
GSS.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
- AUTHORS  
1 (bases 1 to 732)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, D.J.,  
Adams, M.D. and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
2 (bases 1 to 732)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, D.J.,  
Adams, M.D. and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)

TITLE  
JOURNAL  
COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
Location/Qualifiers

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/gene="CTHRC1"  
/locus\_tag="HCM0106"

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Query Match 57.9%; Score 727.2; DB 9; Length 732;  
Best Local Similarity 99.6%; Pred. No. 2.1e-145;  
Matches 729; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 138 ATGCGACCCGAGGAGCCCGCGCTCCGCGAGGAGTCCGCGGCTCTGCTGCTCTG 197  
DB 1 ATGCGACCCGAGGAGCCCGCGCTCCGCGAGGAGTCCGCGGCTCTGCTGCTCTG 60  
QY 198 CTGCTGAGAGTCCCGGCGCGCTGAGAGCTCTGAGATCCGCAAGGAGAAAGGCG 257  
DB 61 CTGCTGAGAGTCCCGGCGCGCTGAGAGCTCTGAGATCCGCAAGGAGAAAGGCG 120  
QY 258 CAGCTCCGCGAGAGAGTGTGAGCCTGTATATGAATGTGCTTACAGGCGCAGCA 317  
DB 121 CAGCTCCGCGAGAGAGTGTGAGCCTGTATATGAATGTGCTTACAGGCGCAGCA 180  
QY 318 GGAAGTCCGTGTCGAGACGAGAGCCCTGGGCGCAATGTATTCGCGGTACACTGGAGTC 377  
DB 181 GGAAGTCCGTGTCGAGACGAGAGCCCTGGGCGCAATGTATTCGCGGTACACTGGAGTC 240  
QY 378 CCAGTGGGAGTGTATTCAAAGAGAAAGGGGAAATGTCTGAGGAAAGCTTTGAGAG 437  
DB 241 CCAGTGGGAGTGTATTCAAAGAGAAAGGGGAAATGTCTGAGGAAAGCTTTGAGAG 300  
QY 438 TCTGACACCACTACAGAGTGTTCATGAGTTCATGAAATTAATGAGCATTAATCTT 497  
DB 301 TCTGACACCACTACAGAGTGTTCATGAGTTCATGAAATTAATGAGCATTAATCTT 360  
QY 498 GGGAAATTTGGAGTGTATTCATTAAGAGATCGTTCAATATGCTCTTAAGAGTTTG 557  
DB 361 GGGAAATTTGGAGTGTATTCATTAAGAGATCGTTCAATATGCTCTTAAGAGTTTG 420  
QY 558 TTCAGTGGCTCACTGGGCTAAATGAGAAATGAGTGTCTGAGGTTGGATTTTACA 617  
DB 421 TTCAGTGGCTCACTGGGCTAAATGAGAAATGAGTGTCTGAGGTTGGATTTTACA 480  
QY 618 TTCATGAGAGTGAATGTTGAGAGCTCTTCCATTTGAAGTATTAATTTATTTGACCA 677  
DB 481 TTCATGAGAGTGAATGTTGAGAGCTCTTCCATTTGAAGTATTAATTTATTTGACCA 540



QY 678 GGAAGCCCTGAATGAATCAACAATTAATTCATCGACTTCTGTGAGAGACTT 737  
DB 541 GGAAGCCCTGAATGAATCAACAATTAATTCATCGACTTCTGTGAGAGACTT 600  
QY 738 TGTGAAGGAATGTGCTGATTAATGATGATGATGATGATGATGATGATGAT 797  
DB 601 TGTGAAGGAATGTGCTGATTAATGATGATGATGATGATGATGATGATGAT 660  
QY 798 TACCCAAAGAGAGAGCTTCTACTGATGATGATGATGATGATGATGATGAT 857  
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QY 858 CTACCAAAATAA 869  
DB 721 CTACCAAAATAA 732

RESULT 17  
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LOCUS AGENCOURT\_7902947 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6157844  
DEFINITION 5', mRNA sequence.  
ACCESSION BQ425098  
VERSION BQ425098.1 GI:21120413  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 922)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC/DC/DTP  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL1504 row: f column: 21  
High quality sequence stop: 714.  
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2 kb. Library constructed by Life  
Technologies."

ORIGIN  
Query Match 57.0%; Score 716.4; DB 5; Length 922;  
Best Local Similarity 89.4%; Pred. No. 4.5e-143;  
Matches 816; Conservative 0; Mismatches 92; Indels 5; Gaps 4;

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QY 205 AGCTGCCCCGCGCTGAGCGCTCTGAGATCCCAAGGAGGAAAGAGGCGAGCTCC 264  
DB 190 AGCTGCCCCGCGCTGAGCGCTCTGAGATCCCAAGGAGGAAAGAGGCGAGCTCC 249  
QY 265 GGCAGAGGAGGTGTGACCTGTAAATGAAATGTGCTTACAGAGGCCAGAGAGTGC 324  
DB 250 GGCAGAGGAGGTGTGACCTGTAAATGAAATGTGCTTACAGAGGCCAGAGAGTGC 309  
QY 325 CTGTGTGAGACGGAGACCTTGCGGCGCAATGTATTTCGCGGATACCTGGAGTCCAGTGC 384  
DB 310 CTGTGTGAGACGGAGACCTTGCGGCGCAATGTATTTCGCGGATACCTGGAGTCCAGTGC 369  
QY 385 GGGATGATTCAAAGAGAAAGGGGGAATGTCTAGAGGAAAGCTTGAAGATCTGTGA 444  
DB 370 GGGATGATTCAAAGAGAAAGGGGGAATGTCTAGAGGAAAGCTTGAAGATCTGTGA 429  
QY 445 CACCAACTACAAGACAGTGTTCATGAGATTCATTAATTAATGACATAGATCTTGGGAAA 504  
DB 430 CACCAACTACAAGACAGTGTTCATGAGATTCATTAATTAATGACATAGATCTTGGGAAA 489  
QY 505 TTGCGAGGTGACATTTACAAAGATGCTTCAATATGCTCTAAGAGTTTGTTCAGTG 564  
DB 490 TTGCGAGGTGACATTTACAAAGATGCTTCAATATGCTCTAAGAGTTTGTTCAGTG 549  
QY 565 GCTCACTCGGCTAAAGTCAAGAAATGCAATGCTGACGCTGATTTACATTCATG 624  
DB 550 GCTCACTCGGCTAAAGTCAAGAAATGCAATGCTGACGCTGATTTACATTCATG 609  
QY 625 GAGCTGAATGTCACAGACCTCTCCCATTAAGCTAATTAATTTGACCAAGAGGCC 684  
DB 610 GAGCTGAATGTCACAGACCTCTCCCATTAAGCTAATTAATTTGACCAAGAGGCC 669  
QY 685 CTGAATGATTAACAATTAATTAATTCATGCACTT-CTTCTGTGAGAGACTTGTG-A 742  
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QY 743 AGGAATGTGTGT-AGATTAGTGATGTTC--TATCTGGTGTGCACTTGTTCAGATTA 799  
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QY 800 CCCAAAGAGAGTGTCTACTGATGAGATTCAGTGTCTGCGATCATTAATGAAGACT 859  
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QY 860 ACCAAATTAATGCTTAATTTCAATTGCTACCTCTTTTATTAATGCTTGAAGTG 919  
DB 850 TTGGAAGAACTAACCAAAATTAATTAATGCTTAATTTTTCATTTGCTGACCTTGA 909  
QY 920 TTCACTTAATGA 932  
DB 910 TTCTTTGAATTA 922

RESULT 18  
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LOCUS Pan troglodytes CTRC1 gene, VIRUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY399085  
VERSION AY399085.1 GI:39755074  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
REFERENCE 1 (bases 1 to 732)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,  
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.D.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

JOURNAL Science 302 (5652), 1960-1963 (2003)  
 REFERENCE 14671302  
 AUTHORS 2 (bases 1 to 732)  
 Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,  
 Todd, M.A., Tanenbaum, D.W., Civallo, D.R., Lu, F., Murphy, B.,  
 Ferritera, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J.,  
 Adams, M.D. and Cargill, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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 Query Match 56.8%; Score 714.4; DB 9; Length 732;  
 Best Local Similarity 98.1%; Pred. No. 1.2e-142;  
 Matches 718; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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1 ATGCACCCCAAGGAGGCGCCGCTCCCGCAGCGGCTCCGCGGCTCCGCTGCTCCG 60
198 CTGCTGACGCTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGAGGAGGAGCG 257
61 CTGCTGACGCTGCGCGCGCGCTGAGCGCTCTGAGATCCCAAGGAGGAGGAGCG 120
258 CAGCTCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 317
121 CAGCTCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
318 GAGATGCTGCTGAGAGCGGAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 377
181 GAGATGCTGCTGAGAGCGGAGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
378 CCAGGTCGGAGTGCATTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
241 CCAGGTCGGAGTGCATTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
438 TCCTGACACCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 497
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498 GGAAGAAATGGGAGAGTACATTTACAAAGATGCTTAAAGATGCTTAAAGATTTG 557
361 GGAAGAAATGGGAGAGTACATTTACAAAGATGCTTAAAGATGCTTAAAGATTTG 420
558 TTGAGTGGCTACTTCCGCTAAATGCGAAATGATGCTGACGCTGCTGATTTTCA 617
421 TTGAGTGGCTACTTCCGCTAAATGCGAAATGATGCTGACGCTGCTGATTTTCA 480
618 TTCAATGAGAGTGAATGTTGAGAGCTCTTCCCATTTGAAGTATTAATTATTTGA 677
481 TTCAATGAGAGTGAATGTTGAGAGCTCTTCCCATTTGAAGTATTAATTATTTGA 540
678 GGAAGCCCTGAATGAATTAACAATTAAATTCACGACCTCTTCTGAGAGAGAGCT 737
541 GGAAGCCCTGAATGAATTAACAATTAAATTCACGACCTCTTCTGAGAGAGAGCT 600
738 TGTGAAGAATTTGCTGCTGAGATTAGTGAATGCTGATCTGAGGAGGAGCTTTG 797
601 TGTGAAGAATTTGCTGCTGAGATTAGTGAATGCTGATCTGAGGAGGAGCTTTG 660
798 TACCAAGAGAGATGCTTCTACTGATGAGATTCAGTTTCTCGATATTAATTGAAGA 857

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Db 661 TACCAAGAGAGATGCTTCTACTGATGAGATTCAGTTTCTCGATATTAATTGAAGA 720  
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 Db 721 CTACCAAAATTA 732

RESULT 19  
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 LOCUS  
 DEFINITION  
 BM915926 1037 bp mRNA linear EST 12-MAR-2002  
 AGENCOURT 6639781 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:5482196  
 5', mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE  
 1 (bases 1 to 1037)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: csapbs-remail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 CDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 http://image.llnl.gov  
 Plate: L1CM2007 row: n column: 21  
 High quality sequence stop: 482.

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 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
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 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCCGAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC Library."

ORIGIN  
 Query Match 56.1%; Score 705.4; DB 4; Length 1037;  
 Best Local Similarity 91.7%; Pred. No. 1.1e-140;  
 Matches 791; Conservative 0; Mismatches 66; Indels 6; Gaps 4;

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61 CCGGCTGCGCGGAGCGGAGCGATGACACCCAGAGGCCCGCGCTCCCGGAGCG 120
173 GCTCGGCGGCTCTGCTGCTCTGCTGCTGAGCTGCGCGCGCTGAGCGCTTGA 232
121 GCTCGGCGGCTCTGCTGCTCTGCTGCTGAGCTGCGCGCGCTGAGCGCTTGA 180
233 GATCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 292
181 GATCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

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SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 747)  
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 TITLE Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Steven Gicellis/ Rush Presbyterian, Dept. of Orthopedics  
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 The following repetitive elements were found in this CDNA sequence: 1-60, >AT rich#Low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
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 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP Ch1"  
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Ch1 is a cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldi, Lemon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TAGTACGCGT.  
 TAG\_TISSUE=grade-2-chondrosarcoma  
 TAG\_LIB=UI-H-E20  
 TAG\_SEQ=ATCTAATATG"

ORIGIN  
 Query Match 55.7%; Score 700.4; DB 6; Length 747;  
 Best Local Similarity 98.9%; Pred. No. 1.2e-139;  
 Matches 716; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

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 654 GAAAGCTAATTTATTTGAGCAAGAAAGCCCTGAATGAATTCATTAATTAATTCAT 713  
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 564 CGAGCTCTCTCTGGAAGAGCTTTGTAAGAAATGCTGCTGATTAAGAGAGTGGCT 505  
 774 ATCTGGGTGGAGCTTGTTCAGATTACCAAGAGAGAGTGTCTTACATGATGAATTC 833

Db 504 ATCTGGGTGGAGCTTGTTCAGATTACCAAGAGAGAGTGTCTTACATGATGAATTC 445  
 Qy 834 GTTTCCTGCATCATTTATGGAAGAACTACCAAAATPAAATGCTTTAATTTGATGAC 893  
 Db 444 GTTTCCTGCATCATTTATGGAAGAACTACCAAAATPAAATGCTTTAATTTGATGAC 385  
 Qy 894 TCTTTTATTTATGAGCTTGAAGAGTTCATTAAGACATTTAATTAAGTTATGTA 953  
 Db 384 TCTTTTATTTATGAGCTTGAAGAGTTCATTAAGACATTTAATTAAGTTATGTA 325  
 Qy 954 TACATCTGAATGAAGAAAGCAAGCTAATATGTTTACAGACCAAGTGTGATTCACACTG 1013  
 Db 324 TACATCTGAATGAAGAAAGCAAGCTAATATGTTTACAGACCAAGTGTGATTCACACTG 255  
 Qy 1014 TTTTAAATCTGACATTTATTTATTTGCTTCATCAAAAGTGTTCATATTTTATTA 1073  
 Db 264 TTTTAAATCTGACATTTATTTATTTGCTTCATCAAAAGTGTTCATATTTTATTA 205  
 Qy 1074 GTTGTGGAATGACCTTCTTCATGACATTCCTGACCTAATTTGGAATATTTGTT 1133  
 Db 204 GTTGTGGAATGACCTTCTTCATGACATTCCTGACCTAATTTGGAATATTTGTT 145  
 Qy 1134 GTGCTCTTTGTTTTCTCTTACATGACATTTTAAATTAATTAAGCTACCAATC 1193  
 Db 144 GTGCTCTTTGTTTTCTCTTACATGACATTTTAAATTAATTAAGCTACCAATC 85  
 Qy 1194 TTTGACATTTGTTAAATGTTAAATTTTATTTATCTGTTAATTAATTAATTTTCC 1253  
 Db 84 TTTGACATTTGTTAAATGTTAAATTTTATTTATCTGTTAATTAATTAATTTTCC 25  
 Qy 1254 AACA 1257  
 Db 24 AACA 21

RESULT 22  
 BQ008675/c 796 bp mRNA linear EST 26-MAR-2002  
 DEFINITION UI-H-E10-ay1-c-24-0-UI.s1 NCI CGAP\_E10 Homo sapiens cDNA clone  
 IMAGE:5840207 3, mRNA sequence.  
 BQ008675  
 BQ008675.1 GI:19733576  
 EST.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 796)  
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 TITLE Unpublished (1997)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: <http://image.llnl.gov>  
 The following repetitive elements were found in this CDNA sequence: 24-57, >AT rich#Low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
 SOURCE  
 1..796  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5840207"  
 /tissue\_type="Chondrosarcoma"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"

/clone\_1lb="NCI CGAP E10"  
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)  
 with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
 NCI CGAP E10 is a cDNA library containing the following  
 tissue(s): Chondrosarcoma. The library was constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into pT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tag for this library is AACTTGCAC.  
 TAG TISSUE=Chondrosarcoma  
 TAG\_LIB=UT-H-E10  
 TAG\_SEQ=AACTTGCAC"

## ORIGIN

Query Match 55.3%; Score 695.6; DB 5; Length 796;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-138;  
 Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 GCTCACTTGGCTAAATGCAAAATGCAATGCTGTCAGCGTTGTAATTCACATTCAGT 624  
 DB 710 GCTCACTTGGCTAAATGCAAAATGCAATGCTGTCAGCGTTGTAATTCACATTCAGT 651  
 QY 625 GAGCTGAATGTCAGAGCTCTTCCCATGAACTAATTAATTTGAGCAAGAGGCC 684  
 DB 650 GAGCTGAATGTCAGAGCTCTTCCCATGAACTAATTAATTTGAGCAAGAGGCC 591  
 QY 685 CTGAATGTAATCAACAATTAATTAATTCATGCACTCTCTGGAAGAGCACTTGGAG 744  
 DB 590 CTGAATGTAATCAACAATTAATTAATTCATGCACTCTCTGGAAGAGCACTTGGAG 531  
 QY 745 GAATGTCGTCGATTAATGATGATGCTATCTGCTGAGCTTGTTCAGATTCACCA 804  
 DB 530 GAATGTCGTCGATTAATGATGATGCTATCTGCTGAGCTTGTTCAGATTCACCA 471  
 QY 805 AAGGAGATGCTTCTACTGATGGAATTCAGTTCTGCACTATTAATGAAGACTACCA 864  
 DB 470 AAGGAGATGCTTCTACTGATGGAATTCAGTTCTGCACTATTAATGAAGACTACCA 411  
 QY 865 AATAATGCTTAATTTGATTTGCTACTCTTTTATTAATGCTTGAATGCTTGC 924  
 DB 410 AATAATGCTTAATTTGATTTGCTACTCTTTTATTAATGCTTGAATGCTTGC 351  
 QY 925 TTAATGACATTTAAATAGTTAATGATTAATCATCTGAATGAAGCAAGCTAAATATG 984  
 DB 350 TTAATGACATTTAAATAGTTAATGATTAATCATCTGAATGAAGCAAGCTAAATATG 291  
 QY 985 TTTACAGACCAAGTGTGATTTACACAGTGTTTTAAATCTAGACATTAATTTGCTTC 1044  
 DB 290 TTTACAGACCAAGTGTGATTTACACAGTGTTTTAAATCTAGACATTAATTTGCTTC 231  
 QY 1045 AATCAAAAGTGTTCATTAATTTTGTGTTGTTAGAAATCTTCTTCANAGTCACT 1104  
 DB 230 AATCAAAAGTGTTCATTAATTTTGTGTTGTTAGAAATCTTCTTCANAGTCACT 171  
 QY 1105 TCTCTCAACCTTAATTTGGAATATGTTGGTCTTTTGTGTTTCTCTAGTATAGA 1164  
 DB 170 TCTCTCAACCTTAATTTGGAATATGTTGGTCTTTTGTGTTTCTCTAGTATAGA 111  
 QY 1165 TTTTAAAAAATATTAAGTACCAATCTTTGTACATTTGTAATGTTAAAGAAATTTT 1224  
 DB 110 TTTTAAAAAATATTAAGTACCAATCTTTGTACATTTGTAATGTTAAAGAAATTTT 51  
 QY 1225 TTTATATCTGTAATTAATTAATTTATTTCAACA 1257  
 DB 50 TTTATATCTGTAATTAATTAATTTATTTCAACA 18

RESULT 23

EX114800  
 LOCUS 734 bp mRNA linear EST 07-FEB-2003  
 DEFINITION BX114800 Soares NhhMPu\_S1 Homo sapiens cDNA clone IMAGE753428 ;  
 IMAGE:753428, mRNA sequence.  
 ACCESSION BX114800  
 VERSION BX114800.1 GI:27879811  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 734)  
 Ebert, L., Hell, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
 Radloff, U., Schneider, D. and Korn, B.  
 Human Unigeneset - RZPD3  
 TITLE Unpublished (2003)  
 JOURNAL  
 COMMENT RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD: IMAGE998F211852.  
 RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/CloneCards/cgi-  
 bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 ML3r, Primer sequence: TTTCAACAGCAAGAACGTATGAC.

## FEATURES

source

1..734  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE998F211852 ; IMAGE:753428"  
 /tissue\_type="Pooled human melanocyte, fetal heart, and  
 pregnant uterus"  
 /lab\_host="DH10B"  
 /clone\_1lb="Soares NhhMPu\_S1"  
 /note="Organ: mixed (see below); Vector: pT73D-Pac  
 (Pharmacia) with a modified polylinker; Site\_1: Not I;  
 Site\_2: Eco RI; Equal amounts of plasmid DNA from three  
 normalized libraries (melanocyte 2NbH, pregnant uterus  
 NbHPU, and fetal heart NbH19W) were mixed, and ss circles  
 were made in vitro. Following HAP purification, this DNA  
 was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from pools of  
 5,000 clones made from the same 3 libraries. The pools  
 consisted of I.M.A.G.E. clones 260232-265223,  
 340488-345479, and 484488-489479."

## ORIGIN

Query Match 55.1%; Score 693.2; DB 5; Length 734;  
 Best Local Similarity 98.5%; Pred. No. 4.2e-138;  
 Matches 706; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 540 AGTGTCTAAGAGTTTGTGTCAGTGCCTCACTTGGCTTAAATGAGAAATGATGATCTGT 599  
 DB 1 AGTGTCTAAGAGTTTGTGTCAGTGCCTCACTTGGCTTAAATGAGAAATGATGATCTGT 60  
 QY 600 CAGCGTGTGATTTTCACTTCAATGAGCTGAATGTTGAGACCTCTTCCCATTAAGCT 659  
 DB 61 CAGCGTGTGATTTTCACTTCAATGAGCTGAATGTTGAGACCTCTTCCCATTAAGCT 120  
 QY 660 AATAATTTATTTGAGCAAGAGCCCTGAATGATTTCAACAATTAATTAATTTGCACT 719  
 DB 121 AATAATTTATTTGAGCAAGAGCCCTGAATGATTTCAACAATTAATTAATTTGCACT 180  
 QY 720 TCTTCTGGAAGAGCTTGTGAAGAAATGGTGTGATTAATGATTTGATTTGCTATCTGG 779

Db 181 TCTCTGTGAGAGACTTGTGAGAGATGTGCTGATTAAGATGATGCTATCTG 240  
QY 780 GTTGGCACTTGTTCAGATTACCCAAAGAGATGCTTACTGATGGAATTCAGTTCT 839  
Db 241 GTTGGCACTTGTTCAGATTACCCAAAGAGATGCTTACTGATGGAATTCAGTTCT 300  
QY 840 CGCATCTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCACTTCTCTTT 899  
Db 301 CGCATCTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTTCACTTCTCTTT 360  
QY 900 TTTATTAATGCTTGAATGCTTCACTTAATGATCACTTTTAATTAATGATTAATCA 959  
Db 361 TTTATTAATGCTTGAATGCTTCACTTAATGATCACTTTTAATTAATGATTAATCA 420  
QY 960 TGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTCACCTGTTT 1019  
Db 421 TGAATGAAGAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTCACCTGTTT 480  
QY 1020 AATCTAGCATTAATTCATTTGCTTCATCAATCAAAAGTGTTCATAA-TTTTTT 1078  
Db 481 AATCTAGCATTAATTCATTTGCTTCATCAATCAAAAGTGTTCATAA-TTTTTT 540  
QY 1079 TTAGAATATCTTTCTTCATAGTCACTTCTCACTTAATTTGAATTTGTTGCT 1138  
Db 541 TTAGAATATCTTTCTTCATAGTCACTTCTCACTTAATTTGAATTTGTTGCT 600  
QY 1139 CTCTGCTTTTCTCTTGTATGATGATTTTAAATTAATTAATTAATTAATTTT 1198  
Db 601 CTCTGCTTTTCTCTTGTATGATGATTTTAAATTAATTAATTAATTAATTTT 660  
QY 1199 ACAATTTGTAATGTTAAGAAATTTTATATCTGTAAATTAATTAATTTTCCAA 1255  
Db 661 ACAATTTGTAATGTTAAGAAATTTTATATCTGTAAATTAATTAATTTTCCA 717

RESULT 24  
CA431413 723 bp mRNA linear EST 07-NOV-2002  
LOCUS  
DEFINITION  
UI-H-FG1-bgp-g-18-0-UI-s1 NCI CGAP FGI Homo sapiens cDNA clone  
UI-H-FG1-bgp-g-18-0-UI 3', mRNA sequence.  
CA431413  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 723)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-rt@mail.nih.gov  
Tissue Procurement: James Martin  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, bento-soares@uiowa.edu  
The following repetitive elements were found in this cDNA  
sequence: 1-57, >AT rich#Low\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
Source  
Location/Qualifiers  
1..723  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FG1-bgp-g-18-0-UI"  
/tissue\_type="Cell lines"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP FGI"  
/note="Organ: Enchondroma; Vector: pT73-Pac (Pharmacia)  
with a modified polylinker; Site 1: EcoR 1; Site 2: Not I;  
NCI CGAP FGI is a normalized cDNA library obtained from a  
pool of mRNA from 2 cell lines from Enchondroma tissues.  
The library was constructed according to Bonaldo, Lennon  
and Soares, Genome Research, 6:791-806, 1996. First strand  
cDNA synthesis was primed with an oligo-dT primer  
containing a Not I site. Double stranded cDNA was ligated  
to an EcoR I adaptor, digested with Not I, and cloned  
directionally into pT73-Pac vector. The oligonucleotide  
used to prime the synthesis of first-strand cDNA contains  
a library tag sequence that is located between the Not I  
site and the (dT)18 tail. The sequence tag for this  
library is CGATCAGTC. The cell lines were provided by Dr.  
James Martin from the University of Iowa.  
TAG\_TISSUE=Enchondroma cell line (Max of EN1 and EN2)  
TAG\_LIB=UI-H-FGI  
TAG\_SEQ=CGATCAGTC"

## ORIGIN

Query Match 55.0%; Score 691; DB 6; Length 723;  
Best Local Similarity 99.7%; Pred. No. 1.2e-137; Indels 1; Gaps 1;  
Matches 702; Conservative 0; Mismatches 1;

QY 554 TTTGTCAGTGGCTCACTTGGCTAAATGAGAAATGATGCTGACGTTGTAATTT 613  
Db 720 TTTGTCAGTGG-TCACCTGGCTAAATGAGAAATGATGCTGACGTTGTAATTT 662  
QY 614 CACATTCATAGAGCTGAATGTTGAGACCTCTTCCATGGAAGCTATATTTATTTGA 673  
Db 661 CACATTCATAGAGCTGAATGTTGAGACCTCTTCCATGGAAGCTATATTTATTTGA 602  
QY 674 CCAAGGAAGCCCTGAATGAAATCAACATTAATATTCATGCACTTCTCTGTGAAG 733  
Db 601 CCAAGGAAGCCCTGAATGAAATCAACATTAATATTCATGCACTTCTCTGTGAAG 542  
QY 734 ACTTGTGAGAGAAATGCTGCTGATTAAGTATGATGTTGCTATCTGAGTGGCACTGTT 793  
Db 541 ACTTGTGAGAGAAATGCTGCTGATTAAGTATGATGTTGCTATCTGAGTGGCACTGTT 482  
QY 794 AGATTAACCCAAAGAGAGATGCTTACTGAGATGGAATTCAGTTTCCGATCACTTAAT 853  
Db 481 AGATTAACCCAAAGAGAGATGCTTACTGAGATGGAATTCAGTTTCCGATCACTTAAT 422  
QY 854 AGAATACCAAAATTAATGCTTATTTTCACTTCTCTTTTATTAATGCTTG 913  
Db 421 AGAATACCAAAATTAATGCTTATTTTCACTTCTCTTTTATTAATGCTTG 362  
QY 914 GAATGTCCTAATTAATGATCACTTTTAATTAAGTTATGATCACTGAAATGAAGCAA 973  
Db 361 GAATGTCCTAATTAATGATCACTTTTAATTAAGTTATGATCACTGAAATGAAGCAA 302  
QY 974 AGCTTAATATGTTTACAGACCAAGTGTGATTTACACCTGTTTAAATCTACATTAAT 1033  
Db 301 AGCTTAATATGTTTACAGACCAAGTGTGATTTACACCTGTTTAAATCTACATTAAT 242  
QY 1034 CATTTGCTCAATCAAAAGGTTTCAATATTTTATAGTGTAGATATCTTCTT 1093  
Db 241 CATTTGCTCAATCAAAAGGTTTCAATATTTTATAGTGTAGATATCTTCTT 182  
QY 1094 CATAGTCACATTTCTCAACCTATTAATTTGGAATATTTGTTGCTTTTCTC 1153  
Db 181 CATAGTCACATTTCTCAACCTATTAATTTGGAATATTTGTTGCTTTTCTC 122  
QY 1154 TTAGATATGCAATTTTAAATTAATTAAGCTACCAATCTTGTCAATTTGTAATGT 1213  
Db 121 TTAGATATGCAATTTTAAATTAATTAAGCTACCAATCTTGTCAATTTGTAATGT 62  
QY 1214 TTAGAATTTTATATCTGTAAATTAATTAATTTTCCACA 1257  
Db 61 TTAGAATTTTATATCTGTAAATTAATTAATTTTCCACA 18

RESULT 25  
BQ009009/c 724 bp mRNA linear EST 26-MAR-2002  
LOCUS UI-H-E10-aym-e-16-0-UI.s1 NCI\_CGAP\_E10 Homo sapiens cDNA clone  
DEFINITION IMAGE:5840631.3', mRNA sequence.  
BQ009009  
ACCESSION BQ009009.1 GI:19733903  
VERSION  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 724)  
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. Jose Mercuende  
cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/ILN at: http://image.llnl.gov  
The following repetitive elements were found in this cDNA  
sequence: 30-63, >AI\_Fich#Low\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
1..724  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5840631"  
/tissue\_type="Chondrosarcoma"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI\_CGAP\_E10"  
/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)  
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP E10 is a cDNA library containing the following  
tissue(s): Chondrosarcoma. The library was constructed  
according to Bonaldi, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an EcoR I adaptor, digested  
with Not I, and cloned directionally into pT73-Pac  
vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is ACACTTGAC.  
TAG\_TISSUE=chondrosarcoma  
TAG\_LIB=UI-H-E10  
TAG\_SEQ=ACACTTGAC"

ORIGIN  
Query Match 54.9%; Score 690; DB 5; Length 724;  
Best Local Similarity 99.9%; Pred. No. 2e-137;  
Matches 701; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 556 TGTTCAGTGGCTCACTTGGCTTAATGCGAATGCTGACCGTGTATTTCA 615  
DB 724 TGTTCAGTGGCTCACTTGGCTTAATGCGAATGCTGACCGTGTATTTCA 665  
QY 616 CATTCAATGAGCTGATGTTGAGACCTTCCCATTTGAAGTATATTTTGGACC 675  
DB 664 CATTCAATGAGCTGATGTTGAGACCTTCCCATTTGAAGTATATTTTGGACC 605  
QY 676 AAGGAAGCCCTGAATGAATCAATTATATTCATGCGACTTCTTGTGGAAGAC 735  
DB 604 AAGGAAGCCCTGAATGAATCAATTATATTCATGCGACTTCTTGTGGAAGAC 545

QY 736 TTTTGAAGGAATTTGCTGTGATTAGTGAATGTTGCTATCTGGTGGACATTGTTCA 795  
DB 544 TTTTGAAGGAATTTGCTGTGATTAGTGAATGTTGCTATCTGGTGGACATTGTTCA 485  
QY 796 ATTACCCAAAGAGATGCTTCTACTGATGATGATTCAGTTTCTGCAATCATTTAAGA 855  
DB 484 ATTACCCAAAGAGATGCTTCTACTGATGATGATTCAGTTTCTGCAATCATTTAAGA 425  
QY 856 AACTACCAAAATTAATGCTTTAATTTTCACTTTGCTACTTTTATTAATGCTTGA 915  
DB 424 AACTACCAAAATTAATGCTTTAATTTTCACTTTGCTACTTTTATTAATGCTTGA 366  
QY 916 ATGGTTCCTTTAAATGACATTTAAATAGATTATGATATGATGATGATGATGATGAT 975  
DB 365 ATGGTTCCTTTAAATGACATTTAAATAGATTATGATATGATGATGATGATGATGAT 306  
QY 976 CTAAATATGTTTACAGACCAAGTGTGATTTGACACTGTTTAAATCTAGCATTTATCA 1035  
DB 305 CTAAATATGTTTACAGACCAAGTGTGATTTGACACTGTTTAAATCTAGCATTTATCA 246  
QY 1036 TTTTGTCTTCAATCAAAAGTGTGTTCAATATTTTGTAGTGTGATGATGATGATGAT 1095  
DB 245 TTTTGTCTTCAATCAAAAGTGTGTTCAATATTTTGTAGTGTGATGATGATGATGAT 186  
QY 1096 TGTGACATCTCTCAACCTATTAATTTGGAATATTTGTTGCTTTGTTTCTCTT 1155  
DB 185 TGTGACATCTCTCAACCTATTAATTTGGAATATTTGTTGCTTTGTTTCTCTT 126  
QY 1156 AGTATATGATTTTAAATATTAATTAAGTACCAATCTTTGTAGCAATTTGTAATGTTA 1215  
DB 125 AGTATATGATTTTAAATATTAATTAAGTACCAATCTTTGTAGCAATTTGTAATGTTA 66  
QY 1216 AATAATTTTAAATATCTGTTAATTAATTAATTAATTTTCAACA 1257  
DB 65 AATAATTTTAAATATCTGTTAATTAATTAATTAATTTTCAACA 24

RESULT 26  
CN394776 700 bp mRNA linear EST 16-MAY-2004  
LOCUS CN394776  
DEFINITION 1700042453311 GRN\_EB Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN394776  
VERSION CN394776.1 GI:47382371  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 700)  
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebrowski, J. and Stanton, L.W.  
TITLE Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)  
COMMENT Contact: Brandenberger R  
Regenerative Medicine  
Geeron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geeron.com  
Insert Length: 700 Std Error: 0.00.  
FEATURES  
source  
1..700  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, embryoid bodies  
derived from H1, H7 and H9 cells"  
/clone\_lib="GRN EB"  
/note="Oligo dT primed, full-length enriched cDNA library



## ORIGIN

from embryoid body outgrowths derived from hbs cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

Query Match 54.6%; Score 685.8; DB 7; Length 700;  
Best Local Similarity 99.7%; Pred. No. 1.6e-136;  
Matches 687; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GCGCGCGGTAAGGCGCATTTGATGACGCTGGGCGGCGCTCGAGCGCGCGAGGC 67  
DB 12 GCGCGCGGTAAGGCGCATTTGATGACGCTGGGCGGCGCTCGAGCGCGCGAGGC 71  
QY 68 AGAGCGCTGACCAAGTTCCTCTCGATCTCTCCGCTTCGAGCTCCGCGTCCGCGCA 127  
DB 72 AGAGCGCTGACCAAGTTCCTCTCGATCTCTCCGCTTCGAGCTCCGCGTCCGCGCA 131  
QY 128 GCGCGGACCGATGCGACCCCGAGGCGCGCGCTCCCGCGAGCGGCTCCGCGCTCT 187  
DB 132 GCGCGGACCGATGCGACCCCGAGGCGCGCGCTCCCGCGAGCGGCTCCGCGCTCT 191  
QY 188 GCTGCTCTGCTGCTGACAGCTCCCGCGCGCTCGAGCGGCTTCGAGATCCCGAGGAGAA 247  
DB 192 GCTGCTCTGCTGCTGACAGCTCCCGCGCGCTCGAGCGGCTTCGAGATCCCGAGGAGAA 251  
QY 248 GCAAAAGCGCAGCTCCCGCAGAGGAGGCTGTGAACCTGTATTAATGAAATGTGCTTACA 307  
DB 252 GCAAAAGCGCAGCTCCCGCAGAGGAGGCTGTGAACCTGTATTAATGAAATGTGCTTACA 311  
QY 308 AGGGCGACAGAGGCTGCTGTCGAGACGGGAGCCCTGGGCGCAATGTTATTCGGGCTAC 367  
DB 312 AGGGCGACAGAGGCTGCTGTCGAGACGGGAGCCCTGGGCGCAATGTTATTCGGGCTAC 371  
QY 368 ACTCGGATCCCGAGCTCCGCGAGATGATTCAGAGAGAGAGAGGAGATGCTGAGGAGAA 427  
DB 372 ACTCGGATCCCGAGCTCCGCGAGATGATTCAGAGAGAGAGAGGAGATGCTGAGGAGAA 431  
QY 428 CTTTGGAGAGTCTGAGACCCCACTACAGAGATGTTATGAGATTCATTAATTAATAG 487  
DB 432 CTTTGGAGAGTCTGAGACCCCACTACAGAGATGTTATGAGATTCATTAATTAATAG 491  
QY 488 CATAGATCTTGGGAAATTTGGGAGTGTACATTTCAAAAGAGCGTTCAAAATAGGCTCT 547  
DB 492 CATAGATCTTGGGAAATTTGGGAGTGTACATTTCAAAAGAGCGTTCAAAATAGGCTCT 551  
QY 548 AAGAGTTTGTTCAGTGTCTCACTTCGGCTAAATGAGAAATGATGATGTCAGCGTTG 607  
DB 552 AAGAGTTTGTTCAGTGTCTCACTTCGGCTAAATGAGAAATGATGATGTCAGCGTTG 611  
QY 608 GTATTTCACTTCAATGAGCTGAATGTTTCAGGACCTCTTCCCATTTGAAGTAAATTTTA 667  
DB 612 GTATTTCACTTCAATGAGCTGAATGTTTCAGGACCTCTTCCCATTTGAAGTAAATTTTA 671  
QY 668 TTTGACCAAGAGAGCCCTGAATGAATTT 696  
DB 672 TTTGACCAAGAGAGCCCTGAATGAATTT 700

RESULT 27  
CA413294 716 bp mRNA linear EST 07-NOV-2002  
LOCUS UI-H-EZ0-bap-h-20-0-UI s1 NCI CGAP Ch1 Homo sapiens cDNA clone  
DEFINITION UI-H-EZ0-bap-h-20-0-UI 3', mRNA sequence.  
ACCESSION CA413294  
VERSION CA413294.1 GI:24775945  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 716)  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL  
COMMENT

Tumor Gene Index  
Unpublished (1997)  
Contract: Robert Stransberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. Steven Gitellis/ Rush Presbyterian, Dept. of  
Orthopedics  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
1..716  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-EZ0-bap-h-20-0-UI"  
/tissue\_type="Chondrosarcoma Grade II"  
/dev\_stage="Adult"  
/lab\_host="MDH10B (Life Technologies)"  
/clone\_lib="NCI CGAP Ch1"  
/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)  
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP Ch1 is a cDNA library containing the following  
tissue(s): Chondrosarcoma Grade II. The library was  
constructed according to Bonaldi, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT73-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
TGATCAGCT.  
TAG TISSUE=grade-2-chondrosarcoma  
TAG LIB=UI-H-EZ0  
TAG\_SEQ=ATCTAATATAG"

## ORIGIN

Query Match 54.3%; Score 682.2; DB 6; Length 716;  
Best Local Similarity 99.3%; Pred. No. 9.6e-136;  
Matches 695; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 193 TCCGCTGCTGACACTGCGCGCGCGCTCGAGCGGCTTCGAGATCCCGAGGAGACCAA 252  
DB 716 TCCGCTGCTGACACTGCGCGCGCGCTCGAGCGGCTTCGAGATCCCGAGGAGACCAA 257  
QY 253 AGGCGCAGCTCCGCGCAGAGGAGGTGTGAGCTGTATTAATGAAATGTGCTTCAAGGCG 312  
DB 256 AGGCGCAGCTCCGCGCAGAGGAGGTGTGAGCTGTATTAATGAAATGTGCTTCAAGGCG 317  
QY 313 CAGCAGAGTGTCTGTGTCAGACGGAGCCCTGCGGCGCAATGTTATTCGGGTACACCTG 372  
DB 316 CAGCAGAGTGTCTGTGTCAGACGGAGCCCTGCGGCGCAATGTTATTCGGGTACACCTG 377  
QY 373 GGATCCAGGTCGGGAGTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432  
DB 376 GGATCCAGGTCGGGAGTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437  
QY 433 AGGAGTCTTGAGACCCCACTACAGAGAGTTCATGAGATTCATTAATGAGCATAG 492  
DB 436 AGGAGTCTTGAGACCCCACTACAGAGAGTTCATGAGATTCATTAATGAGCATAG 497  
QY 493 ATCTTGGGAAATTTGGGAGTGTACATTTCAAAAGATGCTTCAATTAAGTCTTAAGAG 552  
DB 496 ATCTTGGGAAATTTGGGAGTGTACATTTCAAAAGATGCTTCAATTAAGTCTTAAGAG 557  
QY 553 TTTTGTTCAGTGTCTCACTTCGGCTAAATGAGAAATGATGATGCTGAGCGTGTATTT 612  
DB 556 TTTTGTTCAGTGTCTCACTTCGGCTAAATGAGAAATGATGATGCTGAGCGTGTATTT 617



QY 613 TCACATTCATGAGAGTGAATGTTTCAGACCTCTCCATGAGCTATATATTTTGG 672  
 DB 296 TCACATTCATGAGAGTGAATGTTTCAGACCTCTCCATGAGCTATATATTTTGG 237  
 QY 673 ACCAAGAGAGCCCTGTAATGAATCAATTAATATTCATGACCTCTCTGTGGAAG 732  
 DB 236 ACCAAGAGAGCCCTGTAATGAATCAATTAATATTCATGACCTCTCTGTGGAAG 177  
 QY 733 GACTTTGTGAAGAAATGTTGCTGATTTGATGATTTGCTATCTGGTTGGCACTTGT 792  
 DB 176 GACTTTGTGAAGAAATGTTGCTGATTTGATGATTTGCTATCTGGTTGGCACTTGT 117  
 QY 793 CAGATTACCCAAAGAGAGTCTTCTACATGAGTGAATTCAGTTCTCCGATCATTTATG 852  
 DB 116 CAGATTACCCAAAGAGAGTCTTCTACATGAGTGAATTCAGTTCTCCGATCATTTATG 57  
 QY 853 AAGAACTA-CCAAATTAATGCTTTAATTTTCAATTTGCTA 891  
 DB 56 AAGAACTACCCAAATTAATGCTTTAATTTTCAATTTGCTA 17

RESULT 28  
 BQ010155 702 bp mRNA linear EST 26-MAR-2002  
 LOCUS BQ010155/c  
 DEFINITION UI-H-ED0-axz-f-23-0-UI.81 NCI\_GAP\_ED0 Homo sapiens cDNA clone  
 IMAGE:5835670 3', mRNA sequence.

ACCESSION BQ010155  
 VERSION BQ010155.1 GI:19735056  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 702)  
 NCI-GAP http://www.ncbi.nlm.nih.gov/ncigap.  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cga@bbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be found  
 through the I.M.A.G.E. Consortium/BLN at: http://image.llnl.gov  
 The following repetitive elements were found in this cDNA  
 sequence: 27-60, >AT rich#low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
 source Location/Qualifiers

1..702  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5835670"  
 /issue\_type="Chondrosarcoma"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP ED0"  
 /note="Organ: Left Pubic Bone; Vector: pT773-Pac  
 (Pharmacia) with a modified polylinker; Site 1: EcoR I;  
 Site 2: Not I; NCI\_GAP\_ED0 is a cDNA library containing  
 the following tissue(s): Chondrosarcoma cell line C5. The  
 library was constructed according to Bonaldo, Lennon and  
 Soares, Genome Research, 6:791-806, 1996. First strand  
 cDNA synthesis was primed with an oligo-dT primer  
 containing a Not I site. Double stranded cDNA was ligated  
 to an EcoR I adaptor, digested with Not I, and cloned  
 directionally into pT773-Pac vector. The oligonucleotide  
 used to prime the synthesis of first-strand cDNA contains  
 a library tag sequence that is located between the Not I

ORIGIN  
 Query Match 54.3%; Score 682; DB 5; Length 702;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-135; Mismatches 0; Indels 0; Gaps 0;  
 Matches 682; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 site and the (d)18 tail. The sequence tag for this  
 library is GCTCAGAGCT.  
 TAG\_TISSUE=chondrosarcoma  
 TAG\_LIB=UI-H-ED0  
 TAG\_SEQ=CGTCAGAGCT"

QY 576 CTAATGAGAGAAATGCAATGCTGTGAGGCTTGTGATTTTCATTCATGAGAGCTGATGT 635  
 DB 702 CTAATGAGAGAAATGCAATGCTGTGAGGCTTGTGATTTTCATTCATGAGAGCTGATGT 643  
 QY 636 TCAGAGCTCTCCATGAGAGCTTAATTTATTTTGGACCAAGAGCCCTGAAATGAT 695  
 DB 642 TCAGAGCTCTCCATGAGAGCTTAATTTATTTTGGACCAAGAGCCCTGAAATGAT 583  
 QY 696 TCAGAGCTTAATTTATTCATGAGAGCTTCTGTGAGAGAGCTTGTGAGAGAGTGTGCT 755  
 DB 582 TCAGAGCTTAATTTATTCATGAGAGCTTCTGTGAGAGAGCTTGTGAGAGAGTGTGCT 523  
 QY 756 GGATTAGAGAGAGTGTGATCTATCTGGTGGCACTGTGTCAGATTACCCAAAGAGAGTGT 815  
 DB 522 GGATTAGAGAGAGTGTGATCTATCTGGTGGCACTGTGTCAGATTACCCAAAGAGAGTGT 463  
 QY 816 TCTACTGATGGAATTCAGTTCTGTCGATCATTTATTGAAGACTACCAATTAATGCTT 875  
 DB 462 TCTACTGATGGAATTCAGTTCTGTCGATCATTTATTGAAGACTACCAATTAATGCTT 403  
 QY 876 TTAATTTCAATTTGCTACCTCTTTTATTTATGCTGGAATGCTTCACTTAATGACAT 935  
 DB 402 TTAATTTCAATTTGCTACCTCTTTTATTTATGCTGGAATGCTTCACTTAATGACAT 343  
 QY 936 TTTAATTAAGTTTATGATATCATCTGAAATGAAGCAAGCTTAATGTTTACAGACCA 995  
 DB 342 TTTAATTAAGTTTATGATATCATCTGAAATGAAGCAAGCTTAATGTTTACAGACCA 283  
 QY 996 AAGTGTGATTCACACCTGTTTAAATCTAGCATTAATTCATTTGCTTCATCAAAAGTG 1055  
 DB 282 AAGTGTGATTCACACCTGTTTAAATCTAGCATTAATTCATTTGCTTCATCAAAAGTG 223  
 QY 1056 GTTTCATTAATTTTGTGTTGTTGTTAGAAATCTTCTTCATGTCATCTCAACT 1115  
 DB 222 GTTTCATTAATTTTGTGTTGTTGTTAGAAATCTTCTTCATGTCATCTCAACT 163  
 QY 1116 ATAAATTTGGAATATTTGTTGCTTTTGTGTTTCTTCTAGATATGACATTTTAAAAA 1175  
 DB 162 ATAAATTTGGAATATTTGTTGCTTTTGTGTTTCTTCTAGATATGACATTTTAAAAA 103  
 QY 1176 ATATAAAGCTACCAATCTTTGTACAAATTTGTAATGTTTAAAGATTTTATATCTGT 1235  
 DB 102 ATATAAAGCTACCAATCTTTGTACAAATTTGTAATGTTTAAAGATTTTATATCTGT 43  
 QY 1236 TAAATTAATTAATTTTCCACA 1257  
 DB 42 TAAATTAATTAATTTTCCACA 21

RESULT 29  
 BE607413/c 683 bp mRNA linear EST 25-FEB-2001  
 LOCUS BE607413  
 DEFINITION COLONEST0306c04 colon carcinoma tissue cDNA library Homo sapiens  
 CDNA, mRNA sequence.  
 ACCESSION BE607413  
 VERSION BE607413.1 GI:13123454  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 683)  
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

AUTHORS Huang, Y.W., Wang, K., Zhang, J.Zh., Li, X.Y., Li, Y., Huang, D.Q.,  
Xie, Y., Mao, Y.M., Bao, L. and Sun, Zh.R.  
TITLE Identification of genes differentially over-expressed in human  
colon carcinoma using combination of SSH and cDNA microarray  
analysis  
JOURNAL Unpublished (2000)  
COMMENT Contact: Huang Y.W.  
Department of Experimental Medicine  
Beijing 306 hospital, Beijing  
No.9, Anxiliang Beileiy Road, Beijing, 100101, P.R.China  
Tel: 8610-66356111  
Fax: +86-10-66356111  
Email: hywboy@sina.com.

FEATURES  
source  
1. .683  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="colon carcinoma tissue cDNA library"  
/note="Organ: colon; Vector: pT Adv; Site\_1: EcorI;  
Site\_2: EcorI"

ORIGIN  
Query Match 54.2%; Score 681.4; DB 2; Length 683;  
Best Local Similarity 99.9%; Pred. No. 1.4e-135;  
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 516 ACATTACAAAGATGCGTCAATATGCTCTAAGAGTTTGTTCAGAGGCTCAGCTCGG 575  
DB 683 ACATTACAAAGATGCGTCAATATGCTCTAAGAGTTTGTTCAGAGGCTCAGCTCGG 624  
QY 576 CTAATAATGCAAGATGATGCTGTGACGCTGTGATTTTCATTCATGAGCTGATGT 635  
DB 623 CTAATAATGCAAGATGATGCTGTGACGCTGTGATTTTCATTCATGAGCTGATGT 564  
QY 636 TCAGAGCCTCTCCCATGGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 695  
DB 563 TCAGAGCCTCTCCCATGGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 504  
QY 696 TCAACAATTAATATTCATGCACTCTCTGTGGAAGGACTTGTGAAGGAATGTGTGT 755  
DB 503 TCAACAATTAATATTCATGCACTCTCTGTGGAAGGACTTGTGAAGGAATGTGTGT 444  
QY 756 GGATTAGTGATGTTGCTATCTGGGTGGCACTTGTTCAGATTACCAAGAGATGCT 815  
DB 443 GGATTAGTGATGTTGCTATCTGGGTGGCACTTGTTCAGATTACCAAGAGATGCT 384  
QY 816 TCTACTGATGGAATTCAGTTCTTCGATCATTATTGGAAGAACTACCAAAATTAATGCTT 875  
DB 383 TCTACTGATGGAATTCAGTTCTTCGATCATTATTGGAAGAACTACCAAAATTAATGCTT 324  
QY 876 TAAATTCATTGCTACCTCTTTTATTTATGACCTGGAGATGTTCACTTAAATGACAT 935  
DB 323 TAAATTCATTGCTACCTCTTTTATTTATGACCTGGAGATGTTCACTTAAATGACAT 264  
QY 936 TTAATAATGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 995  
DB 263 TTAATAATGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 204  
QY 996 AAGGTGATTTTCAACGCTTTTAAATCTAGATTAATCTTTTCTTCAATCAAAAGTG 1055  
DB 203 AAGGTGATTTTCAACGCTTTTAAATCTAGATTAATCTTTTCTTCAATCAAAAGTG 144  
QY 1056 GTTTCATATTTTATTTAGTGTAGATATCTTCTCATAGTACATTCCTCAACT 1115  
DB 143 GTTTCATATTTTATTTAGTGTAGATATCTTCTCATAGTACATTCCTCAACT 84  
QY 1116 ATAATTTGGAATATGTTGCTTTTGTGTTTCTTGTATAGATTTTAAAAA 1175  
DB 83 ATAATTTGGAATATGTTGCTTTTGTGTTTCTTGTATAGATTTTAAAAA 24  
QY 1176 ATAATAAGCTACCAATCTTGT 1198

DB 23 ATATAAAGCTACCAATCTTGT 1

RESULT 30  
BE607414 683 bp mRNA linear EST 25-FEB-2001  
LOCUS colonesT0306c10 colon carcinoma tissue cDNA library Homo sapiens  
DEFINITION cDNA, mRNA sequence.  
ACCESSION BE607414  
VERSION BE607414.1 GI:13123455  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Huang, Y.W., Wang, K., Zhang, J.Zh., Li, X.Y., Li, Y., Huang, D.Q.,  
Xie, Y., Mao, Y.M., Bao, L. and Sun, Zh.R.  
TITLE Identification of genes differentially over-expressed in human  
colon carcinoma using combination of SSH and cDNA microarray  
analysis  
JOURNAL Unpublished (2000)  
COMMENT Contact: Huang Y.W.  
Department of Experimental Medicine  
Beijing 306 hospital, Beijing  
No.9, Anxiliang Beileiy Road, Beijing, 100101, P.R.China  
Tel: 8610-66356111  
Fax: +86-10-66356111  
Email: hywboy@sina.com.

FEATURES  
source  
1. .683  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="colon carcinoma tissue cDNA library"  
/note="Organ: colon; Vector: pT Adv; Site\_1: EcorI;  
Site\_2: EcorI"

ORIGIN  
Query Match 54.2%; Score 681.4; DB 2; Length 683;  
Best Local Similarity 99.9%; Pred. No. 1.4e-135;  
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 516 ACATTACAAAGATGCGTCAATATGCTCTAAGAGTTTGTTCAGAGGCTCAGCTCGG 575  
DB 1 ACATTACAAAGATGCGTCAATATGCTCTAAGAGTTTGTTCAGAGGCTCAGCTCGG 60  
QY 576 CTAATAATGCAAGATGATGCTGTGACGCTGTGATTTTCATTCATGAGCTGATGT 635  
DB 61 CTAATAATGCAAGATGATGCTGTGACGCTGTGATTTTCATTCATGAGCTGATGT 120  
QY 636 TCAGAGCCTCTCCCATGGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 695  
DB 121 TCAGAGCCTCTCCCATGGAAGCTAATTTATTTGGACCAAGAAAGCCCTGAATGAAT 180  
QY 696 TCAACAATTAATATTCATGCACTCTCTGTGGAAGGACTTGTGAAGGAATGTGTGT 755  
DB 181 TCAACAATTAATATTCATGCACTCTCTGTGGAAGGACTTGTGAAGGAATGTGTGT 240  
QY 756 GGATTAGTGATGTTGCTATCTGGGTGGCACTTGTTCAGATTACCAAGAGATGCT 815  
DB 241 GGATTAGTGATGTTGCTATCTGGGTGGCACTTGTTCAGATTACCAAGAGATGCT 300  
QY 816 TCTACTGATGGAATTCAGTTCTTCGATCATTATTGGAAGAACTACCAAAATTAATGCTT 875  
DB 301 TCTACTGATGGAATTCAGTTCTTCGATCATTATTGGAAGAACTACCAAAATTAATGCTT 360  
QY 876 TAAATTCATTGCTACCTCTTTTATTTATGACCTGGAGATGTTCACTTAAATGACAT 935  
DB 361 TAAATTCATTGCTACCTCTTTTATTTATGACCTGGAGATGTTCACTTAAATGACAT 420  
QY 936 TTAATAATGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 995

Db 421 TTTAATAAGTTATGTATACATCTGAATGAAAGCAAGCTAATATGTTTACAGACCA 480  
Qy 996 AAGTGTATTCACACTGTTTTTAAATCTAGCATTTATTCATTTGGTTCATCAAGAG 1055  
Db 481 AAGTGTATTCACACTGTTTTTAAATCTAGCATTTATTCATTTGGTTCATCAAGAG 540  
Qy 1056 GTTTCATATTTTTTTTGTGTTAGAAATACCTTTCTCATAGTCACATTTCTCAACCT 1115  
Db 541 GTTTCATATTTTTTTTGTGTTAGAAATACCTTTCTCATAGTCACATTTCTCAACCT 600  
Qy 1116 ATAAATTTGCAATATTTGTGTGTTGTTTCTTTCTTATGATNGCAATTTTAAAAA 1175  
Db 601 ATAAATTTGCAATATTTGTGTGTTGTTTCTTTCTTATGATNGCAATTTTAAAAA 660  
Qy 1176 ATATAAGCTACCAATCTTGT 1198  
Db 661 ATATAAGCTACCAATCTTGT 683

RESULT 31  
AL570753/c 836 bp mRNA linear EST 05-APR-2004  
LOCUS AL570753 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS0D1022YF04 3-PRIME, mRNA sequence.  
ACCESSION AL570753  
VERSION AL570753.3 GI:46236906  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 836)  
Li W.B., Gruber C., Jessee J. and Polayes D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 16, 2001 this sequence version replaced gi:31292170.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
4941.f

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CS0D1022YF04&c=4941.f.  
Location/Qualifiers  
1. 836  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1022YF04"  
/issue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized." sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Query Match 54.1%; Score 679.8; DB 1; Length 836;  
Best Local Similarity 94.3%; Pred. No. 3.2e-135;  
Matches 713; Conservative 4; Mismatches 37; Indels 2; Gaps 2;

Qy 402 GAAAGGGGGAATGCTGAGGAGAGCTTGAAGAGTCTTGACACCACTCAAGAGCAG 461  
Db 766 GAGAAAGGGGGAATGCTGAGGAGAGCTTGAAGAGTCTTGACACCACTCAAGAGCAG 707  
Qy 462 TGTTCATGAGATTCATTTATTTATGCAATGATCTTGGGAAATTCGGAGGTGTACATT 521  
Db 706 TGTTCATGAGATTCATTTATTTATGCAATGATCTTGGGAAATTCGGAGGTGTACATT 648

Qy 522 ACAAGATGCGTTCAATAGTGTCTGAAGAGTTTGTTCAGTGGCTCACTTGGCTAAA 581  
Db 647 ACAAGATGCGTTCAATAGTGTCTGAAGAGTTTGTTCAGTGGCTCACTTGGCTAAA 588  
Qy 582 TGCAGAAATGATGCTGTGACGGTGTGATTTTACATTCATATGAGCTGAATGTTCA 641  
Db 587 TGCAGAAATGATGCTGTGACGGTGTGATTTTACATTCATATGAGCTGAATGTTCA 528  
Qy 642 CCTCTTCCATGAGCTATTAATTTATTTGACCAAGAGAGCCCTGAAATGAATTCACA 701  
Db 527 CCTCTTCCATGAGCTATTAATTTATTTGACCAAGAGAGCCCTGAAATGAATTCACA 468  
Qy 702 ATTAATATTCATGACACTCTTCTGGAAGAGACTTTGGAAGAGTTGTCGTGATTA 761  
Db 467 ATTAATATTCATGACACTCTTCTGGAAGAGACTTTGGAAGAGTTGTCGTGATTA 408  
Qy 762 GTGATGTTGCTATCTGAGTGGGCTGCTGCTGAGATTAACCAAGAGAGATCTTACT 821  
Db 407 GTGATGTTGCTATCTGAGTGGGCTGCTGCTGAGATTAACCAAGAGAGATCTTACT 348  
Qy 822 GGATGATTCATGCTTTCTGCTGCTATTTTGAAGAGCTTCAAAATTAATGCTTTAATT 881  
Db 347 GGATGATTCATGCTTTCTGCTGCTATTTTGAAGAGCTTCAAAATTAATGCTTTAATT 288  
Qy 882 TCATTTGCTACTCTTTTCTTTTATTTATGCTTGAAGAGCTTCAAAATTAATGCTTTA 941  
Db 287 TCATTTGCTACTCTTTTCTTTTATTTATGCTTGAAGAGCTTCAAAATTAATGCTTTA 228  
Qy 942 TAAATTTATGATATCATCTGAATGAAAGCAAGCTAATATGTTTACAGACCAAGTGT 1001  
Db 227 TAAATTTATGATATCATCTGAATGAAAGCAAGCTAATATGTTTACAGACCAAGTGT 168  
Qy 1002 GATTTCACACTGTTTAAATTTAGCATTTATTCATTTGCTTCATCAAAAGTGTGTTCA 1061  
Db 167 GATTTCACACTGTTTAAATTTAGCATTTATTCATTTGCTTCATCAAAAGTGTGTTCA 108  
Qy 1062 AATATTTTATTTA-GTTGTTAGATATCTTCTGATGACATTTCTCAACTATAAT 1120  
Db 107 AATATTTTATTTA-GTTGTTAGATATCTTCTGATGACATTTCTCAACTATAAT 48  
Qy 1121 TTGGAATATGTTGTGCTCTTTGTTTCTTCTTAA 1156  
Db 47 TTGGAATATGTTGTGCTCTTTGTTTCTTCTTAA 12

RESULT 32  
AL553798 709 bp mRNA linear EST 30-MAR-2004  
LOCUS AL553798 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS0D1077YB01 5-PRIME, mRNA sequence.  
ACCESSION AL553798  
VERSION AL553798.3 GI:45858563  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 709)  
Li W.B., Gruber C., Jessee J. and Polayes D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 15, 2001 this sequence version replaced gi:31275612.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized. Library was  
constructed by Life Technologies, a division of Invitrogen. This sequence  
belongs to sequence cluster 4941.f

ORIGIN  
Query Match 54.1%; Score 679.8; DB 1; Length 836;  
Best Local Similarity 94.3%; Pred. No. 3.2e-135;  
Matches 713; Conservative 4; Mismatches 37; Indels 2; Gaps 2;

Qy 402 GAAAGGGGGAATGCTGAGGAGAGCTTGAAGAGTCTTGACACCACTCAAGAGCAG 461  
Db 766 GAGAAAGGGGGAATGCTGAGGAGAGCTTGAAGAGTCTTGACACCACTCAAGAGCAG 707  
Qy 462 TGTTCATGAGATTCATTTATTTATGCAATGATCTTGGGAAATTCGGAGGTGTACATT 521  
Db 706 TGTTCATGAGATTCATTTATTTATGCAATGATCTTGGGAAATTCGGAGGTGTACATT 648



Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	655	GAGCTGAATGTTCAAGACCTCTTCCCATTAAGCATATA- TTATNTGGACCAAGGAAGCC	597					
Qy	685	CTGAAATGAATTCACAACTTAATATTCATGCACTCTCTGTGGAGGAAGCTTTGTGAAG	744					
Db	596	CTGAAATGAATTCACAACTTAATATTCATGCACTCTCTGTGGAGGAAGCTTTGTGAAG	537					
Qy	745	GAATTTGGTGTGCGAATTTAGTGTGATATCTGGGTTGGGACCTTTGTCAGATTAACCAA	804					
Db	536	GAATTTGGTGTGCGAATTTAGTGTGATATCTGGGTTGGGACCTTTGTCAGATTAACCAA	477					
Qy	805	AAGAGAGATGCTTCTACTGATGATGAATTCAGTTTCTCGCATCATTTATGAAAGACTACCA	864					
Db	476	AAGAGAGATGCTTCTACTGATGATGAATTCAGTTTCTCGCATCATTTATGAAAGACTACCA	417					
Qy	865	AATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTATATGCTTGAATGAGTTCAC	924					
Db	416	AATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTATATGCTTGAATGAGTTCAC	357					
Qy	925	TTAATATGATTTTAAATAAAGTTTATATGATATCATCTGAATGAAGAAAGCAAGCTAAATATG	984					
Db	356	TTAATATGATTTTAAATAAAGTTTATATGATATCATCTGAATGAAGAAAGCAAGCTAAATATG	297					
Qy	985	TTTACAGACCAAGGTGATTTCAACAGTCTTTTAAATCTAGCAATTAATTCATTTTGTCTTC	1044					
Db	296	TTTACAGACCAAGGTGATTTCAACAGTCTTTTAAATCTAGCAATTAATTCATTTTGTCTTC	237					
Qy	1045	AATCAAAAGTGGTTCAATATTTTTTTTATGTTGGTTGAATATCTTCTTCAATAGTCAAT	1104					
Db	236	AATCAAAAGTGGTTCAATATTTTTTTTATGTTGGTTGAATATCTTCTTCAATAGTCAAT	177					
Qy	1105	TCTCTCAACCTATATTAATTTGGAAATTTGTTGGTCTTTTGTGTTTCTTCTTAATATAGCA	1164					
Db	176	TCTCTCAACCTATATTAATTTGGAAATTTGTTGGTCTTTTGTGTTTCTTCTTAATATAGCA	117					
Qy	1165	TTTTTAAATTAATTAATTAAGTACCAATCTTTGTATCAATTTGTAAATGTTAAGATTTT	1224					
Db	116	TTTTTAAATTAATTAATTAAGTACCAATCTTTGTATCAATTTGTAAATGTTAAGATTTT	57					
Qy	1225	TTTATATCTGTTAAATTAATTAATTTATTTTCAACA	1257					
Db	56	TTTATATCTGTTAAATTAATTAATTTATTTTCAACA	24					
RESULT 34								
LOCUS	BM915288	1099 bp	mRNA	linear	EST 12-MAR-2002			
DEFINITION	AGENCOURT_6702310 NIH_MGC_41 Homo sapiens CDNA clone IMAGE:5481457							
ACCESSION	BM915288							
VERSION	BM915288.1	GI:19365667						
KEYWORDS	EST.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.							
TITLE	1 (bases 1 to 1099)							
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .							
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)							
	Unpublished (1999)							
	Contact: Robert Strausberg, Ph.D.							
	Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>							
	Tissue Procurement: DCTD/DRP							
	CDNA Library Preparation: Rubin Laboratory							
	DNA Sequencing by: Agencourt Bioscience Corporation							
	Clone distribution: MGC clone distribution information can be							
	found through the I.M.A.G.E. Consortium/LLNL at:							
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>							
	Plate: LLCM2005 row: p column: 02							
	High quality sequence start: 26							
	High quality sequence stop: 565.							
FEATURES	Location/Qualifiers							
SOURCE	1..1099							

[illegible]

RESULT	35
LOCUS	B0648112
DEFINITION	B0648112 986 bp mRNA linear EST 15-JUL-2002 AGENCOURT_8507019 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6297812 5', mRNA sequence.
ACCESSION	B0648112
VERSION	B0648112
KEYWORDS	B0648112.1 GI:21772284 EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 986) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1998)
AUTHORS	Contact: Robert Strausberg, Ph.D.
TITLE	
JOURNAL	
COMMENT	

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Plate: LLCM2507 row: n column: 21
High quality sequence stop: 520.
location/qualifiers
1. .986
FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6297812"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_100"
/notes="Organ: liver; Vector: pOT87; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

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Query Match	Best Local Similarity	53.5%;	Score 672.6;	DB 5;	Length 986;
Matches 698;	Conservative	0;	Mismatches 19;	Indels	4; Gaps 1;
QY	37	GCTGTGCGCGGCTCTCGAGACCGCGCGAGACGCTGACCAAGTTCTCTCTCGATC	96		
Db	1	GCTGTGCGCGGCTCTCGAGACCGCGCGAGACGCTGACCAAGTTCTCTCTCGATC	60		
QY	97	TCTTCCGCTTCAGCTCCGCGCTGCGCGGCAGCCGGAAGCCATGCAATCCAGGATCCG	156		
Db	61	TCTTCCGCTTCAGCTCCGCGCTGCGCGGCAGCCGGAAGCCATGCAATCCAGGATCCG	120		
QY	157	CCGCTCCCGCCAGCGAGTCCGCGGCGCTTCTGCTGCTCTGCTGAGTGTCCGCGC	216		
Db	121	CCGCTCCCGCCAGCGAGTCCGCGGCGCTTCTGCTGCTCTGCTGAGTGTCCGCGC	180		
QY	217	CGTGTGACGCTCTGAGATCCCAAGGAGGAAGCAAAAGGCGCAGCTCCGCGAGAGG	276		
Db	181	CGTGTGACGCTCTGAGATCCCAAGGAGGAAGCAAAAGGCGCAGCTCCGCGAGAGG	240		
QY	277	TGCTGACCTGTATTAATGGAATGTCTTACAAGGCCAGAGAGTGCCTGTGTGAGAC	336		
Db	241	TGCTGACCTGTATTAATGGAATGTCTTACAAGGCCAGAGAGTGCCTGTGTGAGAC	300		
QY	337	GGAGCCTGGGGCCAATGTTATTCCGGGTACACTGTGAATCCAGGTGGAGATGATTC	396		

Db 301 GGAACCTTGGGCGCAATGGCATTCCGGTACCTGGATCCAGGTGGGATGGATTCA 360

Qy 397 AAGAGAAAAGGGGAAATGCTTGAGGAAAGCTTTGAGAGTCTCGACACCCAACTACA 456

Db 361 AAGAGAAAAGGGGAAATGCTTGAGGAAAGCTTTGAGAGTCTCGACACCCAACTACA 420

Qy 457 AGCAGTCTTCAGAGGTCATTGAATTAAGCANAAGATCTTGGGAAAATTGCGAGGTGA 516

Db 421 AGCAGTGTTCATGAGATTCATTGAATTAATGACATGATCTTGGGAAAATTGCGAGGTGA 480

Qy 517 CATTACAAAGATGCGTTCAAATAGTGTCTTAAGGTTTTGTCAAGGCTCACTTCGCG 576

Db 481 CATTACAAAGATGCGTTCAAATAGTGTCTTAAGGTTTTGTCAAGGCTCACTTCGCG 540

Qy 577 TAAAAATCAGAAATGATGATGTCAGACGCTGGATTTCACTCAATAGSAGCTGAATGTT 636

Db 541 TAAATGCAAAATGATGATGTCAGACGCTGGATTTCACTCAATAGSAGCTGAATGTT 600

Qy 637 CAGGACTCTTCCCATTTGAAGCTATTAATTGATGACCAAGAAAGCCCTGAATGAATT 696

Db 601 CAGGACTCTTCCCATTTGAAGCTATTAATTGATGACCAAGAAAGCCCTGAATGAATT 660

Qy 697 CAACAAATTAATTTATC---GCACTTCTTGTGAAAGACTTTGTGAAGAAATGTGT 752

Db 661 CAACAAATTAATTTATCTCCGACACTCTTGTGTGGAAAGACTTTGTGAAGAAATTTGG 720

Qy 753 G 753

Db 721 G 721

RESULT 36			
EX386416			
LOCUS			
DEFINITION	EX386416	707 bp	mRNA linear EST 27-APR-2000
ACCESSION	EX386416	Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DD1077YB01.5-PRIME, mRNA sequence.	
VERSION	EX386416		
KEYWORDS	EX386416.2	GI:46627527	
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	I.J.W.B., Gruber,C., Jessee,J. and Polayes,D.		
AUTHORS	Full-length cDNA libraries and normalization		
TITLE	Unpublished (2001)		
JOURNAL	On May 8, 2003 this sequence version replaced gi:30457424.		
COMMENT			

Contact: Genoscope  
 Genoscope - Centre National de Séquençage  
 BP 191 91006 EVRY cedex - France  
 Email: [segreg@genoscope.cns.fr](mailto:segreg@genoscope.cns.fr), web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 ends enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 4941.f  
 For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna/s=CSINA1020ZB01QP1c=4941.f>.  
 Location/Qualifiers  
 I. .707

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1077B01"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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Db 323 GGATGATTCMAAGGGGAAAAAGGAGATGCTTAAAGGAAAGCTTTGAGAGTCTTGAC 382
QY 446 ACCCACTCAAGACAGTGTTCATGAGTTCATGATTAATGATGATCTTGGGAAAT 505
Db 383 CCGAAACCTAAGACAGTGTTCGAGAGTTCGAACTAATGATGATCTTGGGAAAT 442
QY 506 TCGGAGTGTACATTTACAAAGATGCGTTCAATATAGTCTTAAAGATTTTGTTCAGTGG 565
Db 443 TCGGAGTGTACATTTACAAAGATGCGTTCACATGATCTTGGGAGTCTTGTTCAGTGG 502
QY 566 CTCACCTGCGCTTAAATGAGAAATGATGCTGTCAGCGTTGATTTACATTCATG 625
Db 503 CTCGCTTCGCGCTTAAATGAGAAATGATGCTGTCAGCGTTGATTTACATTCATG 562
QY 626 AGCTGAATGTTCAGAGCTCTTCCCATTAAGATTAATTTATTTGACCAAGAGAGCC 685
Db 563 AGCTGAATGTTCAGAGCTCTTCCCATTAAGATTAATTTATTTGACCAAGAGAGCC 622
QY 686 TGAATGAATTCACATTTAATATATGATGCACTCTTCTGTGGAAGAGATTTGTGAAG 745
Db 623 TGAATGAATTCACATTTAATATATGATGCACTCTTCTGTGGAAGAGATCTGTGAAG 682
QY 746 AATTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 805
Db 683 GATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 742
QY 806 AGAGAGATGCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 865
Db 743 AGAGAGATGCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 802
QY 866 ATAAATGCTTTAA-TTTTCAATTTGCTACCT-----CTTTTATTAATGCTTGAAT 917
Db 803 ATAAATGCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 862
QY 918 GGTTCATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 970
Db 863 GGTTCATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 922
QY 971 CAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1030
Db 923 CAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 979
QY 1031 ATTCATTTGCTTCACTGATGATGATGATGATGATGATGATGATGATGATGATG 1081
Db 980 AACCATTTTATTCACGCAAGATGATGATGATGATGATGATGATGATGATGATG 1030

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RESULT 39
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LOCUS UI-H-E11-a2h-m-17-0-UI.s1 NCI_CGAP_E11 Homo sapiens cDNA clone
DEFINITION IMAGE:5848888 3', mRNA sequence.
ACCESSION B0005403
VERSION B0005403
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 723)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-rc@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/BLN at: http://image.jhmi.gov
The following repetitive elements were found in this cDNA

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sequence: 30-62, >AT rich#low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.
FEATURES
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Location/Qualifiers
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/clone_lib="NCI CGAP E11"
/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP E11 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldi, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
ACACTTGAC.
TAG TISSUE=chondrosarcoma
TAG LIB=UI-H-E11
TAG_SEQ=ACACTTGAC"

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## ORIGIN

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Query Match 52.1%; Score 655.4; DB 5; Length 723;
Best Local Similarity 99.4%; Pred. No. 5,4e-130;
Matches 689; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
QY 565 GCTCACTTGGCTAAATGCAAAATGATGCTGTCAGCGTTGATTTACATTCATG 624
Db 713 GCTCACTTGGCTAAATGCAAAATGATGCTGTCAGCGTTGATTTACATTCATG 654
QY 625 GAGCTGAATGTTCAAGACCTCTCCATTAAGATTAATTTATTTGACCAAGAGCC 684
Db 653 GAGCTGAATGTTCAAGACCTCTCCATTAAGATTAATTTATTTGACCAAGAGCC 594
QY 685 CTGAATGAATTCACAAATTAATTTATTCATGCACTCTTCTGTGAAGAGACTTTGGAG 744
Db 593 CTGAATGAATTCACAAATTAATTTATTCATGCACTCTTCTGTGAAGAGACTTTGGAG 534
QY 745 GAATTGCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 804
Db 533 GAATTGCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 474
QY 805 AAGAGATGCTTCTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 864
Db 473 AAGAGATGCTTCTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 414
QY 865 AATTAATGCTTTAATTTATTTGCTACCTCTTTTATTAATGCTTGAATGCTTTC 924
Db 413 AATTAATGCTTTAATTTATTTGCTACCTCTTTTATTAATGCTTGAATGCTTTC 354
QY 925 TTAATGAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 984
Db 353 TTAATGAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 294
QY 985 TTAACAGACCAAGTGTGATTCACAGCTGTTTAAATCTAGCATTAATTTGCTTC 1044
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QY 1045 AATCAAAAGTGTTCATATTTTATTTAGTGTGAAGTCTTTCTTCATAGTCACAT 1104
Db 233 AATCAAAAGTGTTCATATTTTATTTAGTGTGAAGTCTTTCTTCATAGTCACAT 174
QY 1105 TCTTCAACCTAATTAATTTGAATATTTGTTGCTCTTTTGTCTTCTAGTATAGCA 1164

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Db	173	TCTGTCAACCTTAATTT-GAATATTGTTGTGG-CTTTTGTTTTTTCCTTAGATACGA	
Oy	1165	TTTTTAAAAAAATATPAAAAGCTACCAATCTTTGTACAATTTGTAAGTGAATTTTT	12244
Db	115	TTTTTAAAAAAATAATPAAAAGCTACCAATCTTTGTACAATTTGTAAGTGAAGAA-TTTT	57
Oy	1225	TTTATATCTCGTAAATTAATAATTTATTTCCACA	1257
Db	56	TTTATATCTCTTTAAATTAATAATTTATTTCCACA	24
RESULT 40			
AKO76498			
LOCUS	AKO76498	1168 bp	mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833429011 product:hypothetical Collagen triple helix repeat containing protein, full insert sequence.		
ACCESSION	AKO76498		
VERSION	AKO76498.1	GI:26096845	
KEYWORDS	HTC, CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meeth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Saeki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsuma, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE	5		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE	6 (bases 1 to 1168)		
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, P., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Niehi, K., Nomura, K., Numasaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saio, H., Saichou, H., Sakaki, C., Sakai, K., Sakazume, N., Sanjo, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T.,		

TITLE	Submitted (16-APR-2002) Yoshihide Hayaishizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-res@isc.riken.jp, URL: http://genome.isc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)			
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.isc.riken.jp/ URL: http://fantom.esc.riken.jp/ Location/Qualifiers			
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	/mol_type="mRNA"			
	/strain="C57BL/6J"			
	/db_xref="FANTOM_DB:4833429011"			
	/db_xref="taxon:10090"			
	/clone="4833429011"			
	/issue_type="head"			
	/clone_id="RIKEN full-length enriched mouse cDNA library"			
	/dev_stage="0 day neonate"			
	76. . 814			
misc_feature	/note="hypothetical Collagen triple helix repeat containing protein (Interpro IPR000087, evidence: InterPro)			
	putative"			
polya_signal	1148. .1153			
	/note="putative"			
polya_site	1168			
	/note="putative"			
ORIGIN				
Query Match	51.8%; Score 651.6; DB 3; Length 1168;			
Best Local Similarity	78.3%; Pred. No. 3.8e-129;			
Matches 878; Conservative	0; Mismatches 219; Indels 25; Gaps 7			
Db	92	CGGTCCTCCGCTCCAGCTCCGCGCTGCCGCGAGCCGAGCCATGCGACCCAGGG	151	
Db	30	CCGACCCCTTTACTCTCTGCTCCGCGCTTCGACGACACCGACACATGACCCCAAG	89	
QY	152	CCCCGCCGCTCCCGCAGCGAGTCCCGG-----CCTCGTGTGCTCTGCTGTCA	205	
Db	90	CCGCGCGGCCCCCGCAGCTGCTGCTGGTCTCTTCTTGCTGTGTGTGTGTCA	149	
QY	206	GCTGCCCGCGCGCTCGAGGCGCTCGAGATCCCAAGGGAGCAAAAGCGAGCTCG	265	
Db	150	GTTGTCCGACCGATCAAGCGCTCTGAGAACCCAAAGTGAACCAAAAGCGTATCCG	209	
QY	266	GCAAGGAGGTGTGTGACCTGTATATATGATGTGCTTCAAAAGGCCAGAGAGTCC	325	
Db	210	GCAAGAGGAGGTGTGTGACCTGTATATATGAGATGTCTCAAGAGCACAGAGAGTCC	269	
QY	326	TGTTCGAGACGGGAGCGCTGGGGGCCAATGTATTCCGGGTACACTGGGATCCAGGTG	385	
Db	270	CGGTCTGTATGGAGACCTCTGGGGCCACAGGCAATCTCGGACACTGGGATCCAGGTG	329	
QY	386	GGATGTGATTCAAAGAGAAAAGGGGAGATGTCTGAGGAAAGCTTTGAGAGTCTGAC	445	
Db	330	GGATGTGATTCAAAGGAGAAAAGGGGAGATGTCTTAAAGGAAAGCTTTGAGAGTCTGAC	389	
QY	446	ACCCATCTCAAGCAAGTGTTCATGTGAGTTCATTGAATTAATGCAATGATCTTGGAAAT	505	
Db	390	CCCAACTATTAAGCAGTGTCTGTGAGATTCGCTGAACTAATGCAATGATCTTGGAAAT	449	

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QY 506 TCCGAGAGTGTACATTTACAAAGATGCGTTCAATATAGTCTTAAGAGTTTGTTCAGTGG 565
DB 450 TCCGAGAGTGTACATTTACAAAGATGCGTTCAATATAGTCTTAAGAGTTTGTTCAGTGG 509
QY 566 CTCACCTTCCGCTAAATGAGAAATGATGCTGTCAGCGCTGGTATTTCAATTCAGTGG 625
DB 510 CTCGCTTCCGCTCAATATGAGAAATGATGCTGTCAGCGCTGGTATTTCAATTCAGTGG 569
QY 626 ACCTGAATGTGAGAGC-TCTTCCATGGAAGCTATATATTTATTTGACCAAGAGAGCC 684
DB 570 ACCTGAATGTGAGAGCCTTCTTCCATGGAAGAGCTATATCTATCTGAGCAAGAGAGCC 629
QY 685 CTGAATGATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 744
DB 630 CTGAATGATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 689
QY 745 GAATGTGCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 804
DB 690 GATATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 749
QY 805 AAGGAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 864
DB 750 AAGGAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 809
QY 865 AATTAATGCTTTAA--TTTTCATTTGCTACT--CTTTTATTTATGCTTGAAG 916
DB 810 AATTAATGCTTGAAGATTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 869
QY 917 TGGTTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 969
DB 870 TGGTTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 929
QY 970 GGAAGCTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1029
DB 930 GGAAGCTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 986
QY 1030 TATTCATTTTGTCTTCATCAAAAGTGTTCATATTTTATTTATTTATTTATTTATTT 1089
DB 987 TACCATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1046
QY 1090 TCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1149
DB 1047 CTAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1106
QY 1150 TCTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1191
DB 1107 TTTCTTTTGAAGACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1148

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RESULT 41
BUE24465/c 671 bp mRNA linear EST 23-SEP-2002
LOCUS BUE24465
DEFINITION UI-H-FGI-Bgk-c-06-0-UI.s1 NCI CGAP FGI Homo sapiens cDNA clone
ACCESSION BUE24465
KEYWORDS UI-H-FGI-Bgk-c-06-0-UI 3', mRNA sequence.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 671)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: James Martin
cDNA library preparation by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained

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FEATURES
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location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FGI-Bgk-c-06-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FGI"
/note="Organ: Enchondroma; Vector: pRT3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FGI is a normalized cDNA library obtained from a
pool of mRNA from 2 cell lines from Enchondroma tissues.
The library was constructed according to Bonaldo, Lennon
and Soares, Genome Research 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pRT3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is CGGTCACTC. The cell lines were provided by Dr.
James Martin from the University of Iowa.
TAG LIB=UI-H-FGI
TAG_SEQ=CGGTCACTC"

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ORIGIN
Query Match 51.7%; Score 649.8; DB 5; Length 671;
Best Local Similarity 99.5%; Pred. No. 8.6e-129;
Matches 651; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 231 GAGATCCCAAGGAGAGCAAAAGCGCACTCCGAGAGGAGTGTGACCTGTAT 290
DB 671 GAGATCCCAAGGAGAGCAAAAGCGCACTCCGAGAGGAGTGTGACCTGTAT 612
QY 291 AATGAAATGTGCTTCAAGAGGCGACAGAGAGTGTGCGAGAGGAGCCCTGGGGCC 350
DB 611 AATGAAATGTGCTTCAAGAGGCGACAGAGAGTGTGCGAGAGGAGCCCTGGGGCC 552
QY 351 AATGTTATTCGCGTACACCTGGATCCAGGTCGAGATGATTCAAAGAGAGAGGGG 410
DB 551 AATGATTCGCGGATACACCTGGATCCAGGTCGAGATGATTCAAAGAGAGAGGGG 492
QY 411 GAATGTGAGGAGAAAGCTTTGAGAGTCTGAGACACCACTACAGACAGTGTTCATGG 470
DB 491 GAATGTGAGGAGAAAGCTTTGAGAGTCTGAGACACCACTACAGACAGTGTTCATGG 432
QY 471 AGTTCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530
DB 431 AGTTCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
QY 531 CGTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 590
DB 371 CGTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 312
QY 591 GCATGCTGTACAGCTGTGATTTTCAATTCATGAGAGTGAATGTTCCAGAGCTTCTCC 650
DB 311 GCATGCTGTACAGCTGTGATTTTCAATTCATGAGAGTGAATGTTCCAGAGCTTCTCC 252
QY 651 ATTGAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 710
DB 251 ATTGAAGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 192
QY 711 CATCCACTTCTTCTGTGAGAGAGCTTTGTGAAGAAATGTGATGATGATGATGATGATGAT 770

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Db 191 CATCGACCTTCTTCTGTGAGAGACTTTGTGAAGAAATTGTCGATTAATGATGTT 132  
 Qy 771 GCTATCTGGGTTGGACCTGTTCAAGATTAACCAAAAGAGATGCTTCTAATGATGAT 830  
 Db 131 GCTATCTGGGTTGGACCTGTTCAAGATTAACCAAAAGAGATGCTTCTAATGATGAT 72  
 Qy 831 TCAGTTTCTCGCATATTATTAAGAACTACCAAAATAATGCTTAAATTTTCA 884  
 Db 71 TCAGTTTCTCGCATATTATTAAGAACTACCAAAATAATGCTTAAATTTTCA 18

RESULT 42  
 BE387335 688 bp mRNA linear EST 21-JUL-2000  
 LOCUS 601276538F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3617432 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BE387335  
 VERSION BE387335.1 GI:9332700  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 688)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: ATCC/DCPD/DTF  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: L10M284 row: 1 column: 09  
 High quality sequence start: 10  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /clone="IMAGE:3617432"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 20"  
 /note="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCAACAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN  
 Query Match 51.1%; Score 641.8; DB 2; Length 688;  
 Best Local Similarity 99.5%; Pred. No. 4.5e-127;  
 Matches 654; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 GGAAGAGAGCGCGCGGTGAAGAGCGCATGATGAGCTGCGGCGCTCGAGCGCGG 60  
 Db 33 GGAAGAGAGCGCGCGGTGAAGAGCGCATGATGAGCTGCGGCGCTCGAGCGCGG 92  
 Qy 61 CGAGAGCAGAGCGCTGACACGCTTCTCTCGTGGCTCCGAGCTCGGCGCTG 120  
 Db 93 CGAGAGCAGAGCGCTGACACGCTTCTCTCGTGGCTCCGAGCTCGGCGCTG 152  
 Qy 121 CCGGAGCGCGGAGCGCATGCGACCCGAGCGCGCGCTCCCGAGCGCGCTCGCG 180  
 Db 153 CCGGAGCGCGGAGCGCATGCGACCCGAGCGCGCGCGCTCCCGAGCGCGCTCGCG 212

Qy 181 GCTCTCTGCTGCTCTGCTGCTGAGCTGCCGCGCGCTGAGCGCTGAGATCCCA 240  
 Db 213 GCTCTCTGCTGCTCTGCTGCTGAGCTGCCGCGCGCTGAGCGCTGAGATCCCA 272  
 Qy 241 AGGGAGCAAAAGCGAGCTCCGCGAGAGAGGTGTGAGCTGTATTAATGAATGT 300  
 Db 273 AGGGAGCAAAAGCGAGCTCCGCGAGAGAGGTGTGAGCTGTATTAATGAATGT 332  
 Qy 301 GCTTCAAGGGCGAGAGAGTGTGTGAGAGCGGAGCGCGCGCAATGTTATTC 360  
 Db 333 GCTTCAAGGGCGAGAGAGTGTGTGAGAGCGGAGCGCGCGCAATGTTATTC 392  
 Qy 361 CGGATACACCTTGGATCCAGAGTGTGATTAAGAGAAAGGAGAAATGTCTGA 420  
 Db 393 CGGATACACCTTGGATCCAGAGTGTGATTAAGAGAAAGGAGAAATGTCTGA 452  
 Qy 421 GGGAAAGCTTTGAGAGTCTCTGAGACCCAACTAAGACAGTGTTCATGAGTTCA 480  
 Db 453 GGGAAAGCTTTGAGAGTCTCTGAGACCCAACTAAGACAGTGTTCATGAGTTCA 512  
 Qy 481 ATTATGATATGATCTTGGAGAAATTTGGAGTGTATTAATTAAGATCGTTCAATA 540  
 Db 513 ATTATGATATGATCTTGGAGAAATTTGGAGTGTATTAATTAAGATCGTTCAATA 572  
 Qy 541 GTGCTCTAAGATTTTGTTCAGTGTCTCACTTCGGCTTAAATGAGAAATGATGCTGTC 600  
 Db 573 GTGCTCTAAGAG-TTGTGTTCAGTGTCTCACTTCGGCTTAAATGAGAAATGATGCTGTC 631  
 Qy 601 AGCGTGTATTTTCAATTCATGAGTGAATTTTCAAGACCTTCCCATTTGAAG 657  
 Db 632 AGCGTGTATTTTCAATTCATGAGTGAATTTTCAAGACCTTCCCATTTGAAG 688

RESULT 43  
 BE896915 688 bp mRNA linear EST 20-OCT-2000  
 LOCUS 601439437F1 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:3924560 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BE896915  
 VERSION BE896915.1 GI:10361827  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 688)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: ATCC/DCPD/DTF  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L10M9762 row: 1 column: 09  
 High quality sequence stop: 685.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /clone="IMAGE:3924560"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 72"  
 /note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 2 kb. Library constructed by Life  
 Technologies."



RESULT 45  
BU624261/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BU624261 654 bp mRNA linear EST 23-SEP-2002  
UT-H-R01-bj1-j-13-0-UI.g1 NCI CGAP\_R01 Homo sapiens CDNA clone  
UT-H-R01-bj1-j-13-0-UI 3', mRNA sequence.  
BU624261  
BU624261.1 GI:23290476  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 654)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: James Martin  
CDNA library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA library arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, bento-soares@uiowa.edu  
The following repetitive elements were found in this CDNA  
sequence: 1-28, >AT richLow\_complexity  
Seq primer: M13 FORWARD  
POLYA=Yes.

**FEATURES**  
**SOURCE**

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location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FG1-bj1-13-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1b="NCI CGAP Fg1"
/notes="Organ: Enchondroma; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Fg1 is a normalized cDNA library obtained from a pool of mRNA from 2 cell lines from Enchondroma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGGTCACTC. The cell lines were provided by Dr. James Martin from the University of Iowa. TAG T73SUB-Enchondroma cell line (Mix of EN1 and EN2) TAG LIB-UI-H-FG1 TAG SEQ=CGGTCACTC"

```

## ORIGIN

	Query Match	Similarity	Score	DB	Length
	Best local	99.7%	Pred. No. 2.3e-125		654
	Matches	635	Conservative	0	Mismatches 2; Indels 0; Gaps 0
Qy	248	GCAAAGGCGCAGCTCCGSCAGAGGAGGTGTGACCTGTATTAATGAAATGCTTACA	307		
Db	654	GCAAAAGGCGCAGCTCCGSCAGAGGAGGTGTGACCTGTATTAATGAAATGCTTACA	595		
Qy	308	AGGGCCAGCAGAGAGTGCCTGTGTGAGACGGAGCCCTGGGGCCCAATGTATTCCGGGTAC	367		
Db	594	AGGGCCAGCAGAGAGTGCCTGTGTGAGACGGAGACCTGGGGCCCAATGTCAATTCGGGTAC	535		
Qy	368	ACCTGGGATCCCAAGTCGGGATGGAATTCAAAGAGAAAAGGGGAATGTCTGAGGGAAG	427		

Db 534 ACCGGGATCCAGGTGGATGGATTCCAGAGAGAAAGGGGAAATGTCTGAGGAAAG 475

QY 428 CTTTGAGAGTCTCTGACACCCAACTAACAAGAGTGTTCATGGAGTTCAATGAATTATGG 487

Db 474 CTTTGAGAGTCTCTGACACCCAACTAACAAGAGTGTTCATGGAGTTCAATGAATTATGG 415

QY 488 CATGATCTTGGGAAAAATTGGGAGTGTACATTATCAAAATGCGTTCAAAATAGTGTCT 547

Db 414 CATGATCTTGGGAAAAATTGGGAGTGTACATTATCAAAATGCGTTCAAAATAGTGTCT 355

QY 548 AAGAGTTTGTTCAGTGGCTCACTTCGCGCTAAATGCGAATAATGCATGCTGCAGCGTTG 607

Db 354 AAGAGTTTGTTCAGTGGCTCACTTCGCGCTAAATGCGAATAATGCATGCTGCAGCGTTG 295

QY 608 GTATTTCACATTCAGTGGAGTGAATGTTCAGACCTCTTCCCATTTGAAGCTATTAATT 667

Db 294 GTATTTCACATTCAGTGGAGTGAATGTTCAGACCTCTTCCCATTTGAAGCTATTAATT 235

QY 668 TTTGGACCAAGGAAGCCCTGAATGAATTCACAATTAATTATCATGSCACTTCTTGT 727

Db 234 TTTGGACCAAGGAAGCCCTGAATGAATTCACAATTAATTATCATGSCACTTCTTGT 175

QY 728 GGAAGACCTTGTGAAGAAATTGGTGTGATTAATGATGATTTGCTATCTGGTGGCAC 787

Db 174 GGAAGACCTTGTGAAGAAATTGGTGTGATTAATGATGATTTGCTATCTGGTGGCAC 115

QY 788 TTGTTCAGATTACCCAAAAGAGATGCTTCTACCTGAGTGAATTCAGTTTCTGSCATCAT 847

Db 114 TTGTTCAGATTACCCAAAAGAGATGCTTCTACCTGAGTGAATTCAGTTTCTGSCATCAT 55

QY 848 TATTGAAGACTACCAAAATAAATGCTTAATTTTCA 884

Db 54 TATTGAAGACTACCAAAATAAATGCTTAATTTTCA 18

RESULT 46  
AL553771/C 676 bp mRNA linear EST 30-MAR-2004  
LOCUS AL553771 Homo sapiens PLACE/NT COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS01077YB01.3-PRIME, mRNA sequence.  
ACCESSION AL553771  
VERSION AL553771.3 GI:45858536  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 676)  
AUTHORS Li, W.B., Graber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On Feb 15, 2001 this sequence version replaced gi:3127585.

For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?b=CSDID077CA0NP1&c=494.1>  
 location/Qualifiers

FEATURES

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QY 667 ATTGGACCAAGAGCCCTGAATGAA-TTCAACAATTATAT 710  
 DB 628 ATTGGACCAAGAGCCCTGAATGAA-TTCAACAATTATAT 672  
 RESULT 48  
 BG421228 1023 bp mRNA linear EST 14-MAR-2001  
 LOCUS 602451719P1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:458956 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG421228  
 VERSION BG421228.1 GI:13327734  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 1023)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LNCM1324 row: f column: 05  
 High quality sequence stop: 679.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:458956"  
 /tissue\_type="renal cell adenocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1ib="NIH MGC 14"  
 /note="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
 ORIGIN  
 Query Match 48.2%; Score 606.2; DB 4; Length 1023;  
 Best Local Similarity 91.3%; Pred. No. 2.1e-119;  
 Matches 722; Conservative 0; Mismatches 58; Indels 11; Gaps 7;

DB 257 AAGGGACCAAAAGCCGAGCTCCGGCAGAGGAGGTGTGACCTGTATATGAAATG 316  
 QY 300 TGGTTCAAGAGGCGACAGAGAGTGCCTGTGTGAGACGGGAGCCCTGGGGCCAAATTAT 359  
 DB 317 TGGTTCAAGAGGCGACAGAGAGTGCCTGTGTGAGACGGGAGCCCTGGGGCCAAATTAT 376  
 QY 360 CCGGGTACACCTGGGATCCAGGTGGGATGGAATCAAGAGGAAAGGGGAAATGTCTG 419  
 DB 377 CCGGGTACACCTGGGATCCAGGTGGGATGGAATCAAGAGGAAAGGGGAAATGTCTG 436  
 QY 420 AGGAAAGCTTTGAGAGTCTTGACACCCAACTACAGAGTGTTCATGAGTTCAATTG 479  
 DB 437 AGGAAAGCTTTGAGAGTCTTGACACCCAACTACAGAGTGTTCATGAGTTCAATTG 496  
 QY 480 A-ATTATGCAATGATCTTGGGAAA--TTGGGAGGTACATTACAAAGATGCGTTC 535  
 DB 497 ACATTATGGCATGATCTTGGGAAA--TTGGGAGGTACATTACAAAGATGCGTTC 556  
 QY 536 --AAATAGTCTCTAAGAGTCTTGTTCAGTGTCTCACTTGGCTAAAATGCAAAATGCA 593  
 DB 557 CAATATGCTCTTAAAGATTTTGTCAAGTGTCTCACTTGGCTAAAATGCAAAATGCA 616  
 QY 594 -TGGTACAGCTTTGATTTTCAATTCAATGAGCTGAATGTTCAGAGACCTTCCCAT 652  
 DB 617 TTGCTGCACGCTGGGATTTTCAATTCAATGAGCTGAATGTTCAGAGACCTTCCCAT 676  
 QY 653 TGA--GCTATATTTATTTTGGACCAAGAGAGCCCTGAATATTTCAATTAATAT 710  
 DB 677 TGAAGGCTATATTTATTTTGGGACCAAGAGAGCCCTGAATATTTCAATTAATAT 736  
 QY 711 CATGCACCTTCTCTGTGG--AAGACTTGTGAGGAATTTGCTGATTAATGATGT 769  
 DB 737 ATCCGACCTCTTGGGAGGAAGACTTGTGAGGAATTTGCTGATTAATGATGT 796  
 QY 770 TGTATCTGGG 780  
 DB 797 TGCCATCTGGG 807  
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 LOCUS CB201936  
 DEFINITION AGNCOCURT\_11289616 NIH\_MGC\_135 Mus musculus cDNA clone  
 IMAGE:30140382 5', mRNA sequence.  
 ACCESSION CB201936  
 VERSION CB201936.1 GI:28236469  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 849)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: Dr. David Rowe  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: NDAM0046 row: f column: 07  
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Qy		903	ATTATGCTTGAATGTTCACTTAATGACATTTTAAATAAGTTATGTAACATCTGA	962
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Qy		963	ATGAAAAGCAAGCTAAATATGTTTACAGACCAAGTGATTCACAGCTGTTTAAAT	1022
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Qy		1143	TGTTTTTCTCTAGTATAGCAATTTTAAATAATATAAAAGCTACCAATCTTTGACAA	1202
Db		127	TGTTTTTCTCTAGTATAGCAATTTTAAATAATATAAAAGCTACCAATCTTTGACAA	68
Qy		1203	TTTGTAAATGTTAAGAAATTTTATATCTGTAAATATAAAATTAATTTTCCACA	1257
Db		67	TTTGTAAATGTTAAGAA- TTTTATATCTGTAAATATAAAATTAATTTTCCACA	14

Search completed: December 25, 2004, 00:26:01  
 Job time : 4416 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_p1us\_p2n model

Run on: December 25, 2004, 05:33:27 ; Search time 4928 Seconds  
(without alignments)  
2673.661 Million cell updates/sec

Title: US-10-063-734-122

Perfect score: 1301  
Sequence: 1 MRPGPASPQRRLGILLLL.....GDASTGMSVSRILIEELPK 243

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4526729 segs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=xrge -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human4.cdi -LIST=100  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL  
-OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLIG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:  
1: gb\_da:  
2: gb\_hcga:  
3: gb\_in:  
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5: gb\_ov:  
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7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_srs:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vl:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	100.0	729	6	AR454023 Sequence
2	1301	100.0	732	6	AR454022 Sequence
3	1301	100.0	837	6	AR454024 Sequence
4	1301	100.0	837	6	AR454025 Sequence

5	1301	100.0	1257	6	AX092390 Sequence
6	1301	100.0	1257	6	AX376298 Sequence
7	1301	100.0	1257	6	AX454660 Sequence
8	1301	100.0	1257	6	AX459648 Sequence
9	1301	100.0	1257	6	AX491138 Sequence
10	1301	100.0	1257	6	AX697362 Sequence
11	1301	100.0	1257	6	AY358914 Homo sapi
12	1294	99.5	732	6	C0714369 Sequence
13	1294	99.5	732	6	BD006704 Novel pol
14	1294	99.5	1220	6	AR405953 Sequence
15	1294	99.5	1221	9	AY136825 Homo sapi
16	1294	99.5	1236	6	BC014245 Homo sapi
17	1294	99.5	1257	6	BD269636 Human sec
18	1294	99.5	1284	6	AX829144 Sequence
19	1291	99.2	1342	6	BD223153 Sequence
20	1291	99.2	1342	6	AR243851 Sequence
21	1286	97.3	1286	6	BD223185 Sequence
22	1286	97.3	1286	6	AR243886 Sequence
23	1258.5	96.7	1288	6	BD193030 Sequence
24	1258.5	96.7	1288	6	C0822026 Sequence
25	1216	93.5	1192	6	AR405952 Sequence
26	1216	93.5	1217	10	AY136824 Rattus no
27	1211	93.1	734	6	AR405955 Sequence
28	1132.5	87.0	1190	9	AK130063 Homo sapi
29	1053.5	81.0	1215	9	AF395488 Homo sapi
30	1052	80.9	1290	5	BX35556 Gallus ga
31	919	70.6	1290	5	BC079494 Danio rer
32	734	56.4	403	6	AR405954 Sequence
33	720	55.3	860	6	AX285214 Sequence
34	650	50.0	539	6	C0412972 Sequence
35	628	48.3	516	6	C0407408 Sequence
36	626	48.1	471	6	AX340025 Sequence
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38	626	48.1	683	6	AR283054 Sequence
39	626	48.1	683	6	AR341827 Sequence
40	626	48.1	683	6	AR343822 Sequence
41	626	48.1	683	6	AR351023 Sequence
42	626	48.1	683	6	AR352789 Sequence
43	626	48.1	683	6	AR453603 Sequence
44	626	48.1	683	6	AX302743 Sequence
45	620	47.7	683	6	AX375790 Sequence
46	536	41.2	687	6	AX067343 Sequence
47	476	36.6	555	6	C0514013 Sequence
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49	454	34.9	396	6	C0665181 Sequence
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51	444.5	34.2	116922	9	AC012213 Homo sapi
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53	427	32.8	453	6	C0394673 Sequence
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56	415	31.9	208553	2	AC145088 Mus muscu
57	407	31.3	1544	6	C0498468 Sequence
58	398.5	30.6	235421	2	AC131363 Rattus no
59	388	29.8	74798	2	AC069352 Homo sapi
60	374.5	28.8	158312	5	BX649637 Zebrafish
61	374	28.7	398	6	C0664298 Sequence
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64	368	28.3	560	6	AX339938 Sequence
65	356	27.4	213269	5	AL844521 Zebrafish
66	310	23.8	466	6	C0712169 Sequence
67	276	21.2	475	6	AX284559 Sequence
68	258	19.8	166810	9	AL590222 Human DNA
69	237	18.2	485	6	C0463279 Sequence
70	169	13.0	460	6	AX351434 Sequence
71	139	10.7	198411	10	AL731670 Rattus no
72	133	10.2	217473	2	AC135154 Rattus no
73	132	10.1	2957	10	BC034164 Mus muscu
74	131.5	10.1	2996	9	AJ293624 Homo sapi
75	130.5	10.0	1485	10	M8933 Mouse alpha
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93	129.5	10.0	6728	9	HSPAL1CO	Z74615 H.sapiens m
94	128.5	9.9	189841	5	AC147717	AC147717 Gallus ga
95	127.5	9.8	4778	10	BC043089	BC043089 Mus muscu
96	127.5	9.8	4786	10	BC052398	BC052398 Mus muscu
97	127.5	9.8	4812	10	BC058724	BC058724 Mus muscu
98	127.5	9.8	24150	2	AL358822	AL358822 Human DNA
99	127	9.8	152196	2	BX548004	BX548004 Danio rer
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## ALIGNMENTS

RESULT 1	
AR454023	
LOCUS	AR454023
DEFINITION	Sequence 511 from patent US 6680197.
Accession	729 bp DNA
	linear
	PAT 20-FEB-2004

ORGANISM Unknown.

Unclassified.

REFERENCE  
AUTHORS  
1 (bases 1 to 729)  
Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L.,  
Hepler, W.T. and Henderson, R.A.

TITLE	Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL	Patent: US 6680197-A 511 20-JAN-2004;
NUMBERS	

FEATURES	Location/Qualifiers
source	1. .729

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/organism="unknown"
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ORIGIN

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Alignment Scores:

Area, NO.:	4.6/e-96	Length:	729
Score:	1301.00	Matches:	2430
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Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-063-734-122 (1-243) X AR454023 (1-729)

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QY 41 GlnLeuAArgGlnAArgIuValAlaSplLeuTYrAsnGlyMetCysLeuGlnGlyProAla 60  
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Db	241	CCAGTGGCGGATGGATTCCAAAGAGAAAAAGGGGGGATGTCTGAGGGGAAACCTTGGAGAG	300
QY	101	serTPhrpAmsnTYrlYsgIuCYsSerTPserserIeAenTYrgIyIleApIu	120
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Db	481	TTCAATGAGACTGGAATGTTCCAGACCTCTTCCCATGAGCAATAAATTATTTTGGACCAA	540
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QY	241	LeuProIYs	243
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AR454022

LOCUS	AR454022	732 bp	DNA	linear	PAT 20-FEB-2004
DEFINITION	Sequence 510 from patent US 6680197.				

ACCESSION	AR454022
VERSION	AR454022.1
	GI:42686812

KEYWORDS	.
SOURCE	Unknown
ORGANISM	Unknown

Unclassified.

REFERENCE  
AUTHORS  
1 (bases 1 to 732)  
Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L.,  
Hepler, W.T. and Henderson, R.A.

**TITLE** Compositions and methods for the therapy and diagnosis of breast cancer  
**JOURNAL** Patent: US 6680197-A 510 20-JAN-2004;

FEATURES	Location/Qualifiers
source	1. .732

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US-10-063-734-122 (1-243) X AR454022 (1-732)

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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProlysglylysglnlysAla 40  
 DB 61 CTGCTGCACTGCCCCCGCCCTGAGCGCTCTGAGATCCCCAAGGGAAGCAAAAGGGG 120  
 QY 41 GlnLeuArgGlnArgGlnValValAlaLeuLeuTyraanglymerCysLeuGlnGlnProAla 60  
 DB 121 CAGCTCCGGCAGAGGAGGTGGTGGACCTGTATTAATGATGTCTTACAAAGGCCAGCA 180  
 QY 61 GlyValProGlyValArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80  
 DB 181 GGAGTGCCTGGTTCGAGACGGAGCCCTGGGGCCAAAGTTAATCCGGGTACACCTGGGATC 240  
 QY 81 ProGlyArgAspGlyPheIysGlyGlyValGlyCysLeuArgGlnSerPheGlnGln 100  
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 DB 421 TTCAGTGGCTCACTTCGCTTAAATTCAGAAATGCAATGCTGTCAGCGTTGGATTTCAACA 480  
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 QY 221 TyrProlysglyAspAlaSerThrGlyTyrlsAsnSerValSerArgIleIleIleGlnGln 240  
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 QY 241 LeuProlyse 243  
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 LOCUS AR454024 Sequence 512 from patent US 6680197.  
 DEFINITION AR454024  
 ACCESSION AR454024  
 VERSION AR454024.1 GI:42686814  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 837)  
 AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L.,  
 TITLE Compositions and methods for the therapy and diagnosis of breast  
 JOURNAL Patent: US 6680197-A 512 20-JAN-2004;  
 FEATURES Location/Qualifiers  
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Score: 1301.00 Matches: 243  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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 DB: 6 Gaps: 0  
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 DB 166 CTGCTGCACTGCCCCCGCCCTGAGCGCTCTGAGATCCCCAAGGGAAGCAAAAGGGG 225  
 QY 41 GlnLeuArgGlnArgGlnValValAlaLeuLeuTyraanglymerCysLeuGlnGlnProAla 60  
 DB 226 CAGCTCCGGCAGAGGAGGTGGTGGACCTGTATTAATGATGTCTTACAAAGGCCAGCA 285  
 QY 61 GlyValProGlyValArgAspGlySerProGlyValAsnValIleProGlyThrProGlyIle 80  
 DB 286 GGAGTGCCTGGTTCGAGACGGAGCCCTGGGGCCAAAGTTAATCCGGGTACACCTGGGATC 345  
 QY 81 ProGlyArgAspGlyPheIysGlyGlyValGlyCysLeuArgGlnSerPheGlnGln 100  
 DB 346 CCAAGTCCGGAGTGAATTCAAAGAGAAAGGGGGAATGCTTGAAGGAAGCTTTGAGAG 405  
 QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120  
 DB 406 TCCTGGACACCCAACTACAAAGCAGTGTTCATGAGTTCAATGATTAATGCAATAGATCTT 465  
 QY 121 GlyValIleAlaGlnCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValIleu 140  
 DB 466 GGAAAAATTGCGAGTACATTACAAAGATGCGTTCAAAATGATGCTTAAAGAGTTTGG 525  
 QY 141 PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTrpTyrlsPheThr 160  
 DB 526 TTCAGTGGCTCACTTCGCTTAAATTCAGAAATGCAATGCTGTCAGCGTTGGATTTCAACA 585  
 QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrlsLeuAspGln 180  
 DB 586 TTCAAATGAGCTGAATGTTCAAGACCTCTCCCATTTGAAGCTAATTAATTTATTTGACCAA 645  
 QY 181 GlySerProGlnuMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200  
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 QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220  
 DB 706 TGTGAAGGAATGGTCTGCTGATTAATGATGTTGCTATCTGGGTGGCACTTTTCAGAT 765  
 QY 221 TyrProlysglyAspAlaSerThrGlyTyrlsAsnSerValSerArgIleIleIleGlnGln 240  
 DB 766 TACCCAAAGAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGCATCATTAATGAAGA 825  
 QY 241 LeuProlyse 243  
 DB 826 CTACCAAAA 834  
 RESULT 4  
 AR454025 837 bp DNA linear PAT 20-FEB-2004  
 LOCUS AR454025 Sequence 513 from patent US 6680197.  
 DEFINITION AR454025  
 ACCESSION AR454025  
 VERSION AR454025.1 GI:42686815  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 837)  
 AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L.,  
 TITLE Compositions and methods for the therapy and diagnosis of breast  
 JOURNAL Patent: US 6680197-A 513 20-JAN-2004;  
 FEATURES Location/Qualifiers  
 1..837  
 /organism="Unknown"  
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 ORIGIN

TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
JOURNAL Patent: US 6680197-A 513 20-JAN-2004;  
FEATURES Location/Qualifiers  
source 1..837  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 5,466-96 Length: 837  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AR454025 (1-837)

QY 1 MetArgProGlnGlyProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20  
Db 106 ATGCAACCCCAAGGGCCCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 165  
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnysAla 40  
Db 166 CTGCTGCAAGCTCCCGCGCTCGAGCGCTCTGAGATCCCAAGGGCAAGAGCGG 225  
QY 41 GlnLeuArgGlnArgGluValValAspLeuTyraSerGlyMetCysLeuGlnGlyProAla 60  
Db 226 CAGCTCCGCGAGAGGAGGAGGTGTGACCTGTGTAATGAGATGCTTACAGGGCCAGCA 285  
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80  
Db 286 GGAGTGCTGTGTCGAGACGGAGCCCTGGGCGCAATGTTATTCGGGTACACCTGGGATC 345  
QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
Db 346 CCAAGTCGGAGATGATTCAGAGAGAGAGAGAGAGAGAGATGTCAGAGAGAGAGAGAG 405  
QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsGlyIleAspLeu 120  
Db 406 TCCGAGACACCACTACAG 465  
QY 121 GlyIysIleAlaGluCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu 140  
Db 466 GGGAAATTTGGGAGGTGATTAATTACAAAGATCGCTTCAATAGCTCTTAAGAGTTTG 525  
QY 141 PheSerGlySerLeuArgLeuIlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160  
Db 526 TTCAATGAGAGGTGATGTTCAAGAGCTCTCCCATTTGAAGCTTAATTAATTGAGACCA 585  
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlsLeuAspGln 180  
Db 586 TTCAATGAGAGGTGATGTTCAAGAGCTCTCCCATTTGAAGCTTAATTAATTGAGACCA 645  
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200  
Db 646 GGAAGCCCTGAATGAATTCACAAATTAATTCACGACCTTCTGTTGAGAGAGACTT 705  
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrlsGlyThrCysSerAsp 220  
Db 706 TGTAAAGAAATTTGCTGCTGAGATGAGATGTTGCTATCTGGGTGGCACTTGTTCAGAT 765  
QY 221 TyrProIysGlyAspAlaSerThrGlyTyraSerSerValSerArgIleIleIleGluGln 240  
Db 766 TACCAAAAAGAGAGATGCTTCTACTGAGATGAGATTCAGTTTCTCGCATCTTAATTGAAGA 825  
QY 241 LeuProIys 243  
Db 826 CTACCAAAA 834

RESULT 5  
AX092390

LOCUS AX092390 1257 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 121 from Patent WO0116318.  
ACCESSION AX092390  
VERSION AX092390.1 GI:13444509  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding the same  
Patent: WO 0116318-A 121 08-MAR-2001;  
Genentech, Inc. (US)

FEATURES  
source 1..1257  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 8,656-96 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AX092390 (1-1257)

QY 1 MetArgProGlnGlyProAlaIaSerProGlnArgLeuArgGlyLeuLeuLeu 20  
Db 138 ATGCAACCCCAAGGGCCCGCGCTCCCGCAGCGGCTCCGCGCTCTGCTGCTCTG 197  
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnysAla 40  
Db 198 CTGCTGCAAGCTCCCGCGCTCGAGCGCTCTGAGATCCCAAGGGCAAGAGCGG 257  
QY 41 GlnLeuArgGlnArgGluValValAspLeuTyraSerGlyMetCysLeuGlnGlyProAla 60  
Db 258 CAGCTCCGCGAGAGGAGGAGGTGTGACCTGTATATGAGATGTGCTTACAGGGCCAGCA 317  
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80  
Db 318 GGAGTGCTGTGTCGAGACGGAGGCTCGGCGCAATGTTATTCGGGTACACCTGGGATC 377  
QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
Db 378 CCAAGTCGGAGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437  
QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsGlyIleAspLeu 120  
Db 438 TCCGAGACACCACTACAG 497  
QY 121 GlyIysIleAlaGluCysThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeu 140  
Db 498 GGGAAATTTGGGAGGTGATTAATTACAAAGATCGCTTCAATAGCTCTTAAGAGTTTG 557  
QY 141 PheSerGlySerLeuArgLeuIlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 160  
Db 558 TTCAATGAGAGGTGATGTTCAAGAGCTCTCCCATTTGAAGCTTAATTAATTGAGACCA 617  
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrlsLeuAspGln 180  
Db 618 TTCAATGAGAGGTGATGTTCAAGAGCTCTCCCATTTGAAGCTTAATTAATTGAGACCA 677  
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200  
Db 678 GGAAGCCCTGAATGAATTCACAAATTAATTCACGACCTTCTGTTGAGAGAGACTT 737

Qy 201 CygIuGlyIleGlyValaGlyLeuValaIleIleTPValGlyThrCysSerap 220  
Db 738 TGTGAAGAAATGGCTGATGATGAGATGATGATGATGATGATGATGAT 797  
Qy 221 TyrProlyseGlyAspAlaSerThrGlyTyrPasnSerValSerArgIleIleIleIleGlu 240  
Db 798 TACCCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGAT 857  
Qy 241 LeuProlys 243  
Db 858 CTACCAAAA 866  
RESULT 6  
AX376298 1257 bp DNA linear PAT 01-MAR-2002  
LOCUS Sequence 365 from Patent WO0168848.  
DEFINITION AX376298  
ACCESSION AX376298  
VERSION AX376298.1 GI:19170540  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P., J.,  
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and  
Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0168848-A 365 20-SEP-2001;  
Genentech, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1.1257  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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ORIGIN  
Alignment Scores:  
Pred. No.: 8.65e-96 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
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Qy 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProIysGlyValGlnVala 40  
Db 198 CTGCTGAGTGGCCCGCGCGCTCGAGGCTCTGAGTATCCCAAGGAGCAAAAGCG 257  
Qy 41 GlnLeuArgGlnArgGlnValaIleAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60  
Db 258 CAGCTCCGCGAGAGGAGGAGTGTGAGACCTGATATATGAAATGCTTACAAAGGCCAGCA 317  
Qy 61 GlyValProGlyArgAspGlySerProGlyValaAsnValIleProGlyThrProGlyTle 80  
Db 318 GGAGTGCCTGTGAGAGCGGAGCGCTGGGGCCATGTTATTCGGGTACACCTGGGATC 377  
Qy 81 ProGlyArgAspGlyPheIysGlyValGlnGlyLeuArgGlyIleSerPheGlnGlu 100  
Db 378 CCAAGTGGGATGATTCAAAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437  
Qy 101 SerTrpThrProAsnTyrIysGlnCysSerTrpSerSerLeuAsnTyrGlyIleAspLeu 120  
Db 438 TCTCGACACCCACATCAAGAGCTGTCTATGAGATTCATGAAATATGCAATGATCTT 497

Qy 121 GlyIysIleAlaGluCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValleu 140  
Db 498 GGGAAATTTGGGAGATGATACATTTACAAAGATGCTTCAAAATAGTCTTAAGAGCTTTG 557  
Qy 141 PheSerGlySerLeuArgLeuIysCysArgAsnAlaCysCysGlnArgTrpTyrPheThr 160  
Db 558 TTCAGTGGCTCATTCCGCTAAATGCAAAATGCAATGCAATGCAATGCAATGCAATGCA 617  
Qy 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGlnValaIleIleTyrLeuAspGln 180  
Db 618 TTCATGAGCTGAATGATGAGGACCTCTCCCATTAAGATTAATTAATTAATTAATTAAT 677  
Qy 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200  
Db 678 GGAAGCTCTGAATATGATATTCACATTAATTAATTAATTAATTAATTAATTAATTAAT 737  
Qy 201 CygIuGlyIleGlyValaGlyLeuValaIleIleTPValGlyThrCysSerap 220  
Db 738 TGTGAAGAAATGGCTGATGATGAGATGATGATGATGATGATGATGATGAT 797  
Qy 221 TyrProlyseGlyAspAlaSerThrGlyTyrPasnSerValSerArgIleIleIleIleGlu 240  
Db 798 TACCCAAAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGAT 857  
Qy 241 LeuProlys 243  
Db 858 CTACCAAAA 866  
RESULT 7  
AX454660 1257 bp DNA linear PAT 06-JUL-2002  
LOCUS Sequence 245 from Patent WO0208284.  
DEFINITION AX454660  
ACCESSION AX454660  
VERSION AX454660.1 GI:21713954  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P., J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 245 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)  
FEATURES  
source Location/Qualifiers  
1.1257  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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ORIGIN  
Alignment Scores:  
Pred. No.: 8.65e-96 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-10-063-734-122 (1-243) x AX454660 (1-1257)  
Qy 1 MetArgProGlnGlyProAlaIleAspProGlnArgLeuArgGlyLeuLeuLeuLeu 20

Db 138 ATGCCACCCGAGGCCCCCGCCCTCCCGACAGCCGCTCCGCGCTCTGCTCTG 197  
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuVal 40  
Db 198 CTGCTGCAAGCTCCCGCCGCTCGAGCGCTCTGAGATCCCGAGGGAGCAAAAGGGG 257  
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60  
Db 258 CAGCTCCGCGAGAGGAGGTGGTGGACCTGTATTAATGATGGCTTACAGAGGGCAGCA 317  
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QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
Db 378 CCAAGTCCGGAGTGGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437  
QY 101 SerThrProAsnTyrIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
Db 438 TCCTGGACACCCCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 497  
QY 121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValIle 140  
Db 498 GGGAAATTTGGCGAGGTACATTACAAAGATGCGTTCAAAATAGTCTTAAGAGATTGG 557  
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Db 558 TTCAGTGCCTCACTTCGGCTAAATGCAAAATGATGCTGTCAGGTTGGATTTTCA 617  
QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180  
Db 618 TTCATGAGAGCTGAATGTTCAAGACCTCTCCCATTAATTAATTATTTGAGCA 677  
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200  
Db 678 GGAAGCCCTGAATGAATTAACAATTAATTAATTAATTAATTAATTAATTAATTAAT 737  
QY 201 CysGluGlyIleGlyValAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220  
Db 738 TGTGAAGAAATGGTGGCTGATTAATGATGTTGATGTTGATGTTGATGTTGATGAT 797  
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGln 240  
Db 798 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGCATTAATTGAAGA 857  
QY 241 LeuProlys 243  
Db 858 CTACCAAAA 866

RESULT 8  
AX459648 1257 bp DNA linear PAT 08-JUL-2002  
LOCUS AX459648  
DEFINITION Sequence 2 from Patent WO0216602.  
ACCESSION AX459648  
VERSION AX459648.1 GI:21725519  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
AUTHORS 1 Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Polakis, P.,  
Williams, P.M., Wood, W.I., Wu, T.D. and Zhang, Z.  
TITLE Compositions and methods for the diagnosis and treatment of tumor  
JOURNAL Patent: WO 0216602-A 2 28-FEB-2002;  
GENENTECH, INC. (US)  
FEATURES  
SOURCE 1. 1257  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:  
Pred. No.: 8,656-96 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AX459648 (1-1257)

QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGlyLeuLeuLeu 20  
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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyLeuVal 40  
Db 198 CTGCTGCAAGCTCCCGCCGCTCGAGCGCTCTGAGATCCCGAGGGAGCAAAAGGGG 257  
QY 41 GlnLeuArgGlnArgGluValAlaAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60  
Db 258 CAGCTCCGCGAGAGGAGGTGGTGGACCTGTATTAATGATGGCTTACAGAGGGCAGCA 317  
QY 61 GlyValProGlyArgAspGlySerProGlyValAlaAsnValIleProGlyThrProGlyIle 80  
Db 318 GGAGTGCCTGGTGGAGCGGAGCCCTGGGGCCAAATGTTATTCGGGTACACCTGGAGATC 377  
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QY 101 SerThrProAsnTyrIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
Db 438 TCCTGGACACCCCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 497  
QY 121 GlyValIleAlaGluCysThrPheThrIleMetArgSerAsnSerAlaLeuArgValIle 140  
Db 498 GGGAAATTTGGCGAGGTACATTACAAAGATGCGTTCAAAATAGTCTTAAGAGATTGG 557  
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QY 161 PheAsnGlyAlaGluCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180  
Db 618 TTCATGAGAGCTGAATGTTCAAGACCTCTCCCATTAATTAATTATTTGAGCA 677  
QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200  
Db 678 GGAAGCCCTGAATGAATTAACAATTAATTAATTAATTAATTAATTAATTAATTAAT 737  
QY 201 CysGluGlyIleGlyValAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220  
Db 738 TGTGAAGAAATGGTGGCTGATTAATGATGTTGATGTTGATGTTGATGTTGATGAT 797  
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleIleGluGln 240  
Db 798 TACCCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTCGCATTAATTGAAGA 857  
QY 241 LeuProlys 243  
Db 858 CTACCAAAA 866

RESULT 9  
AX491138 1257 bp DNA linear PAT 16-AUG-2002  
LOCUS AX491138  
DEFINITION Sequence 245 from Patent WO0200690.  
ACCESSION AX491138  
VERSION AX491138.1 GI:22323906  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Masters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I., and Ye, W.  
TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
JOURNAL Patent: WO 0200690-A 245 03-JAN-2002;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1. 1257  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores:  
Pred. No.: 8.65e-96 Length: 1257  
Score: 1301.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AX491138 (1-1257)

QY 1 MetAArgProGInGlyProAlaAaSerProGInArgLeuArgGlyLeuLeuLeuLeu 20  
Db 138 ATGCGACCCAGGGGCCCCGCGCTCCCGACGCGGCTCCGCGCTCTGCTCTCTG 197

QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlyGlyGly 40  
Db 198 CTGCTCGACGTGCGCGCGCGCTCGAGCGCTCTGAGTCCCAAGGAGGAGGAGCG 257

QY 41 GInLeuArgGInArgGlyValValAlaPLeuTyraSnglyMetCysLeuGInGlyProAla 60  
Db 258 CAGCTCCGGCAGAGGAGGTGTGTGACCTGTATATGTAATGTGCTTCAAGGCGCAGCA 317

QY 61 GlyValProGlyArgAspGlySerProGlyValAlaAsnValLeuProGlyThrProGly 80  
Db 318 GAGGTGCTGTGTGAGAGCGGAGCCCTGGGCGCAATGTATTCGGGTACACCTGGGATC 377

QY 81 ProGlyArgAspGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
Db 378 CCAAGTCGGATGATTCAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437

QY 101 SerTrpThrProAsnTyrlYsGInCysSerTrpSerSerLeuAsnTyrlYleAspLeu 120  
Db 438 TCTTGACACCCCACTACAGACAGGTTCATGAGTTCATTGATTAATGAGCATGATCTT 497

QY 121 GlyValLeuAlaGlyCysThrPheThrIysMetArgSerAsnSerAlaLeuArgValLeu 140  
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Db 558 TTCAGTGTGCTACCTCGCTAAATGCAAGAAATGCAATGCTGCTGCTGCTGCTGCTGCA 617

QY 161 PheAsnGlyValaGlyCysSerGlyProLeuProGlyGluAlaIleIleTyrlYleAspGln 180  
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QY 221 TyrlYleProGlyGlyAspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGlyGlu 240

Db 798 TACCCAAAGAGATCTTACTGATGATGATTCAGTTCCTGCGATCATTAATGAGAA 857  
QY 241 LeuProLys 243  
Db 858 CTACCAAAA 866

RESULT 10  
AX697362  
LOCUS Sequence 430 from Patent WO0078961. 1257 bp DNA linear PAT 02-APR-2003  
DEFINITION AX697362  
ACCESSION AX697362  
VERSION AX697362.1 GI:29498494  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L., Baton, D.L., Gao, W.Q., Pan, J., Borstein, D., Fong, S., Goddard, A., Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.I., Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A., and Watanabe, C.K.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: WO 0078961-A 430 28-DEC-2000;  
Genentech Inc. (US)  
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US-10-063-734-122 (1-243) x AX697362 (1-1257)

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QY 41 GInLeuArgGInArgGlyValValAlaPLeuTyraSnglyMetCysLeuGInGlyProAla 60  
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ORGANISM Homo sapiens (human)  
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1 (bases 1 to 1257)  
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
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Lee,J., Lewis,L., Liao,D., Mark,M., Robble,E., Sanchez,C.,  
Schoenfeld,J., Seshagiri,S., Simons,L., Singh,J., Smith,V.,  
Stinson,J., Vagte,A., Vandlen,R., Watanabe,C., Wiesend,V.,  
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
Goddard,A., Wood,W.I. and Godowski,P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
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2 (bases 1 to 1257)  
Clark,H.F.  
Direct Submission  
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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Alignment Scores:  
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VERSION CQ714369.1 GI:42275226  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

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 1 Venter, C.J., Adams, M.C., Li, P.W., and Myers, E.W.  
 Kite, such as nucleic acid arrays, comprising a majority of  
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 Patent: WO 02068579-A 303 06-SEP-2002;  
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 1 (bases 1 to 732)  
 Ito, Y., Mogi, S., Tanaka, H., Okubo, S. and Ogi, K.  
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 PF 19-MAY-2000 JP 2000147530  
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AUTHORS    Lindner,V. and Friesel,R.E.
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TITLE      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL    Lehner,W., Moore,D.P., Harmon,K.J., Mancini,M.L. and Lindner,V.
            Expression of the novel collagen triple helix repeat-containing
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REFERENCE   2  (bases 1 to 1221)
AUTHORS    Lindner,V.
TITLE      Direct Submission
JOURNAL    Submitted (29-JUL-2002) Center for Molecular Medicine, Maine
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DB 164 CTCTGCGAGTCCCGGCGCGCTCGAGCGCTTCGAGATCCCGAGGAGGAGGAGGCG 223
QY 41 GlnLeuArgGlnArgGlnValAlaAspLeuTyAsnGlyMetCysLeuGlnGlyProAla 60
DB 224 CAGCTCCGCGAGGAGGAGTGTGAGCATCTGTATATGATGATGCTTACAGGCGCAGCA 283
QY 61 GlyValProGlyArgAspGlySerProGlyAlaAsnValIleProGlyThrProGlyIle 80
DB 284 GAGATGCTGCTGTCGAGACGCGGAGCCCGGCGCAATGCGCATTCGCGGTACACCTGGGATC 343
QY 81 ProGlyArgAspGlyPheGlyGlyGlnValGlyCysLeuArgGlnLeuPheGlnGln 100
DB 344 CCGAGTCCGAGATGATTCAGAGGAGGAGGAGGAGATGCTGAGGAGGAGGAGGAG 403
QY 101 SerTrpThrProAsnTyArgGlnCysSerTrpSerSerLeuAsnTyArgIleAspLeu 120
DB 404 TCTCGAGCACCAACTACAGCAAGTGTTCATGAGTTCATGATTAATGATGATGATCTT 463
QY 121 GlyValIleAlaGlnCysThrPheThrIleMetCysSerSerLeuAsnValAlaGlnVal 140
DB 464 GGGAAATTCGAGGAGTGTACATTTACAAACATGCTCAATAGTGTCTTAAAGATTTTG 523
QY 141 PheSerGlySerLeuArgLeuValCysArgAsnAlaCysCysGlnArgTyrPheThr 160
DB 524 TTGAGTGGCTCACTTCGCTTAAATGCAAAATGCAATGCTGCTGAGCGCTGATTTTCACA 583
QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleIleTyLeuAspGln 180
DB 584 TTCATGAGAGCTGAATGTTCAAGACCTCTCCCATTAACATAATTTATTTGAGACCA 643
QY 181 GlySerProGlnMetLeuSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200
DB 644 GGAAGCCCTGAAATGAATTCACAAATTAATTCATGCACTTCTCTGAGAGGAGCTT 703
QY 201 CysGlnGlyIleGlyAlaGlyLeuValAspValAlaIleTrpValGlyThrCysSerAsp 220

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DB 704 TGTGAAGGAATTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 763
QY 221 TTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
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QY 241 LeuProGly 243
DB 824 CTACCAAAA 832

RESULT 16
BC014245
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1236)
Strausberg,R.D., Collins,F.S., Wagner,L.H., Derge,J.G.,
Altechul,S.F., Zeeberg,B., Buetow,K.H., Scheffer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Datchenko,M., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldi,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carinci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hilyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shevchenko,Y.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalek,A., Smallus,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1236)
Strausberg,R.
Direct Submission
Submitted (10-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:15559789.
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Ahter,N., Ayle,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,L.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Latic,P., Legaspi,R.,
Maduro,Q.L., Masello,C., Maskeri,B., Mastrillo,S.D., McKloskey,J.C.,
McDowell,J., Pearson,R., Stantrop,S., Thomas,P.J., Touchman,J.W.,
Teurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILN.ac: <http://image.llnl.gov>  
Series: IRBL Plate: 30 Row: 1 Column: 18  
This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction.

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Location/Qualifiers  
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## ORIGIN

## Alignment Scores:

Pred. No.: 3.12e-95 Length: 1236  
Score: 1294.00 Matches: 242  
Percent Similarity: 99.59% Conservative: 0  
Best Local Similarity: 99.59% Mismatches: 1  
Query Match: 99.46% Indels: 0  
DB: 9 Gaps: 0

US-10-063-734-122 (1-243) x BC014245 (1-1236)

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Db 100 ATGCAACCCAGAGGGCCGCCGCTCCCGAGCGGCTCGGCTGCTGCTCCG 159  
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLLeProLyGlyGInLyAla 40  
Db 160 CTGCTGCAAGCTGCCGCCGCTGCGAGCGCTCTGAGATCCCAAGGGGAGCAAAAGGCG 219  
QY 41 GInLeuATGInATgInuAlaValAspLeuTyraenGlyMetCysLeuGInGlyProAla 60  
Db 220 CAGCTCCGGCAGAGGAGGTGCTGACCTGTATATGATGTGCTTACAAAGGGCCAGCA 279  
QY 61 GlyValProGlyATGAspGlySerProGlyAlaAsnValLLeProGlyThrProGlyLle 80  
Db 280 GAGAGCTGCTGCGAGCGGAGCCCTGGGCAATGCAATTCGCGGTACACTTGAGGATC 339  
QY 81 ProGlyATGAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
Db 340 CCAAGTCCGGAGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399  
QY 101 SerTPThrProAsnTyrlLeGInCysSerTPSerSerLeuAsnTyrlGlyLLeAspLeu 120  
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QY 121 GlyTysLLeaGInCysThrPheThrLysMetATGAspSerAsnSerAlaLeuATgValLeu 140  
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QY 141 PheSerGlySerLeuATgLeuATgCysATgAsnAlaCysCysGInATgTrpTyrrPheThr 160

Db 520 TTCATGTGCTACTTCGGCTAAATGCAAGAAATGCAATGCTGACGCTTGATTTTACA 579  
QY 161 PheAsnGlyAlaGInCysSerGlyProLeuProLLeGInValLLeTyrrLeuAspGIn 180  
Db 580 TTCATGTGAGCTGATGATGTTTACAGACTTCCTCCATTAGATTAATTAATTTTGACCAA 639  
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Db 700 TGTGAAGAAATGATGCTGATTTAGTGATTTGCTGATCTGCGGTGGCACTTGTTGAGAT 759  
QY 221 TyrProLyGlyAspAlaSerThrGlyTTPAsnSerValSerATgLeLLeGInGly 240  
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QY 241 LeuProLyS 243  
Db 820 CTACCAAAA 828

RESULT 17  
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LOCUS BD269636  
DEFINITION Human secretory proteins.  
ACCESSION BD269636  
VERSION BD269636.1 GI:33079404  
KEYWORDS JP 2002537805-A/5.  
SOURCE JP 2002537805-A/5.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1257)  
Tang,T.Y., Lai,P., Baughn,M.R., Yue,H., Young,J.A., Lu,D.A.M. and  
Azimzal,Y.  
Human secretory proteins  
Patent: JP 2002537805-A 5 12-NOV-2002;  
INCYTE PHARMACEUTICALS INC  
OS Homo sapiens (human)  
PN JP 2002537805-A/5  
PF 12-NOV-2002  
PI 03-MAR-2000 JP 2000602763  
PR 05-MAR-1999 US 60/123117  
PI TOM Y TANG, PREETI LAL, MARIAH R BAUGHN, HENRY YUE, JANICE AU PI  
YOUNG.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

PI DYUNG AINA M LU, YALDA AZIMZAI  
PC C12N15/09,A01K67/027,A61K38/00,A61K45/00,A61P1/00,  
PC A61P9/00,  
PC A61P25/00,A61P29/00,A61P31/00,A61P35/00,C07K14/47,C07K16/18,  
PC C12N1/15,  
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PC C12N5/00,A61K37/02,  
PC A61K37/24  
CC Incyte ID No: 978433CBI  
FH Key Location/Qualifiers  
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## ORIGIN

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Percent Similarity: 99.59% Conservative: 0  
Best Local Similarity: 99.59% Mismatches: 1  
Query Match: 99.46% Indels: 0  
DB: 6 Gaps: 0

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QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGlnLeuProArgGlyLeuArgAla 40  
 DB 192 CTGCTGACGCTGCGCCCGCGCTGAGCGCTCTGAGATGCCCAAGGAGGAGGAGGCG 251

QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyraGlnGlyMetCysLeuGlnGlyProAla 60  
 DB 252 CAGCTCCGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 311

QY 61 GlyValProGlnValArgAspGlySerProGlyAlaAsnValLeuProGlyThrProGlyIle 80  
 DB 312 GGAGTCCCTGCTGCAACCGGAGCCCTGGGGCCAAATGCAATCCGGGTACACCTGGGATC 371

QY 81 ProGlnValArgAspGlyPheLeuArgGlyValArgGlyValCysLeuArgGlyLeuPheGlnGlu 100  
 DB 372 CAGGTCGGGATGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 431

QY 101 SerTrpThrProAsnTyrlsGlnCysSerTrpSerSerLeuAsnTyrlsIleAspLeu 120  
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QY 121 GlyValIleAlaGlnCysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140  
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QY 141 PheSerGlySerLeuArgLeuLysCysArgAsnAlaCysCysGlnArgTrpPheThr 160  
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QY 161 PheAsnGlyAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyrlsLeuAspGln 180  
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QY 181 GlySerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeu 200  
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QY 201 CysGlnGlyIleGlyValArgValAspValAlaIleTrpValGlyThrCysSerAsp 220  
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QY 221 TyrProLysGlyAspAlaSerThrGlyTyraAsnSerValSerArgIleIleIleGlnGlu 240  
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QY 241 LeuProLys 243  
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 ACCESSION AX829144  
 VERSION AX829144.1 GI:39838921  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Mack, D.H., Gish, K.C. and Afar, D.  
 TITLE Methods of diagnosis of breast cancer, compositions and methods of screening for modulators of breast cancer  
 JOURNAL Patent: WO 02059377-A 37 01-AUG-2002;  
 FEATURES EOS Biotechnology, Inc. (US)  
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QY 41 GlnLeuArgGlnArgGlnValValAspLeuTyraGlnGlyMetCysLeuGlnGlyProAla 60  
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QY 61 GlyValProGlnValArgAspGlySerProGlyAlaAsnValLeuProGlyThrProGlyIle 80  
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QY 81 ProGlnValArgAspGlyPheLeuArgGlyValArgGlyValCysLeuArgGlyLeuPheGlnGlu 100  
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 DB 503 GGAGAAATTCGCGAGTGTACATTTACAAAGATGCGTTCAAAATGATGCTCTTAAGAGTTTGG 562

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 DEFINITION 98 human secretory proteins.  
 ACCESSION BD223153

VERSION BD223153.1 GI:33032923  
KEYWORDS JP 2002521055-A/88.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1342)  
AUTHORS Komatsu, G.A., Rosen, C.A., Ruben, S.M., Duan, R., Moore, P.A., Shi, Y., Lafleur, D., Wei, Y.F., Ni, J., Florence, K.A., Young, P.E., Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H.S. and Mucenski, M.  
TITLE 98 human secretory proteins  
JOURNAL Patent: JP 2002521055-A 88 16-JUL-2002;  
COMMENT HUMAN GENOME SCIENCES INC  
OS Homo sapiens (human)  
PN JP 2002521055-A/88  
PD 16-JUL-2002  
PF 29-JUL-1999 JP 2000562480  
PR 30-JUL-1998 US 60/094657, 05-AUG-1998 US 60/095486 PR  
06-AUG-1998 US 60/095455, 06-AUG-1998 US 60/095454 PR  
12-AUG-1998 US 60/096319  
PI GEORGE A KOMATSOULIS, CRAIG A ROSEN, STEVEN M RUBEN, ROXANNE DUAN  
PI PAUL A MOORE, YANGU SHI, DAVID LAFLEUR, YING FEI WEI, JIAN NI, PI KIMBERLY A FLORENCE, PAUL E YOUNG, LAURIE A BREWER, DANIEL R PI SOPEY,  
PI GREGORY A ENDRESS, REINHARD EBNER, HENRIK S OLSEN, MICHAEL PI MUCENSKI  
PC C12N15/09, A61K31/713, A61K38/00, A61K48/00, C07K44/47, C07K6/18, PC C12N1/15,  
PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/68, G01N33/15,  
PC G01N33/50, G01N33/53//A61P1/18, A61P5/02, A61P5/06, A61P5/14, A61P9/10,  
PC A61P11/06, A61P17/06, A61P19/02, A61P25/02, A61P25/14, A61P25/16, PC A61P25/28,  
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PC A61K37/02  
CC 98 human secretory proteins  
FH Key Location/Qualifiers  
FT source 1. 1342  
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Query Match: 99.23% Indels: 0  
Gaps: 0  
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DB 381 CCAGTCCGGATGATTCGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 440  
QY 101 SerTPThrProAsnTyrLeuGlyGlySerTyrSerSerLeuAsnTyrGlyIleAspLeu 120  
DB 441 TCCTGAGACCCCACTACACAGACAGTTCATGAGGATTCATGATTCATGATTCATGATTC 500  
QY 121 GlyValIleAlaGlyCysThrPheThrIleSerIleSerIleSerIleSerIleSerIle 140  
DB 501 GGGAAATTCGGAGATGACATTCATTCAAAGATGCTTCATTCATTCATTCATTCATTCAT 560  
QY 141 PheSerGlySerLeuArgLeuLeuGlyCysArgAsnAlaCysCysGlnArgTyrPheThr 160  
DB 561 TTCAGTGGCTCAGCTTCGGCTAAATGACGAAATGCATGCTGTGAGCGTGTGATTCACA 620  
QY 161 PheAsnGlyAlaGlyCysSerGlyProLeuProIleGlnAlaIleTyrLeuAspGln 180  
DB 621 TTCATGAGCTGAGATGTCAGACCTCTCCATTCATTCATTCATTCATTCATTCATTCAT 680  
QY 181 GlySerProGlyLeuAsnSerThrIleAsnIleHisArgThrSerSerValGlyGlyLeu 200  
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QY 201 CysGlyGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220  
DB 741 TGTGAGGAAATGAGTGGCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 800  
QY 221 TyrProGlyGlyAspAlaSerThrGlyTyrAsnSerValSerArgIleIleGlyGlu 240  
DB 801 TACCCAAAGAGATGCTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 860  
QY 241 LeuProLys 243  
DB 861 CTACCAAAA 869  
RESULT 20  
AR243851  
LOCUS AR243851 1342 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 89 from patent US 6476195.  
ACCESSION AR243851  
VERSION AR243851.1 GI:27291344  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1342)  
AUTHORS Komatsu, G., Rosen, C.A., Ruben, S.M., Duan, R.D., Moore, P.A., Shi, Y., Lafleur, D.W., Wei, Y.F., Ni, J., Florence, K.A., Young, P.E., Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H. and Mucenski, M.  
TITLE Secreted protein HNF6P20  
JOURNAL Patent: US 6476195-A 89 05-NOV-2002;  
FEATURES  
source 1. 1342  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 5,97e-95 Length: 1342  
Score: 1291.00 Matches: 241  
Percent Similarity: 99.59% Conservative: 1  
Best Local Similarity: 99.18% Mismatches: 1  
Query Match: 99.23% Indels: 0  
Gaps: 0  
US-10-063-734-122 (1-243) x AR243851 (1-1342)



QY 1 MetArpProGInGlyProAlaAlaSerProGInArGLeuArGlyLeuLeuLeuLeu 20  
DB 141 ATGCACCCCGAGGCCCCCGCCCTCCCGACGGCTCCGCGCTCTGCTGCTCTG 200  
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProGlyGlyGInGlyAla 40  
DB 201 CTGCTGACAGCTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAAGCAAGGCG 260  
QY 41 GInLeuArGInArGInGlyAlaValAlaAspLeuTyraAsnGlyMetCysLeuGInGlyProAla 60  
DB 261 CAGCTCCGCGACAGGAGGTGGTGGACCTGTATTAATGAAATGTGCTTACAAAGGGCCAGCA 320  
QY 61 GIVAlaProGIVArAspGlySerProGIVAlaAanValIleProGIVThrProGIVyle 80  
DB 321 GGAGTCCGCTGTGAGACCGGAGCCCTGGGGCCAAAGGCATTCCGGGTAACCTGGAGATC 380  
QY 81 ProGIVArAspGIVPheLeuGIVGlyGIVGlyCysLeuArGIVSerPheGIVGIn 100  
DB 381 CCAGGTCCGGAGTGAATTCAAAGAGAAAGGGGAAATGCTGAGGAAAGCTTTGAGAG 440  
QY 101 SerTPThrProAsnTyriLeGInCysSerTPSerSerLeuAsnTyriGIVleAspLeu 120  
DB 441 TCCTGACACCCCACTACACAGCAGTGTTCATGAGATTGATTAATGATAGATCTT 500  
QY 121 GIVySIIeAlaGIVCyEThrPheThriYsMetArGSerAsnSerAlaLeuArGValleu 140  
DB 501 GGGAAATTTGCGAGGTGATTCATTACAAAGATGCGTTCAATATGCTCTTAAGAGTTTG 560  
QY 141 PheSerGIVSerLeuArGLeuYsCysArGAsnAlaCysCysGInArGTrPlyPheThr 160  
DB 561 TTCAATGCTGCTCACTTCGCTTAATACAGAAATGCAATGCTGAGAGCTTGATTTTACA 620  
QY 161 PheAsnGIVAlaGIVCysSerGIVProLeuProIleGIVAlaIleIleTyriLeuAspGIn 180  
DB 621 TTCATATGAGCTGAATGTTGAGACCTCTCCCATTAAGATTAATTAATTGAGCA 680  
QY 181 GIVSerProGIVMetArSerThriLeAsnIleHisArGThrSerSerAlaGIVGlyLeu 200  
DB 681 GGAAGCCCTGAAATGATTCACAAATTAATTCATGAGCACTTCTTGTGAAAGACTT 740  
QY 201 CysGIVGlyIleGIVAlaGIVLeuValaAspValaIleTrpValGIVThrCysSerAsp 220  
DB 741 TGTGAAGAAATGCTGCTGATTAAGTGAATGTTGCTGATCTGGGTGGCACTTGTCAGAT 800  
QY 221 TyriProYsGIVAspAlaSerThriTyriPAsnSerValSerArGIVleIleIleGIVGIn 240  
DB 801 TACCAAAAGAGATGCTTCTACTGATGGAATTCAGTTTCTGCAATCATTAATTGAAGA 860  
QY 241 LeuProYs 243  
DB 861 CTACCAAAA 869  
RESULT 21  
BD223185 1286 bp DNA linear PAT 17-JUL-2003  
LOCUS BD223185 98 human secretory proteins.  
DEFINITION BD223185  
ACCESSION BD223185.1 GI:33032955  
VERSION JP 2002521055-A/120.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1286)  
AUTHORS Komatsoulis,G.A., Rosen,C.A., Ruben,S.M., Duan,R., Moore,P.A.,  
Shi,Y., Lafleur,D., Wei,Y.F., Ni,J., Florence,K.A., Young,P.E.,  
Breuer,L.A., Soppet,D.R., Endress,G.A., Edner,R., Olsen,H.S. and  
Mucenski,M.  
TITLE 98 human secretory proteins  
JOURNAL Patent: JP 2002521055-A 120 16-JUL-2002;  
HUMAN GENOME SCIENCES INC  
COMMENT OS Homo sapiens (human)

PN JP 2002521055-A/120  
PD 16-JUL-2002  
PF 29-JUL-1999 JP 2000562480  
PR 30-JUL-1998 US 60/094577,05-AUG-1998 US 60/095486 PR  
06-AUG-1998 US 60/095455,06-AUG-1998 US 60/095454 PR  
12-AUG-1998 US 60/096319  
PI GEORGE A KOMATSOLIS, CRAIG A ROSEN, STEVEN  
M RUBEN, ROXANNE DUAN,  
PI PAUL A MOORE, YANGGU SHI, DAVID LAFLEUR, YING FRI WEI, JIAN NI, PI  
KIMBERLY A FLORENCE, PAUL E YOUNG, LAURIE A BREWER, DANIEL R PI  
SOPET,  
PI GEORGY A ENDRESS, REINHARD EBNER, HENRIK S OLSEN, MICHAEL PI  
MUCENSKI  
PC C12N15/09,A61K31/713,A61K38/00,A61K48/00,C07K14/47,C07K16/18,  
PC C12N1/15,  
PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/68,G01N33/PC  
15,  
G01N33/50,G01N33/53//A61P1/18,A61P5/02,A61P5/06,A61P5/14,A61P9/PC  
10,  
PC A61P11/06,A61P17/06,A61P19/02,A61P25/02,A61P25/14,A61P25/16,  
PC A61P25/24,  
PC A61P25/28,A61P27/02,A61P29/00,A61P31/18,A61P35/02,C12N15/00,  
PC C12N5/00,  
PC A61K37/02  
CC n equals a,c,t,g, or c  
PH Key Location/Qualifiers  
FT source 1.1286  
/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'  
ORIGIN  
Alignment Scores:  
Pred. No.: 5,92e-93 Length: 1286  
Score: 1266.00 Matches: 241  
Percent Similarity: 99.18% Conservative: 0  
Best Local Similarity: 99.18% Mismatches: 2  
Query Match: 97.31% Indels: 1  
DB: Gaps: 0  
US-10-063-734-122 (1-243) x BD223185 (1-1286)  
QY 1 MetArpProGInGlyProAlaAlaSerProGInArGLeuArGlyLeuLeuLeuLeu 20  
DB 131 ATGCACCCCGAGGCCCCCGCCCTCCCGACGGCTCCGCGCTCTGCTGCTCTG 190  
QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGInLeuProGlyGlyGInGlyAla 40  
DB 191 CTGCTGACAGCTCCCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAAAGCAAGGCG 250  
QY 41 GInLeuArGInArGInGlyAlaValAlaAspLeuTyraAsnGlyMetCysLeuGInGlyProAla 60  
DB 251 CA-CTCCGCGACAGGAGGTGGTGGACCTGTATTAATGAAATGTGCTTACAAAGGGCCAGCA 309  
QY 61 GIVAlaProGIVArAspGIVSerProGIVAlaAanValIleProGIVThrProGIVyle 80  
DB 310 GGAGTCCGCTGTGAGACCGGAGCCCTGGGGCCAAATGCAATTCGGGTAACCTGGAGATC 369  
QY 81 ProGIVArAspGIVPheLeuGIVGlyGIVGlyCysLeuArGIVSerPheGIVGIn 100  
DB 370 CCAGGTCCGGAGTGAATTCAAAGAGAAAGGGGAAATGCTGAGGAAAGCTTTGAGAG 429  
QY 101 SerTPThrProAsnTyriLeGInCysSerTPSerSerLeuAsnTyriGIVleAspLeu 120  
DB 430 TCCTGACACCCCACTACACAGCAGTGTTCATGAGATTGATTAATGATAGATCTT 489  
QY 121 GIVySIIeAlaGIVCyEThrPheThriYsMetArGSerAsnSerAlaLeuArGValleu 140

Db 490 GGGAAATTGGGAGTGTACATTTCACAAAGATGCTTCAMATAGTCTTCAGAGTTTG 549

Qy 141 PheSerGISeTLeuArgLeuLysCysArgAsnAlaCysCysGIlnArgTrpIyrPheThr 160

Db 550 TTCAAGTGGCTCACTTCGGCTAAATGCAGAAATGATGCTGTCAGCGTTGGATTTCACA 609

Qy 161 PheAnGIyAlaGIuCySeSerGIyProLeuProIIeGIuAlaIleIleTyrLeuAspGln 180

Db 610 TTCAATGAGCTGAATGTTCAGACCTCTCCCATTTGAAGCATATATTATTTGAGACCA 669

Qy 181 GlySerProGIuMetAsnSerThrIleAsnIleHisArgThrSerSerValGIuGIuLeu 200

Db 670 GGAAGCCCTGAAATGAATTCACAAATTAATTCACGACCTTCTGTGGAGAGACTT 729

Qy 201 CysGIuGIyIleGIyAlaGIyLeuValAspValAlaIleTrpValGIyThrCysSerAsp 220

Db 730 TGTGAAGAAATGGTGTGCTGATTAAGTGTGCTACTGCTGCTGGCTTGGCACTTTCAGAT 789

Qy 221 TyrProLysGIyAspAlaSerThrGIyTrpAsnSerValSerArgIleIleIleGIuGln 240

Db 790 TACCCAAAGAGATGCTTCTACTGATGAGATTCAGTTTCTGCATCATTTATGAAGA 849

Qy 241 LeuProLys 243

Db 850 CTACCAAAA 858

RESULT 22

AR243886 1286 bp DNA linear PAT 20-DEC-2002

LOCUS Sequence 124 from patent US 6476195.

DEFINITION AR243886

ACCESSION AR243886

VERSION AR243886.1 GI:27291379

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1286)

AUTHORS Komatsu, G., Rosen, C.A., Ruben, S.M., Duan, R.D., Moore, P.A., Shi, Y., Lafleur, D.W., Wei, Y.-F., Ni, J., Florence, K.A., Young, P., Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H. and Mucenki, M.

TITLE Secreted protein HNF20

JOURNAL Patent: US 6476195-A 124 05-NOV-2002;

FEATURES

source Location/Qualifiers

1..1286

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 5,92e-93 Length: 1286

Score: 1266.00 Matches: 241

Percent Similarity: 99.18% Conservatave: 0

Best Local Similarity: 99.18% Mismatches: 2

Query Match: 97.31% Indels: 1

Gaps: 0

US-10-063-734-122 (1-243) x AR243886 (1-1286)

Qy 1 MetArgProGIuNGIyProAlaAlaSerProGIlnArgLeuArgIyLeuLeuLeuLeu 20

Db 131 ATGGAGACCCAGGGGCCCGCGCTCCCGCAGCGGCTCCGCGGCTCTCTGCTCTG 190

Qy 21 LeuLeuGIlnLeuProAlaProSerSerAlaSerGIuIleProLysGIyLysGIlnLysAla 40

Db 191 CTGCTGAGCTGCCCCCGCGCTCAAGCCCTCTGAGATCCCAAGGGAGCAAGAGCG 250

Qy 41 GlnLeuArgIlnArgIlnValAlaAspLeuTyrAsnGIyMetCysLeuGIlnGIyProAla 60

Db 251 CA-CTCCGGAGAGAGAGGTGTGAGCTGTATATGGAATGTGCTTCAAGGGCGACCA 309

Qy 61 GlnValProGIyArgAspGIySerProGIyAlaAsnValIleProGIyThrProGIyIle 80

Db 310 GAGAGCTGCTGTGAGACGGAGCCCTGGGGCCAAATGAGCATTCGGGTACACCTGGGATC 369

Qy 81 ProGIyArgAspGIyPheLysGIyGIuLysGIyGIuCySeLeuArgGIuSerPheGIuGln 100

Db 370 CCAAGTCCGAGTGAATTCATCAAGAGGAAAGGGGAAATGCTTGAGGAAACCTTTGAGAG 429

Qy 101 SerTrpThrProAsnTyrLysGlnCysSerTrpSerSerLeuAsnTyrGIyIleAspLeu 120

Db 430 TCTGAGACACCACTAACAGACAGTGTTCATGAGATTCAATGAATTAATGACATAGATCTT 489

Qy 121 GlyLysIleAlaGIuCySerThrPheThrLysMetArgSerAsnSerAlaLeuGValLeu 140

Db 490 GGGAAATTGGGAGGTGTACATTTACAAAGATGCTTCAATATGTGCTCTCAAGAGTTTG 549

Qy 141 PheSerGISeTLeuArgLeuLysCysArgAsnAlaCysCysGIlnArgTrpIyrPheThr 160

Db 550 TTCAAGTGGCTCACTTCGGCTAAATGCAGAAATGATGCTGTCAGCGTTGGATTTCACA 609

Qy 161 PheAnGIyAlaGIuCySeSerGIyProLeuProIIeGIuAlaIleIleTyrLeuAspGln 180

Db 610 TTCAATGAGCTGAATGTTCAGACCTCTCCCATTTGAAGCATATATTATTTGAGACCA 669

Qy 181 GlySerProGIuMetAsnSerThrIleAsnIleHisArgThrSerSerValGIuGIuLeu 200

Db 670 GGAAGCCCTGAAATGAATTCACAAATTAATTCATGACCTTCTGTGGAGAGACTT 729

Qy 201 CysGIuGIyIleGIyAlaGIyLeuValAspValAlaIleTrpValGIyThrCysSerAsp 220

Db 730 TGTGAAGAAATGGTGTGCTGATTAAGTGTGCTACTGCTGCTGGCTTGGCACTTTCAGAT 789

Qy 221 TyrProLysGIyAspAlaSerThrGIyTrpAsnSerValSerArgIleIleIleGIuGln 240

Db 790 TACCCAAAGAGATGCTTCTACTGATGAGATTCAGTTTCTGCATCATTTATGAAGA 849

Qy 241 LeuProLys 243

Db 850 CTACCAAAA 858

RESULT 23

BD193030 1288 bp DNA linear PAT 17-JUL-2003

LOCUS 207 human secreted proteins.

DEFINITION BD193030

ACCESSION BD193030.1 GI:133002769

VERSION JP 2002516573-A/124.

KEYWORDS

SOURCE JP 2002516573-A/124.

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 1288)

AUTHORS Young, P., Greene, J.M., Ferrle, A.M., Ruben, S.M., Rosen, C.A., Hu, J.S., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y., Florence, C., Florence, K., Lafleur, D.W., Ni, J., Fan, P., Wei, Y.F., Fischer, C.L., Soppet, D.R., Li, Y., Ze, Z., Kyaw, H., Yu, G.L., Feng, P., Dillon, P.J., Endress, G.A. and Carter, K.C.

TITLE 207 human secreted proteins

JOURNAL Patent: JP 2002516573-A 124 04-JUN-2002;

HUMAN GENOME SCIENCES INC

PN JP 2002516573-A/124

PD 04-JUN-2002

PF 04-JUN-1998 JP 1999502815

PR 06-JUN-1997 US 60/048915, 06-JUN-1997 US 60/048882 PR

06-JUN-1997 US 60/048892, 06-JUN-1997 US 60/048901 PR

06-JUN-1997 US 60/048900, 06-JUN-1997 US 60/048893 PR

06-JUN-1997 US 60/048864, 06-JUN-1997 US 60/048884 PR

06-JUN-1997 US 60/048894, 06-JUN-1997 US 60/048971 PR

06-JUN-1997 US 60/048881, 06-JUN-1997 US 60/049375 PR

06-JUN-1997 US 60/048896, 06-JUN-1997 US 60/048860 PR

06-JUN-1997 US 60/048876, 06-JUN-1997 US 60/049020 PR

06-JUN-1997 US 60/049019, 06-JUN-1997 US 60/048935 PR

06-JUN-1997 US 60/048870, 06-JUN-1997 US 60/048916 PR

06-JUN-1997 US 60/048970, 06-JUN-1997 US 60/048972 PR

06-JUN-1997 US 60/048949, 06-JUN-1997 US 60/048974 PR

06-JUN-1997 US 60/048883, 06-JUN-1997 US 60/048897 PR



US-10-063-734-122 (1-243) x CQ822026 (1-1288)

QY 1 MetArgProGInGlyProAlaIAsrProGInArgLeuArgGlyLeuLeuLeu 20  
 Db 130 ATGCACCCCGAGGCGCGCGCTCCCGCAGCGGCTCCGGCGCTCTGCTGCTCG 189  
 QY 21 LeuLeuGInLeuProAlaProSerSerAlaSerGluIleProGlyGlyGlyGln 40  
 Db 190 CTGCTGCGAGCTCCCGCGCGCTCCGAGCGCTCTGAGATCCCAAGGGAGCAAAAGCG 249  
 QY 41 GInLeuArgGInArgGluValAlaIAsrLeuTyraGlyMetCysLeuGInGlyProAla 60  
 Db 250 C-ATCCCGCAGAGGAGGTGCTGAGCCTGTATATGAAATGCTTACAGAGGCGCAGCA 307  
 QY 61 GlyValProGlyArgAspGlySerProGlyAlaIAsrValIleProGlyThrProGlyIle 80  
 Db 308 GGAAGTCTGTGTCAGACCGAGCGCTGGGCGCAATGGCATTCCGGGTAACCTGGGATC 367  
 QY 81 ProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
 Db 368 CCAGGTCCGGATGATTCATAAGAGAGAAAGGGGATGCTGAGGGAAGCTTTGAGAG 427  
 QY 101 SerThrProArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120  
 Db 428 TCCGAGACACCACTACAGAGGCTTCATGAGTTCATGAAATATGAGCATAGATCTT 487  
 QY 121 GlyIleAlaIAsrGlyThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeu 140  
 Db 488 GGGAAATTCGGAGGTGATTCATTCAAGAGATGCTTCAAAATAGTCTTAAAGAGTTTG 547  
 QY 141 PheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTyrPheThr 160  
 Db 548 TTCAAGTGGCTACTCGCTAAATGCAAGATGATGCTGTCAGGTTGGATTTTCA 607  
 QY 161 PheLeuGlyAlaGlyCysSerGlyProLeuProIleGluAlaIleIleTyrLeuAspGln 180  
 Db 608 TTCAATGAGGTGATGATGTCAGAGCTCTCCCATTAAGCTAATATTAATTTGACCA 667  
 QY 181 GlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeu 200  
 Db 668 GGAAGCCTGAATGAAATTCACACATTAATTCACGACTCTCTTCGTGAGAGACTT 727  
 QY 201 CysGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAsp 220  
 Db 728 TGTGAGGAAATGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 787  
 QY 221 TyrProGlySerAlaAspAlaSerThrGlyTyrPheSerValSerArgIleIleIleGlu 240  
 Db 788 TACCAAAAGAGAGATGCTTCTACTGATGAGATGAGATGAGATGAGATGAGAT 847  
 QY 241 LeuProLys 243  
 Db 848 CTACCAAAA 856

RESULT 25  
 AR405952 1192 bp DNA linear PAT 18-DEC-2003  
 LOCUS AR405952  
 DEFINITION Sequence 1 from patent US 6630325.  
 ACCESSION AR405952  
 VERSION AR405952.1 GI:40155008  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.  
 REFERENCE 1 (bases 1 to 1192)  
 AUTHORS Lindner V. and Friesel R.E.  
 TITLE Compositions, methods and kits relating to remodell  
 JOURNAL Patent: US 6630325-A 1 07-OCT-2003;  
 FEATURES  
 1. 1192  
 /organism="Unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

## Alignment Scores:

Pred. No.: 5,89e-89 Length: 1192  
 Score: 1216.00 Matches: 231  
 Percent Similarity: 95.51% Conservative: 3  
 Best Local Similarity: 94.29% Mismatches: 2  
 Query Match: 93.47% Indels: 9  
 DB: 6 Gaps: 1

US-10-063-734-122 (1-243) x AR405952 (1-1192)

QY 1 MetArgProGInGlyProAlaIAsrProGInArgLeuArgGly-----LeuLeu 18  
 Db 97 ATGCACCCCGAGGCGCGCGCTCCCGCAGCGTCTGCTGCTCTCTCTTCTTGTCTA 156  
 QY 19 LeuLeuLeuGInLeuProAlaProSerSerAlaSerGluIleProGlyGlyGln 38  
 Db 157 CTGCTGCTTCTGAGCTGTCCGCGCGCTCCAGCGCTCTGAGATCCCAAGTGAGCA 216  
 QY 39 LysAlaGInLeuArgGInArgGluValAlaIAsrLeuTyraGlyMetCysLeuGInGly 58  
 Db 217 AAGCGCTGATCCGACAGAGGAGAGTGTAGACCTGTATATGAGATGCTTACAGAG 276  
 QY 59 ProAlaGlyValProGlyArgAspGlySerProGlyAlaIAsrValIleProGlyThrPro 78  
 Db 277 CCAGCAGAGATTCCTGTGCGGATGAGAGCCCTGGGCCAATGGCATTCCTGCGACACCG 336  
 QY 79 GlyIleProGlyArgAspGlyPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGly 98  
 Db 337 GGAATCCCGAGGTCCGGATGATTCATAAGAGAGAAAGGGAGGCTTAAAGGAAAGCTTT 396  
 QY 99 GluGluSerThrProArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 118  
 Db 397 GAGGATCTGAGCCCAAACTACAGACAGTTCATGAGGATGACTTAAATTAATGACATA 456  
 QY 119 AspLeuGlyLysIleAlaGlyCysThrPheThrLysMetArgSerAsnSerAlaLeuArg 138  
 Db 457 GATCTTGGGAAATTCGGGAATGTACATTCAAAAGATGGATCCAAAGCGCTCTTCCA 516  
 QY 139 ValLeuPheSerGlySerLeuArgLeuGlyCysArgAsnAlaCysCysGlnArgTyrPhe 158  
 Db 517 GTTCTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 576  
 QY 159 PheThrPheLeuGlyAlaGlyCysSerGlyProLeuProIleGluAlaIleIleTyrLeu 178  
 Db 577 TTTACCTTTAATGAGAGCTGATGATGTCAGACCTCTTCCCATTAAGCTATCATCTATCTG 636  
 QY 179 AspGlnGlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlu 198  
 Db 637 GACCAAGAGAGCCCTGAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 696  
 QY 199 GlyLeuGlyGluGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCys 218  
 Db 697 GGACTCTGTGAAGGATGCTGCTGAGCTGTGAGACGTGACCTGCGGCTGCGCACCTGT 756  
 QY 219 SerAspTyrProGlySerAlaAspAlaSerThrGlyTyrPheSerValSerArgIleIle 238  
 Db 757 TCAATTAATCCCAAGAGAGAGCGCTTCTACTGAGTGAATTCGTGTGCGCATCATCAT 816  
 QY 239 GluGluLeuProLys 243  
 Db 817 GAAGAACTACCAAAA 831

RESULT 26  
 AY136824 1217 bp mRNA linear ROD 01-DEC-2002  
 LOCUS AY136824  
 DEFINITION Rattus norvegicus collagen triple helix repeat-containing protein 1  
 (Chcrl1) mRNA, complete cds.  
 ACCESSION AY136824  
 VERSION AY136824.1 GI:25989618  
 KEYWORDS  
 SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 1217)  
AUTHORS Lehnert, W., Moore, D. P., Harmon, K. J., Mancini, M. L. and Lindner, V.  
TITLE Expression of the novel collagen triple helix repeat-containing  
gene (Cthrc1) suggests functions in multiple organ systems  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1217)  
AUTHORS Lindner, V.  
TITLE Direct Submission  
JOURNAL Submitted (29-JUL-2002) Center for Molecular Medicine, Maine  
Medical Center Research Institute, 81 Research Drive, Scarborough,  
ME 04074, USA  
FEATURES  
source location/Qualifiers  
1..1217  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/tissue\_type="8 day balloon-injured carotid artery"  
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/gene="Cthrc1"  
117..854  
/gene="Cthrc1"  
/note="matrix protein"  
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/product="collagen triple helix repeat-containing protein  
1"  
/protein\_id="AA15748.1"  
/db\_xref="GI:2598619"  
/translation="MHQRRASPOLLLGLPIVLLILLDLSAPSSASENPKYKRALI  
KREAVDLNGMLQDPAGVPRSDSGMNGIPGTGIRGRGFKESKESPEE  
SWTPYKQCSWSLNYGIDLGKIAECTFKMSNSALRYLFGSLRLKCRNACQGRWY  
FTFNAGCSGLPIEALIVLDGSPELNNTINIHRTSVYGLCEGIGLVVAIWWG  
TSDYPKGDASTGMNSVSRRIIEELPK"  
ORIGIN  
Alignment Scores:  
Pred. No.: 6,03e-89 Length: 1217  
Score: 1216.00 Matches: 231  
Percent Similarity: 95.51% Conservative: 3  
Best Local Similarity: 94.29% Mismatches: 9  
Query Match: 93.47% Indels: 2  
DB: 10 Gaps: 1  
US-10-063-734-122 (1-243) x AY136824 (1-1217)  
QY 1 MetArgProGlnGlyProAlaAlaSerProGlnArgLeuArgGly-----LeuLeuLeu 18  
DB 117 ATGCACCCCCAAGGCGCGCGCTCCACACAGCTGCTCGGCTCTTCTTGCTA 176  
QY 19 LeuLeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGln 38  
DB 177 CTGCTGCTTCTGACGTGCTCGGCGCTCCAGGCTCTGAGAAATCCCAAGGGAAGCAA 236  
QY 39 LysAlaGlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGly 58  
DB 237 AAAGCGCTGATCCGAGAGGAGGAGTGTAGACTGTATATATGAGATGCTTACAAAGA 296  
QY 59 ProAlaGlyValProGlyTyrArgAspGlySerProGlyValAlaAsnValLeuProGlyThrPro 78  
DB 297 CCAGCAGGAGTTCCTGCTGCGAGTGGAGCCCTGGGCGCAATGGCAATTCCTGGCACACCG 356  
QY 79 GlyLeuProGlyValArgAspGlyPheLeuGlyGluLeuGlyGluCysLeuArgGlySerPhe 98  
DB 357 GGAATCCGAGCTCGGATGATTCAAAGAGAGAAAGGAGAGTCTTAAGGAAACCTTT 416  
QY 99 GluGluSerTyrThrProAlaTyrLysGlnCysSerTyrSerSerLeuAlaTyrGlyLeu 118  
DB 417 GAGGATCTCTGGACCCCAAACTACAGCAGTGTTCATGAGATTCACTAATATATGCAAT 476

QY 119 AspLeuGlyLysIleAlaGluCysThrPheThrLysMetArgSerAsnSerAlaLeuArg 138  
DB 477 GATCTGGGAAATATGCGGAATGTACATTCACAAAGATGCCATCCACAGCGCTCTTCA 536  
QY 139 ValLeuPheSerGlySerLeuArgLeuLysCysValGlnAlaCysCysGlnArgTyr 158  
DB 537 GTTCTGTTACAGTGCTCTGCTTCCGCTCAATGACAGAAATGCTGTGTCACAGCTGGAT 596  
QY 159 PheThrPheAsnGlyValAlaGluCysSerGlyProLeuProIleGluAlaIleLeuTyrLeu 178  
DB 597 TTTACCTTAAATGAGAGCTGAATGTTCAGACCTCTTCCATTGAACTATCATCTATCTG 656  
QY 179 AspGlnGlySerProGluMetAsnSerThrIleAsnIleHisArgThrSerSerValGlu 198  
DB 657 GACCAAGAGAGCCCTGAGTAAATTCACATTAATATTCATCGTACTTCCCTCGGAGAA 716  
QY 199 GlyLeuCysGluGlyTyrGlyValAlaGlyLeuValAspValAlaIleTyrValGlyThrCys 218  
DB 717 GGACTCTGAAAGGAGATTTGCTGCTGAGCTGAGACGTGGCCATCTGGGCTCGCACCTGT 776  
QY 219 SerAspTyrTyrProLysGlyAspAlaSerThrGlyTyrPheAsnSerValSerArgIleIle 238  
DB 777 TCAGATTACCCCAAGAGAGACGCTTCTACTGGGTGGAATTCGTGTCCGCAATCAT 836  
QY 239 GluGluLeuProLys 243  
DB 837 GAGAACTACCAAAA 851  
RESULT 27  
LOCUS AR405955 734 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 9 from patent US 6630325.  
ACCESSION AR405955  
VERSION AR405955.1 GI:40155011  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 734)  
AUTHORS Lindner, V. and Friesel, R.E.  
TITLE Compositions, methods and kits relating to remodel  
JOURNAL Patent: US 6630325-A 9 07-OCT-2003;  
FEATURES location/Qualifiers  
source 1..734  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 8,62e-89 Length: 734  
Score: 1211.00 Matches: 230  
Percent Similarity: 95.88% Conservative: 3  
Best Local Similarity: 94.65% Mismatches: 8  
Query Match: 93.08% Indels: 2  
DB: 6 Gaps: 1  
US-10-063-734-122 (1-243) x AR405955 (1-734)  
QY 3 ProGlnGlyProAlaAlaSerProGlnArgLeuArgGly-----LeuLeuLeuLeu 20  
DB 6 CCCAAAGGCGGCGCGCTCCACACAGCTGCTCGGCTCTTCTTGTGCTACTGCTG 65  
QY 21 LeuLeuGlnLeuProAlaProSerSerAlaSerGluLeuProGlyGlyGlnLysAla 40  
DB 66 CTTTCTGACGCTGCTCGGCGCTCCAGCGCTCTGAGAAATCCCAAGGTGAAGAAAAAGCG 125  
QY 41 GlnLeuArgGlnArgGluValValAspLeuTyrAsnGlyMetCysLeuGlnGlyProAla 60  
DB 126 CTGATCCGACAGAGGAGAAATGTAACCTGTATATGGATGTGCTTACAGACACAGCA 185  
QY 61 GlyValProGlyValArgAspGlySerProGlyValAlaAsnValIleProGlyThrProGly 80  
DB 186 GGAATTCCTGCTGCGATGAGAGCCCTGGGCGCAATGCAATTCCTGCGACACCGGGAATC 245



AF395488  
 LOCUS AF395488 1215 bp mRNA linear pri 07-JUN-2003  
 DEFINITION Homo sapiens NTMC1 mRNA, complete cds.  
 ACCESSION AF395488  
 VERSION AF395488.1 GI:27525623  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1215)  
 AUTHORS Sanuki,N., Fujiki,K., Kanai,A., Tanaka,Y. and Iwata,T.  
 TITLE Novel polypeptide found in human cornea cDNA library  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1215)  
 AUTHORS Sanuki,N., Fujiki,K., Kanai,A., Tanaka,Y. and Iwata,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JUN-2001) National Center for Sensory Organs, National Tokyo Medical Center, 2-5-1 Higashi-gaoka, Meguro, Tokyo 152-8902, Japan  
 FEATURES  
 source location/Qualifiers  
 1..1215  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 121..819  
 /codon\_start=1  
 /product="NTMC1"  
 /protein\_id="AA017919.1"  
 /db\_xref="GI:27525624"  
 /translation="MMPGRSITTVKLRKTVSRKLEMGPSAFQGLCGKYNMCLQG PAVGRDGPNGANGIPGPGIRGRDGEGLRESFESMTPTNPKQCSWSLNY GIDLGKIECTTKMRNSALAFVPSGSLRKCRAACQRMWFTNGAEGSGPLIEA IYLDGSGPBNASTINIRHRSVSEGLCEIGALVDVAIWGTGSDYPRGADSTGMS VSRILIEELPYML"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 7,81e-76 Length: 1215  
 Score: 1053.50 Matches: 210  
 Percent Similarity: 80.22% Conservative: 9  
 Best Local Similarity: 76.92% Mismatches: 16  
 Query Match: 80.98% Indels: 38  
 DB: 9 Gaps: 6  
 US-10-063-734-122 (1-243) x AF395488 (1-1215)  
 QY 1 McatArgProGln-----GlyProAlaAlaSerProGlnArgLeuArg-GlyLe 16  
 Db 9 TTAAGGCCCGAAGGAATGAAGGGCCCGCGCTAACCT-----CTAAGGACCTGT 62  
 QY 16 uLeuLeuLeuLeuLeuGlnLeuProAlaProSerSerAlaSerGluIle----- 33  
 Db 63 TTTGCTTCTGTTT-----AAACCAATGGCGAGTCTGTCAATTACACACAC 107  
 QY 34 -----Prolysglyysgln---lysaIaglnLeuArgGlnArgG1 46  
 Db 108 CTTGGCTTTCATATGTCGGCCGACAGTACATCACAGTCAAGTACGGGAGAAAC 167  
 QY 46 uVal-----ValAspLe 50  
 Db 168 AGTTTCCAGGAACCTGGAATGACGCGCCGAGTCTTCCAGGGGCTCATCTGCGGAA 227  
 QY 50 uTyrAnglyMetCysLeuGlnGlyProAlaGlyValProGlyArgAspGlySerProG1 70  
 Db 228 GATATATGGAATGTGTCTTCAAGGGCCACAGAGAGTGTCTGTCGAGACGGAGCCCTG 287  
 QY 70 yAlaAsnValIleProGlyThrProGlyIleProGlyArgAspGlyPheGlyGlyGly 90  
 Db 288 GGCCAAATGGCATTTCCGGGTACACCTGGGATCCAGGTGGAGATTCAAAGAGAAAA 347  
 QY 90 sGlyGluCysLeuArgGluSerPheGluGluSerTyrThrProAsnTyrIleGlnCysSe 110

Db 348 GGGGGAATGTCTGAGGGAAGCTTTGAGAGTCTTGAGACACCAACTACAGCAGTGTTC 407  
 QY rThrsSerSerLeuAsnTyrGlyIleAspLeuGlyValIleIleGlyCysThrPheThrLy 130  
 Db 408 ATGGAGTTCATTGAATATATGAGCATAGATCTGGGAAAAATGGGAGTGTACATTACAA 467  
 QY 130 sMetArgSerAsnSerAlaLeuArgValIlePheSerGlySerLeuArgLeuLeuCysAr 150  
 Db 468 GATGCGTTCAAAATATGTCTTAAGAGTTTGTTCAGTGGCTCATTGGCTAAATATGCG 527  
 QY 150 gAsnAlaCysCysGlnArgTyrPheThrPheAsnGlyValaGluCysSerGlyProle 170  
 Db 528 AAATCATAGCTGTGACCGCTGGTATTTCAATTCAATGAGAGTGAATGTTTCAGACCTCT 587  
 QY 170 uProIleGluAlaIleIleTyrLeuAspGlnGlySerProGluMetAsnSerThrIleAs 190  
 Db 588 TCCCAATGAAGCTAATATTAATTTGACCAAGAAAGCCCTGAATGAATCAACATTTAA 647  
 QY 190 nIleHisArgThrSerSerValGluGlyLeuCysGluGlyIleGlyValaGlyLeuValAs 210  
 Db 648 TATTATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGAAATGCTGCTGATTAATGTA 707  
 QY 210 pValAlaIleTyrValGlyThrCysSerAspTyrProlysglyAspAlaSerThrGlyTr 230  
 Db 708 TGTTCCTATCTGGGTGGCATTGTTCAGATTACCCAAAGAGATGCTTCTACTGATG 767  
 QY 230 pAsnSerValSerArgIleIleIleGluGluLeuPro 242  
 Db 768 GAATTCAGTTCTCGCATCATTAATGAAGAACTACCA 804  
 RESULT 30  
 BX935556 1009 bp mRNA linear VRT 30-MAR-2004  
 LOCUS BX935556  
 DEFINITION Gallus gallus finished cDNA, clone CHEST82913.  
 ACCESSION BX935556  
 VERSION BX935556.2 GI:46018669  
 KEYWORDS  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.  
 REFERENCE 1 (bases 1 to 1009)  
 AUTHORS Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Gardner,C., Chalk,S.E., Croning,M.D.R., Davies,R.M., Francis,M.D., Graham,D.V., Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R., Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G., Tickle,C. and Wilson,S.A.  
 JOURNAL Direct Submission  
 Submitted (29-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickens@ms.unist.ac.uk  
 COMMENT On Apr 1, 2004 this sequence version replaced gi:41636084.  
 BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA sequencing project.  
 This sequence is from the  
 BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,  
 from a library constructed by Elizabeth Bosch. cDNA was prepared  
 from RNA extracted from heads,  
 and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the  
 vector. Vector: pBluescript II KS(+); Site\_1: EcoRI; Site\_2: NotI  
 Host: Escherichia coli DH10B.  
 FEATURES  
 source location/Qualifiers  
 1..1009  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="white Leghorn, HiseX"  
 /db\_xref="taxon:9031"  
 /clone\_lib="CHEST82913"  
 /clone\_id="CHEST82913"  
 /dev\_stage="stage 36"  
 ORIGIN  
 Alignment Scores:

Pred. No.: 8,376-76 Length: 1009  
 Score: 1052.00 Matches: 200  
 Percent Similarity: 89.25% Conservative: 16  
 Best Local Similarity: 82.64% Mismatches: 18  
 Query Match: 80.86% Indels: 8  
 Gaps: 4

US-10-063-734-122 (1-243) x BX935556 (1-1009)

QY 2 ArgProGlnGlyProAlaAlaSerProGlnArgGlyLeuLeuLeuLeu 21  
 Db 11 CGCCCGC---GGCCCCGCC-----ATGCCCGCGCCCGCCTGCTCTCCGCGCTG 58  
 QY 22 LeuGlnLeuProAlaProSerSerAlaSerGlnLeuProGlyLeuGlnLeuGln 41  
 Db 59 CTG-----CTGGGCTCGCGGCTCGCGGACAGCCCGGGGAGAAAGAGAGG--- 106  
 QY 42 LeuArgGlnArgGlnValValAlaSerLeuTyraSerGlyMetCysLeuGlnGlyProAlaGly 61  
 Db 107 GCGGCGCGCGGAGAGTCTGAGAGCGTACAAACGCGCTGCTGCTGCGAGGCGCCAGCGCG 166  
 QY 62 ValProGlyArgAspGlySerProGlyAlaAlaValIleProGlyThrProGlyIlePro 81  
 Db 167 GTCCCGGAGACGGAGACGGAACTCTGACCAACAGGGATCCGAGGACACCGGAGATCCCG 226  
 QY 82 GlnArgAspGlyPheLeuGlyGlnGlyGlnGlyGlnGlnGlnGlnGlnGlnGlnGln 101  
 Db 227 GGGCGGAGCGGCGCCCAAGGGGAAAGGCGAGTCTGCGGAGAGGAGATTGAGAGTCC 286  
 QY 102 ThrThrProAlaThrLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 121  
 Db 287 TGGAGCGCCCACTTCACAGCAGTCTGAGAGCGTACGAGTCTGAGTCTGAGTCTGAGG 346  
 QY 122 LysIleAlaGlnCysThrPheThrIleMetArgSerSerAlaSerAlaLeuArgValLeuPhe 141  
 Db 347 AAATAGGGAATGATGATCTTCAACAGATGCGCTCCACAGTCTCTCAAGATCTCTTTC 406  
 QY 142 SerGlySerLeuArgLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 161  
 Db 407 AGTGAATGCTCTCGGCTGAGAGCGGAGCGGCTGCTGCAAGCTGAGTCTGAGTCTTTC 466  
 QY 162 AsnGlnIleAlaGlnCysSerGlyProLeuProIleGlnAlaIleIleTyraLeuAspGlnGly 181  
 Db 467 AATGAGAGAGATGAGCGCGGCACTTCCATCGAAGCATATATATTATATATATGAAAGC 526  
 QY 182 SerProGlnMetAsnSerThrIleAsnIleHisArgThrSerSerValGlnGlyLeuGlnGln 201  
 Db 527 AGTCGGAGACTGACTTACTATCAACATACACGAACTCTCTAGTGAAGTCTGTGT 586  
 QY 202 GlnGlyIleGlyAlaGlyLeuValAspValAlaIleTyrValGlyThrCysSerAspTyr 221  
 Db 587 GAAGGAGATCAACGCTGCTGAGCATTCGCACTGAGTCTGAGTCTGAGTCTGAGTCTG 646  
 QY 222 ProGlyLeuAspAlaSerThrGlyTyrPasnSerValSerArgIleIleIleGlnGlnLeu 241  
 Db 647 CCCAGGAGATGCTTCTACTGAGATGATTCAGTCTCCGATATCATATGAAAGACTG 706  
 QY 242 ProGly 243  
 Db 707 CCAGAA 712

RESULT 31  
 LOCUS BC079494 1290 bp mRNA linear VRT 03-AUG-2004  
 DEFINITION Danio rerio cDNA clone MGC:101075 IMAGE:7153214, complete cds.  
 ACCESSION BC079494  
 VERSION BC079494.1 GI:50927421  
 KEYWORDS MGC.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

# REFERENCE

1 (bases 1 to 1290)

Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Maruina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Udell, T.B., Toshitsugu, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mulle, S.J., Boeck, S.A., McEwan, P.J., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hu, X., Gibbs, R.A., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Bouffard, G.G., Blakesley, R.W., Madan, A., Young, A.C., Shcherbina, Y., Dickson, M.C., Rodriguez, A.C., Grimm, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smalins, D.E., Schermer, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16699-16903 (2002)

12477932

2 (bases 1 to 1290)

Director MGC Project.

Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Genome Institute of Singapore

cDNA Library Preparation: S. Mathavan, China-Lin Wei, and Yijun Ruan, Genome Institute of Singapore

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland

Web site: <http://www.nisc.nih.gov/>

Contact: [nisc\\_mgc@nsl.nih.gov](mailto:nisc_mgc@nsl.nih.gov)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Khong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stancir, P., Thomas, P.J., Touchman, J.W., Tsurgoun, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 60 Row: m Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers

1. 1290

/organism="Danio rerio"

/mol\_type="mRNA"

/strain="Singapore local strain"

/db\_xref="taxon:7955"

/clone="MGC:101075 IMAGE:7153214"

/tissue\_type="Embryo, 7 different stages (from just fertilized embryos to 72 hours just hatched baby fish)"

/clone\_id="GIS2F001\_ra"

/lab\_host="DH10B"

/note="Vector: pDNR-LIB"

77..772

/codon\_start=1

/product="Unknown (protein for MGC:101075)"

/protein\_id="AAH79494.1"

# REMARK

COMMENT

FEATURES

source

CDS





ORIGIN

Alignment Scores:

Pred. No.: 4.32e-49 Length: 860

Score: 720.00 Matches: 134

Percent Similarity: 98.54% Conservative: 1

Best Local Similarity: 97.81% Mismatches: 2

Query Match: 55.34% Indels: 0

DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AX285214 (1-860)

QY 107 LysGlnCysSerTrpSerLeuAsnTrpGlyValLeuPheGlnGlyLysIleAlaGlnCys 126

DB 837 AGAAACATGTCATGAGTTCATGATTTATGATGATCTGGGAAATGGGAGTGT 778

QY 127 ThrPheTrpIleMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146

DB 777 ACATTTCAAACATGCGTTCATTAATGCTCTAAGAGTTTGTTCAGTGGCTCATTGGG 718

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTrpTrpPheThrPheAsnGlyAlaGlnCys 166

DB 717 CTAAATGCGAAGATGATGCTGCTGAGCGTGGTATTTACATTCATGAGCTGATGT 658

QY 167 SerGlyProLeuProIleGlnAlaIleIleTrpLeuAspGlnGlySerProGlnMetAsn 186

DB 657 TCAGACCTCTCCCATTAAGCTATTAATTTATTTGACCAAGAAAGCCCTGAATGAAT 598

QY 187 SerThrIleAsnIleHisArgThrSerSerValGlnGlyLeuGlnGlyIleGlyAla 206

DB 597 TCACAAATTATATTCATGATGCACTTCTCTGAGAAAGACTTTGTAAAGAAATGGTGT 538

QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCysSerAspTrpProLysGlyAspAla 226

DB 537 GGATTAAGGAGATGTGCTATCTGGGTGGCACTGTTCAGATTACCCCAAGAGATGTCT 478

QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGlnGlnLeuProLys 243

DB 477 TCTACTGATGAAATTCAGTTCTTCGCATCATTTATTAAGAACTAACCAAAA 427

RESULT 34

LOCUS CQ412972 539 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 20043 from Patent WO0170979.

ACCESSION CQ412972

VERSION CQ412972.1 GI:41320753

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Lee, J. and Lillie, J.

TITLE Genes, compositions, kits, and method for identification, assessment, prevention and therapy of ovarian cancer

JOURNAL Patent: WO 0170979-A 20043 27-SEP-2001;

FEATURES

source

1. .539

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 1.14e-43 Length: 539

Score: 650.00 Matches: 116

Percent Similarity: 98.31% Conservative: 0

Best Local Similarity: 98.31% Mismatches: 2

Query Match: 49.96% Indels: 0

DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x CQ412972 (1-539)

QY 51 TyrAsnGlyMetCysLeuGlnGlyProAlaGlyValProGlyArgAspGlySerProGly 70

DB 185 TATATGGAATGTGTTTCAAGGCGCAGAGATGCTGTTCAGACGGAGCCCTGGG 244

QY 71 AlaAsnValIleProGlyThrProGlyIleProGlyArgAspGlyPheLysGlyLys 90

DB 245 GCCAATGCAATTCGCGGTACACCTGGGATCCAGGTGGATGATTCAAAGGAGAAAG 304

QY 91 GlyGlnCysLeuArgGlnSerPheGlnGlySerTrpThrProAsnTrpLysGlnCysSer 110

DB 305 GGGGATGCTGAGGAGAAAGCTTTGAGAGATCTCGACACCCCACTCAAGCAGTGTCA 364

QY 111 TrpSerSerLeuAsnTrpGlyIleAspLeuGlyLysIleAlaGlnCysThrPheTrpLys 130

DB 365 TGGAGTTCATTAATTAAGCATAGATCTTGGGAAATTTGGGAGTCTACATTACAAAG 424

QY 131 MetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArgLeuLysCysArg 150

DB 425 ATGCGTTCAAATAGTGTCTAAGAGTTTGTTCAGTGGCTCATTCCGGCTAAATGACAG 484

QY 151 AsnAlaCysCysGlnArgTrpTrpPheThrPheAsnGlyAlaGlnCysSerGly 168

DB 485 AATGCATGCTGCGCGTGGATTTCACTCATGAGCTGAATGTTGAGGA 538

RESULT 35

LOCUS CQ407408 516 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 14479 from Patent WO0170979.

ACCESSION CQ407408

VERSION CQ407408.1 GI:4135189

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Lee, J. and Lillie, J.

TITLE Genes, compositions, kits, and method for identification, assessment, prevention and therapy of ovarian cancer

JOURNAL Patent: WO 0170979-A 14479 27-SEP-2001;

FEATURES

source

1. .516

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 6.45e-42 Length: 516

Score: 628.00 Matches: 111

Percent Similarity: 96.55% Conservative: 1

Best Local Similarity: 95.69% Mismatches: 4

Query Match: 48.27% Indels: 0

DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x CQ407408 (1-516)

QY 51 TyrAsnGlyMetCysLeuGlnGlyProAlaGlyValProGlyArgAspGlySerProGly 70

DB 167 TATATGGAATGTGTTTCAAGGCGCAGAGATGCTGTTCAGACGGAGCCCTGGG 226

QY 71 AlaAsnValIleProGlyThrProGlyIleProGlyArgAspGlyPheLysGlyLys 90

DB 227 GCCAATGCAATTCGCGGTACACCTGGGATCCAGGTGGATTCAAAGGAGAAAG 286

QY 91 GlyGlnCysLeuArgGlnSerPheGlnGlySerTrpThrProAsnTrpLysGlnCysSer 110

DB 287 GGGGATGCTGAGGAGAAAGCTTTGAGAGATCTCGGACACCCCACTCAAGCAGTGTCA 346

QY 111 TrpSerSerLeuAsnTrpGlyIleAspLeuGlyLysIleAlaGlnCysThrPheTrpLys 130

LOCUS	AX340025	471 bp	DNA	linear	PAT 10-JAN-2002
DEFINITION	Sequence 272 from Patent WO0196388.				
ACCESSION	AX340025				
VERSION	AX340025.1				
KEYWORDS	GI:18136006				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	Jiang, Y., Harlocker, S.L. and Secrist, H.				
JOURNAL	Compositions and methods for the therapy and diagnosis of colon				
FEATURES	Cancer				
source	Patent: WO 0196388-A 272 20-DEC-2001;				
	CORIXA CORPORATION (US)				
	Location/Qualifiers				
	1..471				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
ORIGIN					
Alignment Scores:					
Pred. No.:	8.43e-42		Length:	471	
Score:	626.00		Matches:	117	
Percent Similarity:	100.00%		Conservative:	0	
Best Local Similarity:	100.00%		Mismatch:	0	
Query Match:	48.12%		Indels:	0	
DB:	6		Gaps:	0	
US-10-063-734-122 (1-243) x AX340025 (1-471)					
QY	127 ThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg	146			
Db	1 ACATTTACCAAGATGCTCTCAATATGCTCTCAAGAGTTTGTTCAGTGGCTCACTTGG	60			
QY	147 LeuLysCyAArgAsnAlaCySCysGlnArgTrpYrPheThrPheAsnGlyAlaGluCys	166			
Db	61 CTAAATGACAGAAATGACATGCTGTCAGCGTTGATTTCACTTCAATGAGAGCTAATGT	120			
QY	167 SerGlyProLeuProIleGluAlaIleIleTyrLeuAspGlnGlySerProGluMetLsn	186			
Db	121 TCAGGACCTCTCCATGAGCTATTAATTTATTTGACCAAGAGCCCTGAAATGAT	180			
QY	187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCySGluGlyIleGlyAla	206			
Db	181 TCACAAATTAATATTATTCATCGCACTTCTCTGTGGAGAGCACTTGTGAAAGAAATGGTCT	240			
QY	207 GlyLeuValAspValAlaIleIleTrpValGlyThrCySerAspYrProlyGlyAspAla	226			
Db	241 GGATTAGTGAGTGTGCTATCTGGGTGGCACTTGTTCAGATTACCAAAAGAGATGCT	300			
QY	227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProLys	243			
Db	301 TCTACTGATGGAATTCAGTTTCTTCGCAATATTATTGAAGAACTACCAAAA	351			
RESULT 37					
LOCUS	AR280558	683 bp	DNA	linear	PAT 10-APR-2003
DEFINITION	Sequence 63 from patent US 6518237.				
ACCESSION	AR280558				

VERSION	AR280558.1	GI:29716028
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 683)	
AUTHORS	Yingui, J., Dillon, D. C., Mitcham, J. L. and Xu, J.	
TITLE	Compositions for treatment and diagnosis of breast cancer and methods for their use	
JOURNAL	Patent: US 6518237-A 63 11-FEB-2003;	
FEATURES	Location/Qualifiers	
source	1..683	
ORIGIN	/organism="unknown"	
	/mol_type="genomic DNA"	
Alignment Scores:		
Pred. No.:	1,286-41	683
Score:	626.00	Matches: 117
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	48.12%	Indels: 0
DB:	6	Gaps: 0
US-10-063-734-122 (1-243) x AR280558 (1-683)		
Qy	127	ThrPheThrIysMetArgSerAsnSerAlaLeuArgValIleuPheSerGlySerLeuArg 146
Db	683	ACATTTCAAAGATGCGCTTCAATATAGTCTTAAAGATTTTGTTCAGTGGCTCACTTCGG 624
Qy	147	LeuIysCysArgAsnAlaCysCysGlnArgTPTyRheThrPheAsnGlyAlaGluCys 166
Db	623	CTAAATGCGAATATGATGCTGTCACGCGTTGGATTTTCATTCAATGAGCGTGAATGT 564
Qy	167	SerGlyProIeuProIleGluAlaIleIleTyRheuAspGlnGlySerProGluMetAsn 186
Db	563	TCAGACCTCTTCCCATTTGAGCTATATATTTATTTGACCAAGAGAGCCCTGAATGAT 504
Qy	187	SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGlnGlyIleGlyAla 206
Db	503	TCAACATTATATTCATTCGACCTCTTCTGTGGAAGACTTGTGAAGGATTTGGTCT 444
Qy	207	GlyLeuValAspValAlaIleTTPValGlyThrCysSerAspTyRProLysGlyAspAla 226
Db	443	GGATTAGTGATGTTGCTATCTGGGTGGYACCTGTTACGATTACCCAAAAGGAGATGCT 384
Qy	227	SerThrGlyTPAsnSerValSerArgIleIleIleGluGluIeuProLys 243
Db	383	TCTACTGGATGGAAATTCAGTTTCTCGYATCATTTATGAAGAATCAACAAA 333
RESULT 38		
AR283054/c	683 bp DNA linear PAT 10-APR-2003	
LOCUS	AR283054	
DEFINITION	Sequence 63 from patent US 6528054.	
ACCESSION	AR283054	
VERSION	AR283054.1	
KEYWORDS	GI:29719881	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 683)	
TITLE	Jiang, Y., Dillon, D. C., Mitcham, J. L., Xu, J., Harlocker, S. L. and Hepler, W. T.	
JOURNAL	Compositions and methods for the therapy and diagnosis of breast cancer	
FEATURES	Patent: US 6528054-A 63 04-MAR-2003;	
source	Location/Qualifiers	
	1..683	
ORIGIN	/organism="unknown"	
	/mol_type="genomic DNA"	
Alignment Scores:		

Pred. No.: 1,28e-41 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AR283054 (1-683)

QY 127 ThrPheThrIlyMeArSerSerAseuValleuPheSerGlySerLeuArg 146  
DB 683 ACATTACAAAGATGGCTTCAATATAGCTCTAAGAGTTTGTTCAGTGGCTACTTGG 624  
QY 147 LeuIysCyArGAsnAlaCySeCysGlnArgTrpTyRPhetThrPheAsnGlyIleGlyAla 166  
DB 623 CTAAGATGCAAGAAATCATGCTGCTGAGCGTGTGATTTTCAATTCATGAGAGCTGAATGT 564  
QY 167 SerGlyProLeuProIleGluAlaIleIleTyRLeuAspGlnGlySerProGluMetAsn 186  
DB 563 TCAGAGACCTCTCCCATTTAGCTATTAATTTATTTGAGCCAGAGAGCCCTGAATGAAT 504  
QY 187 SerThrIleAsnIleHisArgTrpSerSerValGluGlyLeuCySeGlnGlyIleGlyAla 206  
DB 503 TCACCAATTAAATTCATGCTGCACTTCTCTGTGAGAGACTTTGTAGAGAAATGGTGTCT 444  
QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCySeSerAspTyRProIysGlyAspAla 226  
DB 443 GGATTAGTGCATGTTGCTATCTGGGTGGVACTTGTTCAGATTACCCAAAGAGATGTCT 384  
QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProIys 243  
DB 383 TCTACTGGATGGAATTCAGTTCTCGATCATTTATTTGAAGAACTACCAAAA 333

RESULT 39  
AR341827/c  
LOCUS AR341827 683 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 63 from patent US 6573368.  
ACCESSION AR341827  
VERSION AR341827.1 GI:33736404  
KEYWORDS  
SOURCE  
ORGANISM  
Unclasseified.

REFERENCE  
AUTHORS Yugu,J., Dillon,D.C., Mitcham,J.L. and Xu,J.  
TITLE Compositions for the treatment and diagnosis of breast cancer and methods for their use  
JOURNAL Patent: US 6573368-A 63 03-JUN-2003;  
FEATURES  
LOCATION/Qualifiers  
SOURCE 1. 683  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 1,28e-41 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AR341827 (1-683)

QY 127 ThrPheThrIlyMeArSerSerAseuValleuPheSerGlySerLeuArg 146  
DB 683 ACATTACAAAGATGGCTTCAATATAGCTCTAAGAGTTTGTTCAGTGGCTACTTGG 624  
QY 147 LeuIysCyArGAsnAlaCySeCysGlnArgTrpTyRPhetThrPheAsnGlyIleGlyAla 166  
DB 623 CTAAGATGCAAGAAATCATGCTGCTGAGCGTGTGATTTTCAATTCATGAGAGCTGAATGT 564  
QY 167 SerGlyProLeuProIleGluAlaIleIleTyRLeuAspGlnGlySerProGluMetAsn 186

DB 563 TCAGAGACCTCTCCCATTTAGCTATTAATTTATTTGAGCCAGAGAGCCCTGAATGAAT 504  
QY 187 SerThrIleAsnIleHisArgTrpSerSerValGluGlyLeuCySeGlnGlyIleGlyAla 206  
DB 503 TCACCAATTAAATTCATGCTGCACTTCTCTGTGAGAGACTTTGTAGAGAAATGGTGTCT 444  
QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCySeSerAspTyRProIysGlyAspAla 226  
DB 443 GGATTAGTGCATGTTGCTATCTGGGTGGVACTTGTTCAGATTACCCAAAGAGATGTCT 384  
QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProIys 243  
DB 383 TCTACTGGATGGAATTCAGTTCTCGATCATTTATTTGAAGAACTACCAAAA 333

RESULT 40  
AR343822/c  
LOCUS AR343822 683 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 63 from patent US 6579973.  
ACCESSION AR343822  
VERSION AR343822.1 GI:33739722  
KEYWORDS  
SOURCE  
ORGANISM  
Unclasseified.

REFERENCE  
AUTHORS Yugu,J., Dillon,D.C., Mitcham,J.L., Xu,J. and Harlocker,S.L.  
TITLE Compositions for the treatment and diagnosis of breast cancer and methods for their use  
JOURNAL Patent: US 6579973-A 63 17-JUN-2003;  
FEATURES  
LOCATION/Qualifiers  
SOURCE 1. 683  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 1,28e-41 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AR343822 (1-683)

QY 127 ThrPheThrIlyMeArSerSerAseuValleuPheSerGlySerLeuArg 146  
DB 683 ACATTACAAAGATGGCTTCAATATAGCTCTAAGAGTTTGTTCAGTGGCTACTTGG 624  
QY 147 LeuIysCyArGAsnAlaCySeCysGlnArgTrpTyRPhetThrPheAsnGlyIleGlyAla 166  
DB 623 CTAAGATGCAAGAAATCATGCTGCTGAGCGTGTGATTTTCAATTCATGAGAGCTGAATGT 564  
QY 167 SerGlyProLeuProIleGluAlaIleIleTyRLeuAspGlnGlySerProGluMetAsn 186  
DB 563 TCAGAGACCTCTCCCATTTAGCTATTAATTTATTTGAGCCAGAGAGCCCTGAATGAAT 504  
QY 187 SerThrIleAsnIleHisArgTrpSerSerValGluGlyLeuCySeGlnGlyIleGlyAla 206  
DB 503 TCACCAATTAAATTCATGCTGCACTTCTCTGTGAGAGACTTTGTAGAGAAATGGTGTCT 444  
QY 207 GlyLeuValAspValAlaIleTrpValGlyThrCySeSerAspTyRProIysGlyAspAla 226  
DB 443 GGATTAGTGCATGTTGCTATCTGGGTGGVACTTGTTCAGATTACCCAAAGAGATGTCT 384  
QY 227 SerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProIys 243  
DB 383 TCTACTGGATGGAATTCAGTTCTCGATCATTTATTTGAAGAACTACCAAAA 333  
RESULT 41  
AR351023/c  
LOCUS AR351023 683 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 63 from patent US 6586572.  
ACCESSION AR351023  
VERSION AR351023.1 GI:33752702  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and Hepler,W.T.  
TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
JOURNAL Patent: US 6586572-A 63 01-JUL-2003;  
FEATURES Location/Qualifiers  
source 1..683  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1 28e-41 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: Gaps: 0

US-10-063-734-122 (1-243) x AR351023 (1-683)

QY 127 ThrPheThrLywMeArGSeRanSerAlaLeuArgValIleuPheSerGlySerLeuArg 146  
DB 683 ACATTTCACAAAGATGCGTTCAATATAGTCTTAAGAGTTTGTTCAGTGCTCAGCTCGG 624  
QY 147 LeuLYeCYaRgARnAlaCYeCYsGlnARGTPTyRPhetThrPheAnGlyAlaGluCYs 166  
DB 623 CTAAATGACGAAATGATGCTGTCAGCGGTGATTCACATTCATGAGAGCTGATGT 564

QY 167 SerGlyProLeuProIleGluAlaIleIeTyRLeuAspGlnGlySerProGluMetAen 186  
DB 563 TCAGGACCTCTTCCCAATGAGCTATTAATTTATTTGACCAAGAGAGCCCTGAATGAT 504  
QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCYsGluGlyIleGlyAla 206  
DB 503 TCACACATTAATATTCATGCACTTCTTGCTGAGAGAGACTTTGTGAAGAAATGCTGCT 444

QY 207 GlyLeuValAspValAlaIleTPValGlyThrCYeSerAspTyRProLYsGlyAspAla 226  
DB 443 GGATTAGTGATGTCTCATCTGCGTGGYACTGTTCAGATTACCCAAAGAGATGCT 384

QY 227 SerThrGlyTPRanSerValSerArgIleIleIleGluGluLeuProLYs 243  
DB 383 TCTACTGATGGAATTCAGTTCTCGATCATTAATGAAGAACTACCAAAA 333

RESULT 42  
AR352789/c  
LOCUS AR352789 683 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 63 from patent US 6590076.  
ACCESSION AR352789  
VERSION AR352789.1 GI:33758194  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Yugu,J., Dillon,D.C., Mitcham,J.L. and Xu,J.  
TITLE Compositions for the treatment and diagnosis of breast cancer and methods for their use  
JOURNAL Patent: US 6590076-A 63 08-JUL-2003;  
FEATURES Location/Qualifiers  
source 1..683  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1 28e-41 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: Gaps: 0

US-10-063-734-122 (1-243) x AR352789 (1-683)

QY 127 ThrPheThrLywMeArGSeRanSerAlaLeuArgValIleuPheSerGlySerLeuArg 146  
DB 683 ACATTTCACAAAGATGCGTTCAATATAGTCTTAAGAGTTTGTTCAGTGCTCAGCTCGG 624  
QY 147 LeuLYeCYaRgARnAlaCYeCYsGlnARGTPTyRPhetThrPheAnGlyAlaGluCYs 166  
DB 623 CTAAATGACGAAATGATGCTGTCAGCGGTGATTCACATTCATGAGAGCTGATGT 564

QY 167 SerGlyProLeuProIleGluAlaIleIeTyRLeuAspGlnGlySerProGluMetAen 186  
DB 563 TCAGGACCTCTTCCCAATGAGCTATTAATTTATTTGACCAAGAGAGCCCTGAATGAT 504  
QY 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCYeGluGlyIleGlyAla 206  
DB 503 TCACACATTAATATTCATGCACTTCTTGCTGAGAGAGACTTTGTGAAGAAATGCTGCT 444

QY 207 GlyLeuValAspValAlaIleTPValGlyThrCYeSerAspTyRProLYsGlyAspAla 226  
DB 443 GGATTAGTGATGTCTCATCTGCGTGGYACTGTTCAGATTACCCAAAGAGATGCT 384

QY 227 SerThrGlyTPRanSerValSerArgIleIleIleGluGluLeuProLYs 243  
DB 383 TCTACTGATGGAATTCAGTTCTCGATCATTAATGAAGAACTACCAAAA 333

RESULT 43  
AR453603/c  
LOCUS AR453603 683 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 63 from patent US 6680197.  
ACCESSION AR453603  
VERSION AR453603.1 GI:42686393  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 683)  
AUTHORS Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L., Hepler,W.T. and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
JOURNAL Patent: US 6680197-A 63 20-JAN-2004;  
FEATURES Location/Qualifiers  
source 1..683  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 1 28e-41 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
DB: Gaps: 0

US-10-063-734-122 (1-243) x AR453603 (1-683)

QY 127 ThrPheThrLywMeArGSeRanSerAlaLeuArgValIleuPheSerGlySerLeuArg 146  
DB 683 ACATTTCACAAAGATGCGTTCAATATAGTCTTAAGAGTTTGTTCAGTGCTCAGCTCGG 624  
QY 147 LeuLYeCYaRgARnAlaCYeCYsGlnARGTPTyRPhetThrPheAnGlyAlaGluCYs 166  
DB 623 CTAAATGACGAAATGATGCTGTCAGCGGTGATTCACATTCATGAGAGCTGATGT 564

Db 623 CTAAGATGAGAAAGCATGCTGTCAGCGTGGATTTCACATTCATGAGCGTGAATG 564  
Qy 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186  
Db 563 TCAGAGACCTCTTCCCATTTGAGCTATATTTATTTGAGCCAGAGAGCCCTGAAATGAAT 504  
Qy 167 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGluGlyIleGlyAla 206  
Db 503 TCAACAAATTAATATTCATGCACTTCTCTGTGGAAGAGACTTTGTAGAGAAATGGTGCT 444  
Qy 207 GlyLeuValAspValAlaIleTTPValGlyThrCysSerAspTyrrProlysglyAspAla 226  
Db 443 GGATTAAGTGAATGTTGCTATCTGGGTGGAGTGTTCGATTCACCAAGAGAGATGCT 384  
Qy 227 SerThrGlyTTPAsnSerValSerArgIleIleIleGluGluLeuProlys 243  
Db 383 TCTACTGGATGGAATTCAGTTTCTCGATCATCTATTGAGAACTACCAAAA 333  
RESULT 44  
AX302743/c 683 bp DNA linear PAT 30-NOV-2001  
LOCUS Sequence 63 from Patent WO0179286.  
DEFINITION AX302743  
ACCESSION AX302743  
VERSION AX302743.1 GI:17383244  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and  
Hepler, W.T.  
TITLE Compositions and methods for the therapy and diagnosis of breast  
cancer  
JOURNAL Patent: WO 0179286-A 63 25-OCT-2001;  
CORIXA CORPORATION (US)  
FEATURES  
source location/Qualifiers  
1. 683  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.28e-41 Length: 683  
Score: 626.00 Matches: 117  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.12% Indels: 0  
Gaps: 0  
DB: 6  
US-10-063-734-122 (1-243) x AX302743 (1-683)  
Qy 127 ThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146  
Db 683 ACATTTACAAAGATCGCTTCAATATGCTCTTAAGAGTTTGTTCAGTGGCTCAGCTCGG 624  
Qy 147 LeuIysCysArgAsnAlaCysCysGlnArgTTPyrrPheThrPheAsnGlyAlaGluCys 166  
Db 623 CTAAGATGAGAAATGAGATGCTGTCAGCGTGGATTTCACATTCATGAGACTGAATGT 564  
Qy 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186  
Db 563 TCAGAGACCTCTTCCCATTTGAGCTATATTTATTTGAGCAAGAGAGCCCTGAATGAAT 504  
Qy 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGluGlyIleGlyAla 206  
Db 503 TCAACAAATTAATATTCATGCACTTCTCTGTGGAAGAGACTTTGTAGAGAAATGGTGCT 444  
Qy 207 GlyLeuValAspValAlaIleTTPValGlyThrCysSerAspTyrrProlysglyAspAla 226  
Db 443 GGATTAAGTGAATGTTGCTATCTGGGTGGAGTGTTCGATTCACCAAGAGAGATGCT 384

Qy 227 SerThrGlyTTPAsnSerValSerArgIleIleIleGluGluLeuProlys 243  
Db 383 TCTACTGGATGGAATTCAGTTTCTCGATCATCTATTGAGAACTACCAAAA 333  
RESULT 45  
AX375790/c 683 bp DNA linear PAT 01-MAR-2002  
LOCUS Sequence 3 from Patent WO0173031.  
DEFINITION AX375790  
ACCESSION AX375790  
VERSION AX375790.1 GI:19170293  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Xu, J. and Stolk, J.A.  
TITLE Compositions and methods for the therapy and diagnosis of ovarian  
cancer  
JOURNAL Patent: WO 0173031-A 3 04-OCT-2001;  
CORIXA CORPORATION (US)  
FEATURES  
source location/Qualifiers  
1. 683  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Alignment Scores:  
Pred. No.: 3.91e-41 Length: 683  
Score: 620.00 Matches: 116  
Percent Similarity: 99.15% Conservative: 0  
Best Local Similarity: 99.15% Mismatches: 1  
Query Match: 47.66% Indels: 0  
Gaps: 0  
DB: 6  
US-10-063-734-122 (1-243) x AX375790 (1-683)  
Qy 127 ThrPheThrIlyMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeuArg 146  
Db 683 ACATTTACAAAGATCGCTTCAATATGCTCTTAAGAGTTTGTTCAGTGGCTCAGCTCGG 624  
Qy 147 LeuIysCysArgAsnAlaCysCysGlnArgTTPyrrPheThrPheAsnGlyAlaGluCys 166  
Db 623 CTAAGATGAGAAATGAGATGCTGTCAGCGTGGATTTCACATTCATGAGACTGAATGT 564  
Qy 167 SerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMetAsn 186  
Db 563 TCAGAGACCTCTTCCCATTTGAGCTATATTTATTTGAGCAAGAGAGCCCTGAATGAAT 504  
Qy 187 SerThrIleAsnIleHisArgThrSerSerValGluGlyLeuCysGluGlyIleGlyAla 206  
Db 503 TCAACAAATTAATATTCATGCACTTCTCTGTGGAAGAGACTTTGTAGAGAAATGGTGCT 444  
Qy 207 GlyLeuValAspValAlaIleTTPValGlyThrCysSerAspTyrrProlysglyAspAla 226  
Db 443 GGATTAAGTGAATGTTGCTATCTGGGTGGAGTGTTCGATTCACCAAGAGAGATGCT 384  
Qy 227 SerThrGlyTTPAsnSerValSerArgIleIleIleGluGluLeuProlys 243  
Db 383 TCTACTGGATGGAATTCAGTTTCTCGATCATCTATTGAGAACTACCAAAA 333  
RESULT 46  
AX067343 687 bp DNA linear PAT 24-JAN-2001  
LOCUS Sequence 47 from Patent WO0078960.  
DEFINITION AX067343  
ACCESSION AX067343  
VERSION AX067343.1 GI:12544967  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Yuglu, J. and Mitcham, J.L.  
 TITLE Compositions and methods for the therapy and diagnosis of breast cancer  
 JOURNAL Cancer  
 Patent: WO 0078960-A 47 28-DEC-2000;  
 CORIXA CORPORATION (US)  
 FEATURES  
 source Location/Qualifiers  
 1.687  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 misc\_feature 1.687  
 /note="n = A,T,C or G"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,376-34 Length: 687  
 Score: 536.00 Matches: 98  
 Percent Similarity: 98.99% Conservative: 0  
 Best Local Similarity: 98.99% Mismatches: 1  
 Query Match: 41.20% Indels: 0  
 DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AX067343 (1-687)

QY 145 LeuArgLeuLysGlyArgAsnAlaCysCysGlnArgTrpPheThrPheAsnGlyAla 164  
 DB 1 CTTGGCTTAAAGTGAAGATGATGCTGTCAGCGTTGGATTTCACATTCAATGAGAGCT 60

QY 165 GluCysSerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGlu 184  
 DB 61 GATGTGATGAGACCTCTTCCCATTTGAAGCTATATTATTGGACCAAGAAAGCCCTGAA 120

QY 185 MetAsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeuGlyGlyIle 204  
 DB 121 ATGAATTTCAACATTAATTAATTCATCCACCTTCTGTGGAGAGACCTTGTGAAGAAAT 180

QY 205 GlyAlaGlyLeuValAspValAlaIleTrpValGlyTyCysSerAspTrpProGlyGly 224  
 DB 181 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

QY 225 AspAlaSerThrGlyTrpAsnSerValSerArgIleIleIleGluGluLeuProGly 243  
 DB 241 GATGCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 297

RESULT 47  
 COS14013 COS14013 555 bp DNA linear PAT 30-JAN-2004  
 LOCUS Sequence 45880 from Patent WO0160860.  
 DEFINITION COS14013  
 ACCESSION COS14013  
 VERSION COS14013.1 GI:41480277  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.  
 TITLE Genes differentially expressed in human prostate cancer and their use  
 JOURNAL Patent: WO 0160860-A 45880 23-APR-2001;  
 Millennium Predictive Medicine, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1.555  
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 /db\_xref="taxon:9606"

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 Alignment Scores:  
 Pred. No.: 1,296-29 Length: 555  
 Score: 476.00 Matches: 88  
 Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 98.88% Mismatches: 0  
 Query Match: 36.59% Indels: 0  
 DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x COS14013 (1-555)

QY 126 CysThrPheThrLysMetArgSerAsnSerAlaLeuArgValLeuPheSerGlySerLeu 145  
 DB 288 TGTACCTTTACCAAGATGCTTCAATATGCTCTTAAGAGTTTGTTCAGTGGCTCAGT 347

QY 146 ArgLeuLysCysArgAsnAlaCysCysGlnArgTrpPheThrPheAsnGlyAlaGlu 165  
 DB 348 CCGTTAAATGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 407

QY 166 CysSerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMet 185  
 DB 408 TGTTCAGGACCTTCTCCCATTAAGCTATTAATTTATTTGGACCAAGAAAGCCCTGAAATG 467

QY 186 AsnSerThrIleAsnIleHisArgThrSerSerValGluGlyLeuGlyGlyIleGly 205  
 DB 468 AATTCACCAATTAATTAATTCATGCACTTCTTGTGGAGAGACCTTGTGAAGAAATGCT 527

QY 206 AlaGlyLeuValAspValAlaIleTrp 214  
 DB 528 GCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 554

RESULT 48  
 AX284686 AX284686 271 bp DNA linear PAT 20-NOV-2001  
 LOCUS Sequence 491 from Patent WO0179556.  
 DEFINITION AX284686  
 ACCESSION AX284686  
 VERSION AX284686.1 GI:17045374  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Little, J., Brown, J.L., Bolt, A. and van Hufel, C.  
 TITLE Novel genes, compositions and methods for the identification, assessment, prevention, and therapy of human cancers  
 JOURNAL Patent: WO 0179556-A 491 25-OCT-2001;  
 Millennium Predictive Medicine, Inc. (US)  
 FEATURES  
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 1.271  
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 /db\_xref="taxon:9606"

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 Best Local Similarity: 98.90% Mismatches: 0  
 Query Match: 35.90% Indels: 1  
 DB: 6 Gaps: 0

US-10-063-734-122 (1-243) x AX284686 (1-271)

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 DB 1 ACATTTACCAAGATGCTTCAATATGCTCTTAAGAGTTTGTTCAGTGGCTCAGT 60

QY 147 LeuLysCysArgAsnAlaCysCysGlnArgTrpPheThrPheAsnGlyAlaGlu 166  
 DB 61 CTAAATGCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120

QY 166 sSerGlyProLeuProIleGluAlaIleIleTyLeuAspGlnGlySerProGluMet 186  
 DB 121 TTCAGGACCTTCTCCCATTAAGCTATTAATTTATTTGGACCAAGAAAGCCCTGAAATGTA 180

QY 186 nSerThrIleAsnIleHisArgThrSerSerValGluGlyLeuGlyGlyIleGly 206

Db 161 TTCAACAATTAATATTCATCGACCTCTTCTGTGGAAGACCTTGTGAAGAAATGGTGC 240  
 Oy 206 aglYleuValaspValAlaIleTtryValgY 216  
 Db 241 TGGATTAGTGAGATTTGCTAATCGGGTGGT 271

RESULT 49  
 CQ665181 396 bp DNA 1linear PAT 03-FEB-2004  
 LOCUS Sequence 10107 from Patent WO02070737.  
 DEFINITION CQ665181  
 ACCESSION CQ665181.1 GI:42147374  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 Liaw,C.C., Marshall,W.E. and Zhang,H.  
 Compositions and methods relating to osteoarthritis  
 Patent: WO 02070737-A 10107 12-SEP-2002;  
 Chondrogene Inc. (CA)  
 FEATURES  
 Source location/Qualifiers  
 1..396  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN  
 Alignment Scores: 5,26e-28 Length: 396  
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 Percent Similarity: 93.33% Mismatches: 6  
 Best Local Similarity: 34.90% Indels: 0  
 Query Match: 6 Gaps: 0

US-10-063-734-122 (1-243) x CQ665181 (1-396)

Oy 154 CysGlnAgyTtryPtryPheThrpheAnGlyAlaGlyCysSerGlyProleuProIleGlu 173  
 Db 67 TGTCAAGCAGTGTATTTTCAATTCATTAAGAGCTGAGTGTCAAGACCTTCCCATGAA 126  
 Oy 174 AlaIleIleYrLeuAspGlnGlySerProGluMetAsnSerThrIleAsnIleHisArg 193  
 Db 127 GCTATTAATTTATTTGACACGACGAGGAGCCCTGAAATGAATTCACAACTTAATTCATGCC 186  
 Oy 194 ThreSerSerValGluGlyLeuGlySerGluGlyIleGlyAlaGlyLeuValaspValAlaIle 213  
 Db 187 ACTTCTTCTGTGGAAGACCTTGCNAGAGAAATGAGCTGAGATTAGCGGATGTCTATTC 246

Oy 214 TryValgYThrCysSerAspTtryProGlyAspAlaSerThrGlyTrypsinSerVal 233  
 Db 247 TGGAGTGCACCTGTGNCAGATTACCAAGAGAGAGTCTTCTAATGATGAGTAATCAAGT 306

Oy 234 SerArgIleIleIleGluGluLeuProIlys 243  
 Db 307 TCTCGCATCATTAATGGAAGAACTACCAAAA 336

RESULT 50  
 LOCUS AC069351 111496 bp DNA 1linear PRI 17-FEB-2002  
 DEFINITION Homo sapiens chromosome 8, clone RP11-432K23, complete sequence.  
 ACCESSION AC069351  
 VERSION AC069351.5 GI:18698795  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 111496)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 Homo sapiens chromosome 8, clone RP11-432K23  
 Unpublished  
 2 (bases 1 to 111496)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,  
 Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,  
 Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,  
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Domingo,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,  
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Grant,G., Hagos,B., Hatford,A., Horton,L.,  
 Howland,J., Ilev,I., Johnson,R., Jones,C., Kam,L., Karatas,A.,  
 Klein,J., Labocque,K., Lamazares,R., Landers,T., Lehoczeky,J.,  
 Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Margus,N.,  
 McCarthy,M., McEwan,P., McGurt,A., McKernan,K., McPheters,R.,  
 Meldrim,J., Menes,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,  
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Testaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (30-MAY-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 111496)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,  
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Charazo,B.,  
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,  
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,  
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,  
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 Hagos,B., Hatford,A., Horton,L., Hulme,W., Ilev,I., Johnson,R.,  
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 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnupack,R.,  
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
 Strause,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,  
 Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,  
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 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (01-SEP-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 4 (bases 1 to 111496)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,  
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Db 105151 AGCATATGTCTGTGTGAGACAGTAAGCACTTTCATCTTATCCCTAAAGTAAATTTA 105210  
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Db 105211 AATTAGCTAAGAAATTTCTGTCTGCTTCAACATAAAGTGGGAAAAATTTCCAAG 105270  
QY 124 ----- 124  
Db 105271 AAATACCAATGATCTGGAAGCAGAAAGTCCATTGGTGTGTTCTTTATTAAGAAAGCA 105330  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Maximum Match 100%  
Listing first 100 summaries

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1222.8	97.3	1286	4	US-09-489-847-124 Sequence 124, App
3	1199.8	95.4	1220	4	US-09-692-081-3 Sequence 3, Appl
4	1197	95.2	1288	4	US-09-305-258-125 Sequence 125, App
5	826	65.7	837	4	US-09-834-759-512 Sequence 512, App
6	826	65.7	837	4	US-09-834-759-513 Sequence 513, App
7	732	58.0	732	4	US-09-834-759-510 Sequence 510, App
8	729	58.0	729	4	US-09-834-759-511 Sequence 511, App
9	681.8	54.2	683	3	US-09-322-575-63 Sequence 63, Appl
10	681.8	54.2	683	4	US-09-389-681-63 Sequence 63, Appl
11	681.8	54.2	683	4	US-09-520-405-63 Sequence 63, Appl
12	681.8	54.2	683	4	US-09-339-338-63 Sequence 63, Appl
13	681.8	54.2	683	4	US-09-433-8268-63 Sequence 63, Appl
14	681.8	54.2	683	4	US-09-604-2874-63 Sequence 63, Appl
15	681.8	54.2	683	4	US-09-285-480-63 Sequence 63, Appl
16	681.8	54.2	683	4	US-09-834-759-63 Sequence 63, Appl
17	681.8	54.2	683	4	US-09-590-7516-63 Sequence 63, Appl
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19	566.6	45.1	734	4	US-09-692-081-6 Sequence 6, Appl
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21	68.8	5.5	1141	4	US-09-641-638-651 Sequence 651, App
22	56.8	4.5	20674	4	US-10-170-097-651 Sequence 651, App
23	55.2	4.4	2109	4	US-09-370-838-153 Sequence 153, App
24	55.2	4.4	2109	4	US-09-854-133-153 Sequence 153, App
25	55	4.4	4818	3	US-08-817-926-27 Sequence 27, Appl
26	54.2	4.3	19124	2	US-08-487-8268-13 Sequence 13, Appl
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28	52.8	4.2	6801	4	US-10-204-708-62 Sequence 62, Appl
29	52.8	4.2	7244	3	US-08-378-313-26 Sequence 26, Appl
30	52.2	4.2	10467	4	US-10-204-708-2 Sequence 2, Appl
31	52	4.1	6243	2	US-09-056-075-1 Sequence 1, Appl
32	51.6	4.1	11049	4	US-10-204-708-24 Sequence 24, Appl
33	51	4.1	1055	4	US-09-806-7088-23 Sequence 23, Appl
34	50.4	4.0	7218	1	US-08-232-463-14 Sequence 14, Appl
35	49.6	3.9	5501	4	US-10-204-708-38 Sequence 38, Appl
36	49.4	3.9	1141	4	US-09-806-7088-22 Sequence 22, Appl
37	48.8	3.9	53332	4	US-09-801-861-3 Sequence 3, Appl
38	48.8	3.9	53332	4	US-10-224-562-3 Sequence 3, Appl
39	48.6	3.9	1866	3	US-08-909-742-1 Sequence 1, Appl
40	48.6	3.9	1866	3	US-09-412-289-1 Sequence 1, Appl
41	48.4	3.9	6020	4	US-10-204-708-7 Sequence 7, Appl
42	48.2	3.8	9347	4	US-10-204-708-35 Sequence 35, Appl
43	48.2	3.8	19513	4	US-10-204-708-40 Sequence 40, Appl
44	47.8	3.8	640681	4	US-09-790-988-1 Sequence 1, Appl
45	47.6	3.8	4383	6	US-08-397-653B-2 Patent No. 5175095
46	47.6	3.8	4383	6	US-07-867-106-2 Patent No. 5175095
47	47.6	3.8	5852	1	US-07-867-106-2 Patent No. 5175095
48	47.6	3.8	6306	4	US-10-204-708-50 Sequence 50, Appl
49	47.4	3.8	5855	4	US-10-204-708-33 Sequence 33, Appl
50	47.4	3.8	6113	4	US-10-204-708-14 Sequence 14, Appl
51	47.2	3.8	3095	6	5231168-1 Patent No. 5231168
52	47.2	3.8	640681	4	US-09-790-988-1 Sequence 1, Appl
53	46.8	3.7	10467	4	US-10-204-708-32 Sequence 32, Appl
54	46.6	3.7	8093	4	US-09-417-485D-5 Sequence 5, Appl
55	46.2	3.7	10640	4	US-09-417-485D-5 Sequence 5, Appl
56	46	3.7	477	4	US-09-489-039A-484 Sequence 484, App
57	46	3.7	2364	4	US-09-489-039A-457 Sequence 457, App
58	46	3.7	4060	1	US-08-308-949A-1 Sequence 1, Appl
59	45.8	3.6	1512	4	US-09-248-796A-1306 Sequence 1306, App
60	45.8	3.6	1785	4	US-09-601-198-156 Sequence 156, App
61	45.6	3.6	636	3	US-08-998-416-1137 Sequence 1137, App
62	45.6	3.6	837	3	US-08-998-416-1137 Sequence 1137, App
63	45.6	3.6	3662	4	US-09-252-991A-7551 Sequence 7551, App
64	45.6	3.6	1611	4	US-09-252-991A-7551 Sequence 7551, App
65	45.6	3.6	1611	4	US-09-252-991A-7551 Sequence 7551, App
66	45.4	3.6	11098	4	US-09-252-991A-7551 Sequence 7551, App
67	45.4	3.6	1135	4	US-09-252-991A-7551 Sequence 7551, App
68	45.4	3.6	1401	4	US-09-252-991A-7551 Sequence 7551, App
69	45.4	3.6	1611	4	US-09-252-991A-7551 Sequence 7551, App
70	45.2	3.6	680	3	US-08-998-416-204 Sequence 204, App
71	45.2	3.6	2450	4	US-09-491-522-9 Sequence 9, Appl
72	45.2	3.6	3909	4	US-09-016-433-1119 Sequence 1119, App
73	45.2	3.6	4580	4	US-09-491-522-8 Sequence 8, Appl
74	45.2	3.6	5562	4	US-10-204-708-63 Sequence 63, Appl
75	45	3.6	390	3	US-08-911-853-20 Sequence 20, Appl
76	45	3.6	390	3	US-09-479-405-20 Sequence 20, Appl
77	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
78	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
79	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
80	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
81	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
82	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
83	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
84	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
85	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
86	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
87	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
88	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
89	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
90	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
91	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
92	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
93	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
94	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
95	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
96	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
97	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
98	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
99	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl
100	45	3.6	390	3	US-08-826-246-3 Sequence 3, Appl

## ALIGNMENTS

```
RESULT 1
US-09-489-847-89
; Sequence 89, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 1342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-847-89

Query Match      98.0%; Score 1231.6; DB 4; Length 1342;
Best Local Similarity 99.6%; Pred. No. 4.3e-284;
Matches 1245; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY      8 GCGCGCGCGGTGAAGGCGCATTTGATGAGCTGCGCGCGGCTCGAGAGCGCGGAGGCC 67
DB      12 GCGCGCGCGGTGAAGGCGCATTTGATGAGCTGCGCGCGGCTCGAGAGCGCGGAGGCC 70
QY      68 AGAGCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
DB      71 AGAGCGCTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 130
QY      128 GCGCGGAGCCATGCGACCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCT 187
DB      131 GCGCGGAGCCATGCGACCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCT 190
QY      188 GCTGCTCTGCTGCTGAGCTGCGCGCGCGCGCGCGCGCGCGCTGAGATCCCAAGGGA 247
DB      191 GCTGCTCTGCTGCTGAGCTGCGCGCGCGCGCGCGCGCGCGCTGAGATCCCAAGGGA 250
QY      248 GCAAAAGCGCGAGCTCCGCGAGAGGAGGAGTGTGAACCTGTAAATGAAATGTCTTACA 307
DB      251 GCAAAAGCGCGAGCTCCGCGAGAGGAGGAGTGTGAACCTGTAAATGAAATGTCTTACA 310
QY      308 AGGGCCAGCAGAGAGTGGCTGTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 367
DB      311 AGGGCCAGCAGAGAGTGGCTGTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 370
QY      368 ACCTGGAGTCCAGGTCGGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
DB      371 ACCTGGAGTCCAGGTCGGAGTGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 430
QY      428 CTTTGAAGAGTCTTGAAGACCACTTAAGAGAGTGTTCAGAGTTCAGTTCAGTTCAGTTCAG 487
DB      431 CTTTGAAGAGTCTTGAAGACCACTTAAGAGAGTGTTCAGAGTTCAGTTCAGTTCAGTTCAG 490
QY      488 CATGATCTTGGGAAATTTGGGAGTGTACATTTTCAAGATGGCTTCAATATGAGCTCT 547
DB      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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DB      491 CATGATCTTGGGAAATTTGGGAGTGTACATTTTCAAGATGGCTTCAATATGAGCTCT 550
QY      548 AAGAGTTTGTTCAGTGGCTCACTTCGGCTAAATGAGAAATGCAATGCTGTAGCTTG 607
DB      551 AAGAGTTTGTTCAGTGGCTCACTTCGGCTAAATGAGAAATGCAATGCTGTAGCTTG 610
QY      608 GTATTTCATTCATGAGCTGATGTTTGAAGAGCTCTTCCATTAAGCTAATTAATTA 667
DB      611 GTATTTCATTCATGAGCTGATGTTTGAAGAGCTCTTCCATTAAGCTAATTAATTA 670
QY      668 TTTGACCAAGAGAGCCCTGAATGAATTCACCAATTAATTAATTCATGCACTTCTCTGT 727
DB      671 TTTGACCAAGAGAGCCCTGAATGAATTCACCAATTAATTAATTCATGCACTTCTCTGT 730
QY      728 GGAAGAGCTTGTGAAGAAATTGGTGTGATTTGAGATGTTGCTATCGGGTGGAC 787
DB      731 GGAAGAGCTTGTGAAGAAATTGGTGTGATTTGAGATGTTGCTATCGGGTGGAC 790
QY      788 TTGTCAGATTACCCAAAGAGAGTGTCTTCACTGATGAGATTCAGTTCTCGCATCAT 847
DB      791 TTGTCAGATTACCCAAAGAGAGTGTCTTCACTGATGAGATTCAGTTCTCGCATCAT 850
QY      848 TATTGAGACTTACCAAAATTAATGCTTTAATTTTCACTTGTCTACTCTTTTATAT 907
DB      851 TATTGAGACTTACCAAAATTAATGCTTTAATTTTCACTTGTCTACTCTTTTATAT 910
QY      908 GCCTTGAATGTTCACTTAATGACATTTTAAATTAATGATTAATGATTAATGATTAATG 967
DB      911 GCCTTGAATGTTCACTTAATGACATTTTAAATTAATGATTAATGATTAATGATTAATG 970
QY      968 AAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTAAATCTAGC 1027
DB      971 AAGCAAGCTAAATATGTTTACAGACCAAGTGTGATTTTCACTGTTTAAATCTAGC 1030
QY      1028 ATTATCTTTTGTCTCAATTAAGAGTGTTCATATTTTGTAGTGTGTAATGAT 1087
DB      1031 ATTATCTTTTGTCTCAATTAAGAGTGTTCATATTTTGTAGTGTGTAATGAT 1090
QY      1088 TTTCTTCACTGATCTCTCTCAACCTTAATTTGAAATGTTGTTGTTTGT 1147
DB      1091 TTTCTTCACTGATCTCTCTCAACCTTAATTTGAAATGTTGTTGTTTGT 1150
QY      1148 TTTCTTCACTGATCTCTCTCAACCTTAATTTGAAATGTTGTTGTTTGT 1207
DB      1151 TTTCTTCACTGATCTCTCTCAACCTTAATTTGAAATGTTGTTGTTTGT 1210
QY      1208 AAATGTTAAGATTTTATATCTGTAAATTAATTAATTTTCCACA 1257
DB      1211 AAATGTTAAGATTTTATATCTGTAAATTAATTAATTTTCCAAA 1260

RESULT 2
US-09-489-847-124
; Sequence 124, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; EARLIER FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
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NUMBER OF SEQ ID NOS: 376  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 124  
LENGTH: 1286  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (1284)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-489-847-124

Query Match 97.3%; Score 1222.8; DB 4; Length 1286;  
Best Local Similarity 99.7%; Pred. No. 5.3e-282;  
Matches 1246; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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QY 8 GCGCGCGGGGTAAAGGCGCATTTGATGACGCTGCGGCGGCGCTCGAGAGCGCGGAGCC 67
DB 2 GCGCGCGGGGTAAAGGCGCATTTGATGACGCTGCGGCGGCGCTCGAGAGCGCGGAG-C 60
QY 68 AACCGTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
DB 61 AACCGTGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 128 GCGGAGCATGACGACCCCAAGGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 187
DB 121 GCGGAGCATGACGACCCCAAGGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
QY 188 GCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
DB 181 GCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 248 GGAAGAGGCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 307
DB 241 GGAAGAGGCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 299
QY 308 AGGCGCAGCAGAGAGTCTCTGTCGACGCGGAGCCCTGCGGCGCAATGTTATCCGCGTAC 367
DB 300 AGGCGCAGCAGAGAGTCTCTGTCGACGCGGAGCCCTGCGGCGCAATGCGATTCGCGGTAC 359
QY 368 ACCTGGATCCAGGTCGCGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
DB 360 ACCTGGATCCAGGTCGCGGATGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
QY 428 CTTTGAAGAGTCTCTGACACCCCACTCAAGCAGTGTTCATGAGATTCATGAAATATAG 487
DB 420 CTTTGAAGAGTCTCTGACACCCCACTCAAGCAGTGTTCATGAGATTCATGAAATATAG 479
QY 488 CATGATCTTGGGAAATGCGGAGTATCATTTACAAAGATGCGTTCAATATAGTCTCT 547
DB 480 CATGATCTTGGGAAATGCGGAGTATCATTTACAAAGATGCGTTCAATATAGTCTCT 539
QY 548 AAGAGTTTGTTCAGTGGCTCACTTGGGCTAAATGAGAGAGAGAGAGAGAGAGAGAGAG 607
DB 540 AAGAGTTTGTTCAGTGGCTCACTTGGGCTAAATGAGAGAGAGAGAGAGAGAGAGAGAG 599
QY 608 GATTTTCACTTCAATGAGAGTGTGATGTCAGAGCTCTTCCATGAGAGATTAATTA 667
DB 600 GATTTTCACTTCAATGAGAGTGTGATGTCAGAGCTCTTCCATGAGAGATTAATTA 659
QY 668 TTTGAGCAAGAGAGCGCTGAATGAATCAACAAATTAATTAATTCATGAGAGTCTCTCT 727
DB 660 TTTGAGCAAGAGAGCGCTGAATGAATCAACAAATTAATTAATTCATGAGAGTCTCTCT 719
QY 728 GGAAGAGCTTTTGAAGAGATGTCGATGATGATGATGATGATGATGATGATGATGATGAT 787
DB 720 GGAAGAGCTTTTGAAGAGATGTCGATGATGATGATGATGATGATGATGATGATGATGAT 779
QY 788 TTTTTCAGATTCACCAAGAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGAT 847
DB 780 TTTTTCAGATTCACCAAGAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGAT 839
QY 848 TATTAAGAGATTCACCAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGAT 907
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DB 840 TATTAAGAGATTCACCAAGAGATGCTTCTACTGATGATGATGATGATGATGATGATGAT 899
QY 908 GCGTGGAGATGTTACTTAATTAATGACATTTTAAATAGTTTATGATGATGATGATGATG 967
DB 900 GCGTGGAGATGTTACTTAATTAATGACATTTTAAATAGTTTATGATGATGATGATGATG 959
QY 968 AAGCAAGCTAAATGTTTACAGACCAAGAGTGTATTCACAGTGTGTTTAAATCTAGC 1027
DB 960 AAGCAAGCTAAATGTTTACAGACCAAGAGTGTATTCACAGTGTGTTTAAATCTAGC 1019
QY 1028 ATTATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTGTGTTAGTTAGATATAC 1087
DB 1020 ATTATTCATTTTGTCTTCAATCAAAAGTGTTCATATTTTGTGTTAGTTAGATATAC 1079
QY 1088 TTTTCTCATGATGACATTTCTGACACCTATTAATTTGGAATATGTTGTTGTTGTT 1147
DB 1080 TTTTCTCATGATGACATTTCTGACACCTATTAATTTGGAATATGTTGTTGTTGTT 1139
QY 1148 TTTTCTCATGATGACATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1207
DB 1140 TTTTCTCATGATGACATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1199
QY 1208 AAATGTTAAGATTTTATTTATATCTGTTAAATTAATTAATTTATTTTCAACA 1257
DB 1200 AAATGTTAAGATTTTATTTATATCTGTTAAATTAATTAATTTATTTTCAACA 1249
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RESULT 3  
US-09-692-081-3  
Patent No. 6630325  
Application US/09692081

GENERAL INFORMATION:  
APPLICANT: LINDNER, Volkhard  
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL  
FILE REFERENCE: 36-13 Lindner et al. (20036.0013)  
CURRENT APPLICATION NUMBER: US/09/692,081  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3  
LENGTH: 1220  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-692-081-3

Query Match 95.4%; Score 1199.8; DB 4; Length 1220;  
Best Local Similarity 99.8%; Pred. No. 1.6e-276;  
Matches 1212; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 43 GCGGCTCTCGAGCGCGGCGGAGCGGAGCGCTGACACGTTCTCTCTGCTGCTCTCTCT 102
DB 6 GCGGCTCTCGAGCGCGGCGGAGCGGAGCGCTGACACGTTCTCTCTGCTGCTCTCTCT 65
QY 103 GCGTCAAGTCTCGCGCTGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 162
DB 66 GCGTCAAGTCTCGCGCTGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 125
QY 163 CCCGCAAGGAGTCTCGCGGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 222
DB 126 CCCGCAAGGAGTCTCGCGGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 185
QY 223 GCGCTCTGAGATCCCAAGGAGGAGCAAAAGGCGCAGCTCTCGGAGAGGAGTGTGTG 282
DB 186 GCGCTCTGAGATCCCAAGGAGGAGCAAAAGGCGCAGCTCTCGGAGAGGAGTGTGTG 245
QY 283 ACCTGTATTAATGAGATGTCCTTACAAAGGCGGAGAGTGTGTGTGTGTGTGTGTGTGT 342
DB 246 ACCTGTATTAATGAGATGTCCTTACAAAGGCGGAGAGTGTGTGTGTGTGTGTGTGTGT 305
QY 343 CTGGGCGCAATGTTTCTCGGAGTCACTGAGATCCCAAGTGTGAGATTCAGAGAG 402
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Db 306 CTGGGGCCAAATGCGATCCGGGTACACCTGGAGTCCAGGTGGATGAGATTCAAGGAG 365  
Qy 403 AAAAGGGGGAATGTCTGAGGGAAGCTTTAGAGAGCTCGACACCCAACTACAAGCACT 462  
Db 366 AAAAGGGGGAATGTCTGAGGGAAGCTTTAGAGAGCTCGACACCCAACTACAAGCACT 425  
Qy 463 GTTCATGAGATTGATTAATTAATGAGATGATCTTGGGAAAATGCGAGTGTACATTTA 522  
Db 426 GTTCATGAGATTGATTAATTAATGAGATGATCTTGGGAAAATGCGAGTGTACATTTA 485  
Qy 523 CAAAGATGCGCTCAATAGTGTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAAT 582  
Db 486 CAAAGATGCGCTCAATAGTGTCTAAGAGTTTGTTCAGTGGCTCACTTGGCTAAAT 545  
Qy 583 GCAGAAATGCAATGCTGTGAGCTGTGATTTTCAATTCATGAGCTGAATGTTCAAGAC 642  
Db 546 GCAGAAATGCAATGCTGTGAGCTGTGATTTTCAATTCATGAGCTGAATGTTCAAGAC 605  
Qy 643 CTCTTCCCATGGAAGCTTAATTAATTTGAGACCAAGAAAGCCCTGAATGAATCAACA 702  
Db 606 CTCTTCCCATGGAAGCTTAATTAATTTGAGACCAAGAAAGCCCTGAATGAATCAACA 665  
Qy 703 TTAATATTCATGCACTCTCTGTGGAAGAGCTTGTGAAGAAATGCTGTGATTTG 762  
Db 666 TTAATATTCATGCACTCTCTGTGGAAGAGCTTGTGAAGAAATGCTGTGATTTG 725  
Qy 763 TGAATGTTGCTATCGGGTGGCACTGTTCAGATTACCAAGAGAGATGCTTCACTG 822  
Db 726 TGAATGTTGCTATCGGGTGGCACTGTTCAGATTACCAAGAGAGATGCTTCACTG 785  
Qy 823 GATGGAATTCAGTTTCTGCACTCAATTATTAAGAACTAACCAAAATGAATGCTTAATTT 882  
Db 786 GATGGAATTCAGTTTCTGCACTCAATTATTAAGAACTAACCAAAATGAATGCTTAATTT 845  
Qy 883 CATTTGACCTCTTTTATTAATGCTTGAAGTGTCACTTAATGAATGAATTTAAT 942  
Db 846 CATTTGACCTCTTTTATTAATGCTTGAAGTGTCACTTAATGAATGAATTTAAT 905  
Qy 943 AAGTTATGATACATCTGAATGAAGCAAGTAATATGTTTACAGACCAAGTGTG 1002  
Db 906 AAGTTATGATACATCTGAATGAAGCAAGTAATATGTTTACAGACCAAGTGTG 965  
Qy 1003 ATTTCACCTGTTTAAATCTAGCATTAATTCATTTGCTTCAATCAAAAGTGTTCOA 1062  
Db 966 ATTTCACCTGTTTAAATCTAGCATTAATTCATTTGCTTCAATCAAAAGTGTTCOA 1025  
Qy 1063 TATTTTGTGTTAGTGTAGAAATCTTCTCATAGTACATTTCTCAACCTATAATTT 1122  
Db 1026 TATTTTGTGTTAGTGTAGAAATCTTCTCATAGTACATTTCTCAACCTATAATTT 1084  
Qy 1123 GGAATATGTTGTGCTTTTGTCTTTCTTATAGATAGCAATTTTAAATAATATAA 1182  
Db 1085 GGAATATGTTGTGCTTTTGTCTTTCTTATAGATAGCAATTTTAAATAATATAA 1144  
Qy 1183 AGCTACCAATCTTTGTACAAATTTGTAAGATTTTAAATCTGTTAAATPA 1242  
Db 1145 AGCTACCAATCTTTGTACAAATTTGTAAGATTTTAAATCTGTTAAATPA 1204  
Qy 1243 AAATTTATTTCCACA 1257  
Db 1205 AAATTTATTTCCACA 1219

## RESULT 4

US-09-205-258-125  
; Sequence 125, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878



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? EARLIER FILING DATE: 1997-06-06
? EARLIER APPLICATION NUMBER: 60/070,923
? EARLIER FILING DATE: 1997-12-19
? EARLIER APPLICATION NUMBER: 60/092,921
? EARLIER FILING DATE: 1998-07-15
? EARLIER APPLICATION NUMBER: 60/094,657
? EARLIER FILING DATE: 1998-07-30
? NUMBER OF SEQ ID NOS: 1227
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO: 125
? LENGTH: 1288
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (1286)
? OTHER INFORMATION: n equals a,t,g, or c
IS-09-205-258-125

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Query Match	95.2%	Score 1197	DB 4	Length 1288
Best Local Similarity	99.3%	Pred. No. 7.5e-276		
Matches 1242; Conservative	2;	Mismatches	2;	Indels 5; Gaps 4;

Qy	8	GGGCGCGGGGTGAAGAGCGCATTTGATGCAAGCTCGCGCGCGCTCGAGCTCGGCGAGCG	67
Db	1	GGCGCGGGGTGAAGAGCGCATTTGATGCAAGCTCGCGCGCGCTCGAGCTCGGCGAGCG	59
Qy	68	AGAGCTGACCAAGTTCTCTCTCGGTCTCTCGGCTCGAGCTCGGCGCTGCGCGCA	127
Db	60	AGAGCTGACCAAGTTCTCTCTCGGTCTCTCGGCTCGAGCTCGGCGCTGCGCGCA	119
Qy	128	GGCGGAGCGCATGCGAAGCCGAGGCGCGCGCGCTCGCGAGCGGCTCGCGCGCTCT	187
Db	120	GCGGAGCGCATGCGAAGCCGAGGCGCGCGCGCTCGCGAGCGGCTCGCGCGCTCT	179
Qy	188	GCTGCTCTGCTGCTCACTGCGCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAA	247
Db	180	GCTGCTCTGCTGCTCACTGCGCGCGCGCTCGAGCGCTCTGAGATCCCAAGGGGAA	239
Qy	248	GCAAAAGCGCAGCTCCGCGAGAGGAGGTGTGACCTGTATATGGAATGTGCTTACA	307
Db	240	GCAAAAGCGCCA--TCCGCGAGAGGAGGTGTGTGACCTGTATATGGAATGTCTTACA	297
Qy	308	AGGCGCAGCAGAGGTGCTGTTGAGAGGGAGCCCTGGGCGCAATGTATTCGGGGTAC	367
Db	298	AGGCGCAGCAGAGGTGCTGTTGAGAGGGAGCCCTGGGCGCAATGTGCAATTCGGGGTAC	357
Qy	368	ACCTGGGATCCAGGTCGGGATGGAATTCAAAGAGAAAGGGGGAATGCTTGAGGGAAAG	427
Db	358	ACCTGGGATCCAGGTCGGGATGGAATTCAAAGAGAAAGGGGGAATGCTTGAGGGAAAG	417
Qy	428	CTTTGAGGAGTCTTGACACCCACATACAGACGTGTCATGAGTTCAATGAATATATGG	487
Db	418	CTTTGAGGAGTCTTGACACCCACATACAGACGTGTCATGAGTTCAATGAATATATATGG	477
Qy	488	CATGATCTTGAGGAAATTCGGGAGTACATTTTCAAAAGATGCGTCAAAATAGTGCCT	547
Db	478	CATGATCTTGAGGAAATTCGGGAGTACATTTTCAAAAGATGCGTCAAAATAGTGCCT	537
Qy	548	AAGAGTTTGTCAGTGGCTCATCTTGCGTAAATATGCAAAATGCAATGCACTGTCAGCGTTG	607
Db	538	AAGAGTTTGTCAGTGGCTCATCTTGCGTAAATATGCAAAATGCAATGCACTGTCAGCGTTG	597
Qy	608	GTAATTTCACTTCAATGAGAGTGAATGTTCAAGACCTCTTCCCATTTGAAGCTATATTTTA	667
Db	598	GTAATTTCACTTCAATGAGAGTGAATGTTCAAGACCTCTTCCCATTTGAAGCTATATTTTA	657
Qy	668	TTTGAACCAAGAGAGCTCGTAATGATATCAACAAATTAATTCATCCGACTTCTGT	727
Db	658	TTTGAACCAAGAGAGCTCGTAATGATATCAACAAATTAATTCATCCGACTTCTGT	717
Qy	728	GGAAGGACTTTGAGAGAAATGCTGCTGGAATTAAGTGAATGTTGCTATCTCGGTTGGAC	787

Db	718	GGAAAGCACTTTGTGAAGAAATTGGAGTCGATTAGTGGATGTGTCTATCTGGTGTGGAC	777
Qy	788	TTGTTTCAGATTACCCAAAAGAGATGCTTCTACCTGATGAAATTCAGTTTCTCCGACAT	847
Db	778	TTGTTTCAGATTACCCAAAAGAGATGCTTCTACCTGATGAAATTCAGTTTCTCCGACAT	837
Qy	848	TATTGAAGACTACCAAAATAAAGCTTAAATTTTCATTGCTACCTCTTTTAAATAT	907
Db	838	TATTGAAGACTACCAAAATAAAGCTTAAATTTTCATTGCTACCTCTTTTAAATAT	897
Qy	908	GCCTTGGATGCTTACCTTAATGACATTTTAAATAAAGTTATGATATACCTGAAATGA	967
Db	898	GCCTTGGATGCTTACCTTAATGACATTTTAAATAAAGTTATGATATACCTGAAATGA	957
Qy	968	AAGCAAACTAAATATGTTTACAGACCAGATGATTTACACCTGTTTTAAATCTAGC	1027
Db	958	AAGCAAACTAAATATGTTTACAGACCAGATGATTTACACCTGTTTTAAATCTAGC	1016
Qy	1028	ATTATTCATTTTGGCTTCATCAAAAAGTGTTCAATATTTTTTAACTGGTTGAATAC	1087
Db	1017	ATTATTCATTTTGGCTTCATCAAAAAGTGTTCAATATTTTTTAACTGGTTGAATAC	1076
Qy	1088	TTTCTTCATTCACATCTCTCAACCTATAATT- GGAATATGTTGGTCTTTGTT	1146
Db	1077	TTTCTTCATTCACATCTCTCAACCTATAATTGGGAATATGTTGGTCTTTGTT	1136
Qy	1147	TTTTCTCTAGATAGCATTTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTG	1206
Db	1137	TTTTCTCTAGATAGCATTTTTTAAAAAAATATAAAAGCTACCAATCTTTGTACAATTTG	1196
Qy	1207	TAAATGTTAAGATTTTTTTTATATCTGTATAAATAAAATATTTCCAAAC	1257
Db	1197	TAAATGTTAAGATTTTTTTTATATCTGTATAAATAAAATATTTCCAAAC	1247

```

US-09-834-759-512
; RESULT 5
; Sequence 512, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiaqichun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS OF AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834.759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 512
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-512

```

Query Match	65.7%	Score 826	DB 4	Length 837
Best Local Similarity	99.9%	Pred. No. 1.8e-187		
Matches	837	Conservative 0	Gaps 1	Gaps 1
Qy	32	ATGCAGCTGGGGGGGAGCTCGAGGGGGGGGAGCCAGACGCTAGCCAGTTCCTCTCT	91	
Db	1	ATGCAGCTGGGGGGGAGCTCGAGGGGGGGGAG-CAGACCTTACCACTTCCTCTCTCT	59	
Qy	92	CGGTTCCTCCGCGCTTCAGACTCCGCGGTCCCGGAGCCGGAGCCATATCGACCCCAAGG	151	
Db	60	CGGTTCCTCCGCGCTTCAGACTCCGCGGTCCCGGAGCCGGAGCCATATCGACCCCAAGG	119	
Qy	152	CCCGCGCGCTCCCGGAGCGGAGTCCGAGGCGCTCTGCTCTGCTGCTGACGTGCC	211	

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Db 120 CCCCCCCCCCTCCCGCAGCGGCTCGCGGCTCCGCTGCTCTCTCTCAGCTGCC 179
Qy 212 CGCGCCGTCGAGCGGCTCTGAGATCCCCAAAGGGGAAAGCAAAAGGGCAGCTCCGGCAGG 271
Db 180 CGCGCCGTCGAGCGGCTCTGAGATCCCCAAAGGGGAAAGCAAAAGGGCAGCTCCGGCAGG 239
Qy 272 GAGAGTGTGAGCCTGTATTAATGATGATGCTTACAGAGGCCAGCAGAGTCTGTGTG 331
Db 240 GAGAGTGTGAGCCTGTATTAATGATGATGCTTACAGAGGCCAGCAGAGTCTGTGTG 299
Qy 332 AGAGGGAGCCCTGGGGCCATGTTATTCGGGTACACCTGGGATCCAGGTGGGATGG 391
Db 300 AGAGGGAGCCCTGGGGCCATGTTATTCGGGTACACCTGGGATCCAGGTGGGATGG 359
Qy 392 ATTCAAGAGGAAAGGGGGAATGCTGAGGGGAAAGCTTGGAGGTCTGTGACACCCAA 451
Db 360 ATTCAAGAGGAAAGGGGGAATGCTGAGGGGAAAGCTTGGAGGTCTGTGACACCCAA 419
Qy 452 CTACAGAGAGTGTTCATGAGATTCATTAATTAATGAGATGATCTTGGGAAATTCGGGA 511
Db 420 CTACAGAGAGTGTTCATGAGATTCATTAATTAATGAGATGATCTTGGGAAATTCGGGA 479
Qy 512 GTGATATTTCAGAAAGATGCTTCAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACT 571
Db 480 GTGATATTTCAGAAAGATGCTTCAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACT 539
Qy 572 TCGGCTAAATAGCAAAATGCAATGCTGTCAAGCGTGTGATTTCAATTCAGATTCAGAGCTGA 631
Db 540 TCGGCTAAATAGCAAAATGCAATGCTGTCAAGCGTGTGATTTCAATTCAGATTCAGAGCTGA 599
Qy 632 ATGTTCAGAGCTCTTCCCATTTGAAGCTATTAATTAATTTGAGCAAGAGCCCTGAAT 691
Db 600 ATGTTCAGAGCTCTTCCCATTTGAAGCTATTAATTAATTTGAGCAAGAGCCCTGAAT 659
Qy 692 GAATTCACCAATTAATTAATTCATTCGACTCTTCTGTGAGAGCACTTTGTGAGAGAAATGG 751
Db 660 GAATTCACCAATTAATTAATTCATTCGACTCTTCTGTGAGAGCACTTTGTGAGAGAAATGG 719
Qy 752 TGTGATTAATGATGATGCTATCTGGGTGGGCACTTGTGAGATTAACCCAAAGAGA 811
Db 720 TGTGATTAATGATGATGCTATCTGGGTGGGCACTTGTGAGATTAACCCAAAGAGA 779
Qy 812 TGTCTTACTGATGATGAATTCAGTTTCTGCATCATTAATGAAGAACTACCAAAATTA 869
Db 780 TGTCTTACTGATGATGAATTCAGTTTCTGCATCATTAATGAAGAACTACCAAAATTA 837
```

## RESULT 6

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US-09-834-759-513
; Sequence 513, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 513
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-759-513
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Query Match 65.7%; Score 826; DB 4; Length 837;
Best Local Similarity 99.9%; Pred. No. 1,8e-187;
Matches 837; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Qy 32 ATGCAAGCTTCGCGGCGGCTCGGAGCGGCGGAGCAGACGCTGACACCACTTCTCTCT 91
Db 1 ATGCAAGCTTCGCGGCGGCTCGGAGCGGCGGAGCAGACGCTGACACCACTTCTCTCT 59
Qy 92 CGGTCTCTCCGCTCCAGCTCCCGGCTCCCGGCAACCGGAGCCATGAGATCCCAAGG 151
Db 60 CGGTCTCTCCGCTCCAGCTCCCGGCTCCCGGCAACCGGAGCCATGAGATCCCAAGG 119
Qy 152 CCCGCGCGCTCCCGGAGCGGCTCCCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 211
Db 120 CCCGCGCGCTCCCGGAGCGGCTCCCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 179
Qy 212 CGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGCAAAAGGCGCAGCTTCGGCAGAG 271
Db 180 CGCGCGCTCGAGCGCTCTGAGATCCCAAGGGAGCAAAAGGCGCAGCTTCGGCAGAG 239
Qy 272 GAGAGTGTGAGCCTGTATTAATGATGATGCTTACAGAGGCCAGCAGAGTGTGTGTG 331
Db 240 GAGAGTGTGAGCCTGTATTAATGATGATGCTTACAGAGGCCAGCAGAGTGTGTGTG 299
Qy 332 AGAGGGAGCCCTGGGGCCATGTTATTCGGGTACACCTGGGATCCAGGTGGGATGG 391
Db 300 AGAGGGAGCCCTGGGGCCATGTTATTCGGGTACACCTGGGATCCAGGTGGGATGG 359
Qy 392 ATTCAAGAGGAAAGGGGGAATGCTGAGGGGAAAGCTTTGAGAGTCTGTGACACCCAA 451
Db 360 ATTCAAGAGGAAAGGGGGAATGCTGAGGGGAAAGCTTTGAGAGTCTGTGACACCCAA 419
Qy 452 CTACAGAGAGTGTTCATGAGATTCATTAATTAATGAGATGATCTTGGGAAATTCGGGA 511
Db 420 CTACAGAGAGTGTTCATGAGATTCATTAATTAATGAGATGATCTTGGGAAATTCGGGA 479
Qy 512 GTGATATTTCAGAAAGATGCTTCAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACT 571
Db 480 GTGATATTTCAGAAAGATGCTTCAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACT 539
Qy 572 TCGGCTAAATAGCAAAATGCAATGCTGTCAAGCGTGTGATTTCAATTCAGATTCAGAGCTGA 631
Db 540 TCGGCTAAATAGCAAAATGCAATGCTGTCAAGCGTGTGATTTCAATTCAGATTCAGAGCTGA 599
Qy 632 ATGTTCAGAGCTCTTCCCATTTGAAGCTATTAATTAATTTGAGCAAGAGCCCTGAAT 691
Db 600 ATGTTCAGAGCTCTTCCCATTTGAAGCTATTAATTAATTTGAGCAAGAGCCCTGAAT 659
Qy 692 GAATTCACCAATTAATTAATTCATTCGACTCTTCTGTGAGAGCACTTTGTGAGAGAAATGG 751
Db 660 GAATTCACCAATTAATTAATTCATTCGACTCTTCTGTGAGAGCACTTTGTGAGAGAAATGG 719
Qy 752 TGTGATTAATGATGATGCTATCTGGGTGGGCACTTGTGAGATTAACCCAAAGAGA 811
Db 720 TGTGATTAATGATGATGCTATCTGGGTGGGCACTTGTGAGATTAACCCAAAGAGA 779
Qy 812 TGTCTTACTGATGATGAATTCAGTTTCTGCATCATTAATGAAGAACTACCAAAATTA 869
Db 780 TGTCTTACTGATGATGAATTCAGTTTCTGCATCATTAATGAAGAACTACCAAAATTA 837
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## RESULT 7

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US-09-834-759-510
; Sequence 510, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jianshun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
```

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
;; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
;; FILE REFERENCE: 210121.470C9  
;; CURRENT APPLICATION NUMBER: US/09/834,759  
;; NUMBER OF SEQ ID NOS: 547  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 510  
;; LENGTH: 732  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-834-759-510

Query Match 58.2%; Score 732; DB 4; Length 732;  
Best Local Similarity 100.0%; Pred. No. 4.3e-165;

Matches 732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 ATGCGACCCGAGGCGCCGCGCTCCGCGAGCGGCTCCGCGCTCTGCTGCTCTG 197  
DB 1 ATGCGACCCGAGGCGCCGCGCTCCGCGAGCGGCTCCGCGCTCTGCTGCTCTG 60  
QY 198 CTGCTGCACTGCTCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 257  
DB 61 CTGCTGCACTGCTCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 120  
QY 258 CAGCTCCGCGAGGAGGCTGAGCTGTATTAAGAAATGCTTACAGGCGCAGCA 317  
DB 121 CAGCTCCGCGAGGAGGCTGAGCTGTATTAAGAAATGCTTACAGGCGCAGCA 180  
QY 318 GAGTGCCTGCTGAGACGCGAGCCCTGGGCGCAATGTTATTCGGGTACACTGGGATC 377  
DB 181 GAGTGCCTGCTGAGACGCGAGCCCTGGGCGCAATGTTATTCGGGTACACTGGGATC 240  
QY 378 CAGGTCGGGATGATTCAGAGGAGAAAGGGGGAATGCTGAGGGAAGCTTTGAGAG 437  
DB 241 CAGGTCGGGATGATTCAGAGGAGAAAGGGGGAATGCTGAGGGAAGCTTTGAGAG 300  
QY 438 TCCTGGACACCACTACAGAGGCTGTATGAGATTCATTAATGAGCATAGATCTT 497  
DB 301 TCCTGGACACCACTACAGAGGCTGTATGAGATTCATTAATGAGCATAGATCTT 360  
QY 498 GGGAAATTTGCGGAGTGTACATTTACAAAGATGCTTCAAAATAGTCTTAAGATTTG 557  
DB 361 GGGAAATTTGCGGAGTGTACATTTACAAAGATGCTTCAAAATAGTCTTAAGATTTG 420  
QY 558 TTCAGTGCCTCACTTGGCTAAATATGAGAAATGATGCTGTCAGGCTTGATTTGACA 617  
DB 421 TTCAGTGCCTCACTTGGCTAAATATGAGAAATGATGCTGTCAGGCTTGATTTGACA 480  
QY 618 TTCATGAGCTGAATGTTACAGACCTCTTCCCATTTGAAGCTATTAATTTGACCA 677  
DB 481 TTCATGAGCTGAATGTTACAGACCTCTTCCCATTTGAAGCTATTAATTTGACCA 540  
QY 678 GGAAGCCTGAATGAATTAACAATTAATTAATTCATGCACTTCTCTGGAAGGACTT 737  
DB 541 GGAAGCCTGAATGAATTAACAATTAATTAATTCATGCACTTCTCTGGAAGGACTT 600  
QY 738 TGTGAAGGAATGCTGATTAAGATGATGATGTTGCTATCTGGGTTGGCACTTGTCAGAT 797  
DB 601 TGTGAAGGAATGCTGATTAAGATGATGATGTTGCTATCTGGGTTGGCACTTGTCAGAT 660  
QY 798 TACCCAAAAGAGAGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATG 857  
DB 661 TACCCAAAAGAGAGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATG 720  
QY 858 CTACCAAAATAA 869  
DB 721 CTACCAAAATAA 732

RESULT 8  
US-09-834-759-511  
; Sequence 511, Application US/09834759

;; Patent No. 6680197  
;; GENERAL INFORMATION:  
;; APPLICANT: Jiang, Yugui  
;; APPLICANT: Dillon, David C.  
;; APPLICANT: Mitcham, Jennifer L.  
;; APPLICANT: Xu, Jiangchun  
;; APPLICANT: Harlocker, Susan L.  
;; APPLICANT: Hepler, William T.  
;; APPLICANT: Henderson, Robert A.  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
;; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
;; FILE REFERENCE: 210121.470C9  
;; CURRENT APPLICATION NUMBER: US/09/834,759  
;; NUMBER OF SEQ ID NOS: 547  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 511  
;; LENGTH: 729  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-834-759-511

Query Match 58.0%; Score 729; DB 4; Length 729;  
Best Local Similarity 100.0%; Pred. No. 2.3e-164;

Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 ATGCGACCCGAGGCGCCGCGCTCCGCGAGCGGCTCCGCGCTCTGCTGCTCTG 197  
DB 1 ATGCGACCCGAGGCGCCGCGCTCCGCGAGCGGCTCCGCGCTCTGCTGCTCTG 60  
QY 198 CTGCTGCACTGCTCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 257  
DB 61 CTGCTGCACTGCTCCGCGCGCTGAGCGCTCTGAGATCCCAAGGGAAGCAAGGCG 120  
QY 258 CAGCTCCGCGAGGAGGCTGAGCTGTATTAAGAAATGCTTACAGGCGCAGCA 317  
DB 121 CAGCTCCGCGAGGAGGCTGAGCTGTATTAAGAAATGCTTACAGGCGCAGCA 180  
QY 318 GAGTGCCTGCTGAGACGCGAGCCCTGGGCGCAATGTTATTCGGGTACACTGGGATC 377  
DB 181 GAGTGCCTGCTGAGACGCGAGCCCTGGGCGCAATGTTATTCGGGTACACTGGGATC 240  
QY 378 CAGGTCGGGATGATTCAGAGGAGAAAGGGGGAATGCTGAGGGAAGCTTTGAGAG 437  
DB 241 CAGGTCGGGATGATTCAGAGGAGAAAGGGGGAATGCTGAGGGAAGCTTTGAGAG 300  
QY 438 TCCTGGACACCACTACAGAGGCTGTATGAGATTCATTAATGAGCATAGATCTT 497  
DB 301 TCCTGGACACCACTACAGAGGCTGTATGAGATTCATTAATGAGCATAGATCTT 360  
QY 498 GGGAAATTTGCGGAGTGTACATTTACAAAGATGCTTCAAAATAGTCTTAAGATTTG 557  
DB 361 GGGAAATTTGCGGAGTGTACATTTACAAAGATGCTTCAAAATAGTCTTAAGATTTG 420  
QY 558 TTCAGTGCCTCACTTGGCTAAATATGAGAAATGATGCTGTCAGGCTTGATTTGACA 617  
DB 421 TTCAGTGCCTCACTTGGCTAAATATGAGAAATGATGCTGTCAGGCTTGATTTGACA 480  
QY 618 TTCATGAGCTGAATGTTACAGACCTCTTCCCATTTGAAGCTATTAATTTGACCA 677  
DB 481 TTCATGAGCTGAATGTTACAGACCTCTTCCCATTTGAAGCTATTAATTTGACCA 540  
QY 678 GGAAGCCTGAATGAATTAACAATTAATTAATTCATGCACTTCTCTGGAAGGACTT 737  
DB 541 GGAAGCCTGAATGAATTAACAATTAATTAATTCATGCACTTCTCTGGAAGGACTT 600  
QY 738 TGTGAAGGAATGCTGATTAAGATGATGATGTTGCTATCTGGGTTGGCACTTGTCAGAT 797  
DB 601 TGTGAAGGAATGCTGATTAAGATGATGATGTTGCTATCTGGGTTGGCACTTGTCAGAT 660  
QY 798 TACCCAAAAGAGAGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATG 857  
DB 661 TACCCAAAAGAGAGCTTCTACTGATGATGATGATGATGATGATGATGATGATGATG 720











QY 816 TCTACTGATGGAATTCAGTTTCGCAATCATTAATGAAGAACTACCAAAATAATGCTT 875  
Db 383 TCTACTGATGGAATTCAGTTTCGCAATCATTAATGAAGAACTACCAAAATAATGCTT 324  
QY 876 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAATGCTTCACTTAATGACAT 935  
Db 323 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAATGCTTCACTTAATGACAT 264  
QY 936 TTTAAATAGATTATGATATGATCATGGAATGAAGAAAGCTAAATATGTTACAGACA 995  
Db 263 TTTAAATAGATTATGATATGATCATGGAATGAAGAAAGCTAAATATGTTACAGACA 204  
QY 996 AAGTGTGATTTCACTGTTTATTAATCAGCAATTAATGCTTCACTTAATGACAT 1055  
Db 203 AAGTGTGATTTCACTGTTTATTAATCAGCAATTAATGCTTCACTTAATGACAT 144  
QY 1056 GTTTCATATTTTATTTAGTGTGATGAATGATCTTCTCATAGTCACTTCTCAACT 1115  
Db 143 GTTTCATATTTTATTTAGTGTGATGAATGATCTTCTCATAGTCACTTCTCAACT 84  
QY 1116 ATAAATTTGGAATATGTTGCTGCTTTGTTTCTCTAGTATGATGATTTTAAAAA 1175  
Db 83 ATAAATTTGGAATATGTTGCTGCTTTGTTTCTCTAGTATGATGATTTTAAAAA 24  
QY 1176 ATATPAAAGCTACCAATCTTTGT 1198  
Db 23 ATATPAAAGCTACCAATCTTTGT 1

RESULT 17  
US-09-590-751A-63/C  
Sequence 63, Application US/09590751A  
Patent No. 6756477

GENERAL INFORMATION:  
APPLICANT: Yucui, Jiang  
APPLICANT: Dillon, Devin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
FILE REFERENCE: 210121.470C6  
CURRENT APPLICATION NUMBER: US/09/590,751A  
CURRENT FILING DATE: 2000-06-08  
NUMBER OF SEQ ID NOS: 479  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 63  
LENGTH: 683  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-590-751A-63

Query Match 54.2%; Score 681.8; DB 4; Length 683;  
Best Local Similarity 99.6%; Pred. No. 3.9e-153;  
Matches 680; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 516 ACATTTTCAAGAGATGCTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 575  
Db 683 ACATTTTCAAGAGATGCTTCAAAATAGTCTCTAAGAGTTTGTTCAGTGGCTCACTTGG 624  
QY 576 CTTAAATATGCAAGATGATGCTGTCAGCGTTGATTTTCAATTCATGAGAGCTGATGT 635  
Db 623 CTTAAATATGCAAGATGATGCTGTCAGCGTTGATTTTCAATTCATGAGAGCTGATGT 564  
QY 636 TCAGAGCTCTTCCCATTTGAGCTATATTTATTTGGACCAAGAAAGCCCTGAATGAT 695  
Db 563 TCAGAGCTCTTCCCATTTGAGCTATATTTATTTGGACCAAGAAAGCCCTGAATGAT 504  
QY 696 TCACAAATTAATATTCATGACATCTTCTGTGAAGACATTTGGAAGAAATGGTGT 755  
Db 503 TCACAAATTAATATTCATGACATCTTCTGTGTGAAGACATTTGGAAGAAATGGTGT 444

QY 756 GGATTAATGATGATGTTGCTATCTGGGTTGGACATTTGTCAGATTACCCAAAGAGATGCT 815  
Db 443 GGATTAATGATGATGTTGCTATCTGGGTTGGACATTTGTCAGATTACCCAAAGAGATGCT 364  
QY 816 TCTACTGATGGAATTCAGTTTCGCAATCATTAATGAAGAACTACCAAAATAATGCTT 875  
Db 383 TCTACTGATGGAATTCAGTTTCGCAATCATTAATGAAGAACTACCAAAATAATGCTT 324  
QY 876 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAATGCTTCACTTAATGACAT 935  
Db 323 TAAATTTCAATTTGCTACCTCTTTTATTAATGCTTGAATGCTTCACTTAATGACAT 264  
QY 936 TTTAAATAGATTATGATATGATCATGGAATGAAGAAAGCTAAATATGTTTACAGACA 995  
Db 263 TTTAAATAGATTATGATATGATCATGGAATGAAGAAAGCTAAATATGTTTACAGACA 204  
QY 996 AAGTGTGATTTCACTGTTTATTAATCAGCAATTAATGCTTCACTTAATGACAT 1055  
Db 203 AAGTGTGATTTCACTGTTTATTAATCAGCAATTAATGCTTCACTTAATGACAT 144  
QY 1056 GTTTCATATTTTATTTAGTGTGATGAATGATCTTCTCATAGTCACTTCTCAACT 1115  
Db 143 GTTTCATATTTTATTTAGTGTGATGAATGATCTTCTCATAGTCACTTCTCAACT 84  
QY 1116 ATAAATTTGGAATATGTTGCTGCTTTGTTTCTCTAGTATGATGATTTTAAAAA 1175  
Db 83 ATAAATTTGGAATATGTTGCTGCTTTGTTTCTCTAGTATGATGATTTTAAAAA 24  
QY 1176 ATATPAAAGCTACCAATCTTTGT 1198  
Db 23 ATATPAAAGCTACCAATCTTTGT 1

RESULT 18  
US-09-692-081-1  
Sequence 1, Application US/09692081  
Patent No. 6630325

GENERAL INFORMATION:  
APPLICANT: LINDNER, Volhard  
APPLICANT: FRIESEL, Robert F.  
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL  
FILE REFERENCE: 36-13 Lindner et al. (200036.0013)  
CURRENT APPLICATION NUMBER: US/09/692,081  
CURRENT FILING DATE: 2000-10-19  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1192  
TYPE: DNA  
ORGANISM: Rattus sp.  
US-09-692-081-1

Query Match 52.6%; Score 661.4; DB 4; Length 1192;  
Best Local Similarity 81.5%; Pred. No. 3.7e-148;  
Matches 844; Conservative 0; Mismatches 171; Indels 20; Gaps 6;

QY 55 GCGGCGGAGCGAGCGTGAACCAAGTTC-CTCTCTCGTCTCTCGGCTCGGCTCGAGCTC 113  
Db 13 GCAAGCTGCGGAGCGAGCGTGAACCAAGTTC-CTCTCTCGTCTCTCGGCTCGGCTCGAGCTC 72  
QY 114 GCGGCTGCGGAGCGGAGCGGAGCCAGTGAACCAAGGCGGCGGCTTCGCCGAGCGG 173  
Db 73 TGGCTTTCGAGCTACCGGAGCAGATGACACCCCAAGGCGGCGGCTTCGCCGAGCGG 132  
QY 174 CTCCGCGGCTC-----CTGCTCTCTGCTGCTGAGTGCCTGCGGCGGCTGAGCGCC 227  
Db 133 CTGCTGCGGCTCTCTCTGCTGCTGAGTGCCTGAGTGCCTGCGGCGGCTGAGCGCC 192  
QY 228 TCTGAGATCCCAAGGAGGAGCAAAAGGCGGAGCTCCGCGAGGAGGAGTGTGAGCTG 287  
Db 193 TCTGAGATCCCAAGGAGGAGCAAAAGGCGGAGCTCCGCGAGGAGGAGTGTGAGCTG 252  
QY 288 TATAATGGAATGTGCTTAAAGGCGGAGAGAGTGTCTGTGAGAGCGGAGCCCTGGG 347



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|||||
Db 253 TATAATGGATGTCCTACAGAGCAGAGGAGTTCTGTGTGCGATGGAGCCCTGGG 312
Qy 348 GCCAATGTTATTCCTGGGTACACCTGGGATCCAGGTGCGGATGGATTTCAAGAGAAAG 407
Db 313 GCCAATGGCAATTCCTGGCACACCGGGAATCCAGGTGCGGATGGATTTCAAGAGAGAA 372
Qy 408 GGGGAATGTCGTAGAGGAAAGCTTTGAGAGTCTCGGACCCCACTACAGAGAGTTC 467
Db 373 GGGGAATGTCGTAGAGGAAAGCTTTGAGAGTCTCGGACCCCACTACAGAGAGTTC 432
Qy 468 TGGAGTTCAATGATATTAATGATAGTCTGGGAAATTCGCGAGTGTACATTACAAAG 527
Db 433 TGGAGTTCAATGATATTAATGATAGTCTGGGAAATTCGCGAGTGTACATTACAAAG 492
Qy 528 ATGCGTTCAATGATAGTCTGTAGAGATTTGTTGTCAGTGGCTCACTTGGCTAAATGAG 587
Db 493 ATGCGATCCAAAGCGGCTCTTCAGAGTTCTGTGAGTGGCTCGCTCAATGACAG 552
Qy 588 AATGCAATGCTGAGGCTGTGATTTCAATTCATGAGTGTAGTTCAGGACCTCTT 647
Db 553 AATGCTGCTGTCACGCTGTGATTTTACCTTAATGAGTGTAGTTCAGGACCTCTT 612
Qy 648 CCCATTGAAGCTAATAATTTATTTGACCAAGAGCCCTGAATGATTCACAAATTAAT 707
Db 613 CCCATTGAAGCTAATCTATCTGACCAAGAGCCCTGAATTAATTAATTAAT 672
Qy 708 ATTCATCGCACTTCTTCTGTGAGAGACTTTGTAAGAAATGGTGTGATTAATGAG 767
Db 673 ATTCATCGCACTTCTTCTGTGAGAGACTTTGTAAGAAATGGTGTGATTAATGAG 732
Qy 768 GTTGCTATCGGGGTGGCACTTGTGAGATTCACCAAGAGAGATGCTTACTGATG 827
Db 733 GTTGCTATCGGGGTGGCACTTGTGAGATTCACCAAGAGAGATGCTTACTGATG 792
Qy 828 AATTCAGTTCTCGCATATTAATTTGAGAACTACCAAAATA-----ATGCTTAAT 879
Db 793 AATTCAGTTCTCGCATATTAATTTGAGAACTACCAAAATAAGCCCTGAGGTTCAAT 852
Qy 880 TTTCATTTGCTACCTCTTTTATTAATGCTTGAATGGTTCATTAATGACATTTTA 939
Db 853 TCCCTGCTCATTTATTTGTAATCAAGCTCTGATGGTTCATTTAATGACATTTTA 912
Qy 940 -AATAGTTTATGATACATGATG-AAAAGCAAGCTAAATATGTTAAGACCAA 997
Db 913 GAAGTCACTATGATGCTGACCAATGAAAGCAAGTTAATGCTTACAGACCAA 972
Qy 998 GTGTGATTTCACTGTTTAAATCTAGCATTAATTCATTTGCTTCAATCAAAAGTGT 1057
Db 973 GTGTGATTTCACTGTTTAAATCTAGCATTAATTCATTTGCTTCAATCAAAAGTGT 1029
Qy 1058 TTCAATATTTTTTTT 1072
Db 1030 TTCAGATTTTATTT 1044

RESULT 19
US-09-692-081-9
; Sequence 9, Application US/09692081
; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: FRIESEL, Robert P.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; CURRENT APPLICATION NUMBER: US/09/692,081
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 9
; LENGTH: 734
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:myc-tagged
; OTHER INFORMATION: REMODEL construct
US-09-692-081-9

Query Match 45.1%; Score 566.6; DB 4; Length 734;
Best Local Similarity 87.0%; Pred. No. 1.2e-125;
Matches 636; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

Qy 142 GACCCCAAGGCCCCCGCTTCCCGCAGCGGCTCCGGGCTCC-----TGTGCTTC 195
Db 4 GCCCCCAAGGCCCCCGCTTCCCGCAGCGGCTCCCGGCTCCCTTCTTGTGCTACATGC 63
Qy 196 TGTGCTGAGTGTGCGCGCGCGCTGAGAGCGCTCTGAGATGCCCAAGGGAGAGCAAAAG 255
Db 64 TGTGCTGAGTGTGCGCGCGCGCTGAGAGCGCTCTGAGATGCCCAAGGGAGAGCAAAAG 123
Qy 256 CCAGACTCCGCGAGAGAGAGTGTGACCTGTATATGATGATGCTTACAAAGGCGCAG 315
Db 124 CCCTGATCCGCGAGAGAGAGTGTGACCTGTATATGATGATGCTTACAAAGGCGCAG 183
Qy 316 CAGAGTGTGCTGTGAGAGCGGAGCGCTGGGCGCAATGTTATTCGGGTACACCTGGGA 375
Db 184 CAGAGTGTGCTGTGAGAGCGGAGCGCTGGGCGCAATGCTTGTGACACCGGCGGA 243
Qy 376 TCCCAAGTGGGATGATTCAAAGAGAGAAAGGGGGAATGTGAGGGGAAAGCTTTGAG 435
Db 244 TCCCAAGTGGGATGATTCAAAGAGAGAAAGGGGAGTGTCTTAAGGAAAGCTTTGAG 303
Qy 436 AGTCTGAGACCCCACTACAGAGAGTTCATGAGATTCATGATTAATGATAGATC 495
Db 304 AATCTGAGACCCCACTACAGAGAGTTCATGAGATTCATGATTAATGATAGATC 363
Qy 496 TTGGGAAATTCGGAAGTGTACATTTACAAAGATGCTTCAATATGCTCTTAAGATT 555
Db 364 TTGGGAAATTCGGAAGTGTACATTTACAAAGATGCTTCAATATGCTCTTAAGATT 423
Qy 556 TGTGAGTGGCTCACTTGGGCTAAATGAGAAATGATGCTGTGAGGTGTGATTTCA 615
Db 424 TGTGAGTGGCTCACTTGGGCTAAATGAGAAATGATGCTGTGAGGTGTGATTTCA 483
Qy 616 CATTCATGAGAGTATGTTGAGAGCTCTTCCATGAGAGCTTAATTTATTTGAGAC 675
Db 484 CTTTAATGAGAGTATGTTGAGAGCTCTTCCATGAGAGCTTAATTTATTTGAGAC 543
Qy 676 AAGGAAGCCCTGAATTAATCAATTAATTAATTCATGACCTTCTGTGAGAGAC 735
Db 544 AAGGAAGCCCTGAATTAATCAATTAATTAATTCATGACCTTCTGTGAGAGAC 603
Qy 736 TTTTGAAGAGATTTGTGTGATTAATGAGATGTTGATCTGGGTGGCACTTGTTCAG 795
Db 604 TGTGTAAGAGATTTGTGTGATTAATGAGATGTTGATCTGGGTGGCACTTGTTCAG 663
Qy 796 ATTACCAAAAGAGATGCTTCACTGATGATGATTCATGATTTCTGCAATTAATGAG 855
Db 664 ATTACCAAAAGAGATGCTTCACTGATGATGATTCATGATTTCTGCAATTAATGAG 723
Qy 856 AACTACCAAAA 866
Db 724 AACTACCAAAA 734

RESULT 20
US-09-692-081-6/c
; Sequence 6, Application US/09692081
; Patent No. 6630325
; GENERAL INFORMATION:
; APPLICANT: LINDNER, Volkhard
; APPLICANT: FRIESEL, Robert P.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
; CURRENT APPLICATION NUMBER: US/09/692,081
; CURRENT FILING DATE: 2000-10-19
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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 403
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE INFORMATION: Description of Artificial Sequence: REMODEL
; OTHER INFORMATION: antisense ribonucleoprobe
US-09-692-081-6

Query Match      26.2%; Score 329.4; DB 4; Length 403;
Best Local Similarity 88.6%; Pred. No. 3.3e-69;
Matches 357; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 425 AAGCTTGGAGAGCTCTGACACCCAACTACAGAGAGTGTTCAGAGTTCATTGAATTA 484
D 403 AAGCTTGGAGAGAGTCTGAGACCCCAACTACAGAGAGTGTTCAGAGTTCATTGAATTA 344
QY 485 TGGCATATGATCTGGGAAAATTGGCGAGTGTACATTTACAAAAGATGCGTTCAATAGTGC 544
D 343 TGGCATATGATCTGGGAAAATTGGCGAAATGTACATTTCAAAAAGATGCGATCCAAAGCGGC 284
QY 545 TCTAAGGTTTGTTCAGAGTGTCTCACTTCGGCTAAATGCAAGATGCTGTCAAGG 604
D 283 TCTTCGAGTTCGTTCAGAGTGTCTCGCTCGCTCAAGAGAGAAATGCTGTGTCAAGG 224
QY 605 TTGGTATTTCAATTCATTAAGAGTGAATGTTCAGAGAGCTCTTCCCATTTGAAGTAAAT 664
D 223 CTGGATATTTTACCTTTAATGAGCTGAATGTTCAGAGAGCTCTTCCCATTTGAAGTAAAT 164
QY 665 TTATTTGACCAAGAGAGAGCCCTGAAATGATTTCAACAAATTAATTCATGCACTTTCTTC 724
D 163 CTATCTGACCAAGAGAGAGCCCTGAGTAAATTCATTAATTCATTCGTACTTCCTC 104
QY 725 TGTGAAGAGCTTGTGTGAAGAAATGTGTGCTGATTAAGTATGTGATCTGAGTGG 784
D 103 CGTGAAGAGAGCTCTGTGAAGAGATTTGTGCTGAGCTGAGAGCGTGGCATCTGGTGG 44
QY 785 CACTTGTTCAGATTAACCCAAAGAGAGATGCTTCTACTGAGATG 827
D 43 CACTTGTTCAGATTAACCCAAAGAGAGAGCTTCTACTGAGATG 1

RESULT 21
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.c., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

Query Match      5.5%; Score 68.8; DB 4; Length 1141;
Best Local Similarity 12.5%; Pred. No. 7.4e-07;
Matches 121; Conservative 353; Mismatches 483; Indels 8; Gaps 3;

QY 291 AATGGAATGCTTACAAAGGCGACAGAGAGTGGCTGTGACAGAGGAGCCCTGGGCGC 350
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D 77 RWMKGMWKKKMYBCCANNSTBRHYHARWKMXTAYBMTITNWKMGKTRHRYHWRBAMBDT 136
QY 351 AATGTTATTCGGGGTACACCTGGAGATCCCAAGTGGGATGATTCACAGAGAGAAAGGG 410
D 137 VDHNYVTAMNNATWTCMMDKDDRTYRMMKNNATGGDDTKYHWMNNNGBTYVWV 196
QY 411 GAATGCTGAGGAAAGCTTTGAGAGTCTGACACCCAACTACAGAGAGTTCATG 470
D 197 RYKTDKMSBKRMVYGBMWKMSYDVTYVWVWDMDCKRKYRWRVTRBMRNMYV--- 253
QY 471 AGTTCATTGAATTTATGCGATGATCTTGGGAAAATTCGCGAGTGTACATTACAAAGATG 530
D 254 --AMDTAHRRRYNNQWMBAMAYRRYTMNNNNNAKAKCKAKYGMWRABVNSTCTTWS 311
QY 531 CGTTCAATATAGTCTTACAGATTTTGTCAAGTGGCTCACTGGGCTAAATACAGAAAT 590
D 312 KTTKVRTSCMANNCBAGDANKDHHKMKMSAMGYNNNNNNNNWYTKAABBARMDVWH 371
QY 591 GCATGCTGTGACGCTGTGATTTTCAATTCATGAGCTGAATGTTTCAGAGACCTCTCC 650
D 372 SAMKMHANNAHYBRKMTBYKRTYNNNNNGTTMREMMAMWYKMDMBGTYNNNNG 431
QY 651 AATGAAGTATATTTATTTGACACCAAGAGAGCCCTGAAATGAATTCACAAATTAAT 710
D 432 GRITYGWTKNKMWYTKMKANNCKMRAMDHKTCTHNNNTYMKYKTYNNCYKMSMTNGK 491
QY 711 CATGCACTTCTCGTGGAGAGAGCTTGTGAAGAAATGTGTGCTGATTAAGATGTT 770
D 492 SHRBAAYVYTYMMWRHYHANNNNNDYMKACTTKYIVCSKMMNNYIAMYTKSSWN 551
QY 771 GCTATCTGGGTTGACCTGTTCAGATTAACCAAGAGAGATCTTCTACTGATGAAT 830
D 552 TSYRYRWKTNNSWFRSDTBSMRANNYARABHYGYMTRMBMSHTMBHBA--GAHY 610
QY 831 TCAGTTCTGCGATCATTTATTTGAAGAACTACCAAAATTAATGCTTTAATTTCAATTTGCT 890
D 611 WMBWYBAKCHCMRAWYKAKYKAGAGSNNNNNNNNNNNNNNNNNNATCARDDYAAARWYA 670
QY 891 ACCTCTTTTATATGACCTTGAATGTTCACTTAATGACATTTTAATAAGTTTAT 950
D 671 MANAKYIYKBAANNA--YTHANNWGCNNNATDTRRTYKNNNNNNAGTWMKNNNNNA 728
QY 951 GTATPACATCTGATGAAGAGAGAGCTAAATATGTTTACAGACCAAGTGTGATTCACA 1010
D 729 KNAASAANKYVAAAAYKAKKMRWANKWAMRGWADAAABTTDKRNNGAYKYTTNNNNNT 788
QY 1011 CTGTTTAAATCTAGCATATTTCTTTGCTTCATCAAAAGTGTTCATATATTTT 1070
D 789 YRGVVTATAADGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 848
QY 1071 TTAGTGTGATGATTAATCTTCTCATATGACATCTCTCAACCTTAATTTGAATATT 1130
D 849 WTNKMYTTTDRMBATTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 908
QY 1131 GTTGTGCTCTTTGTTTCTCTTACATAGATTTTAAAAAATATAAAGCTACGA 1190
D 909 YNRGTARNTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 968
QY 1191 ATCTTGTACAAATTTGTAATGTTAAGATTTTATATCTGTAAATATAAATTAAT 1250
D 969 TTKRYKNNCTWYMTTTRTYWAAATRMKTNATGSMTRCNATGKNNNNYVWGTBWT 1028
QY 1251 TCCAA 1255
D 1029 AYRWA 1033

RESULT 22
US-09-641-638-651
; Sequence 651, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
```

```

APPLICANT: Blumenfeld, Marta
APPLICANT: Bouguetelret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
PRIORITY FILING DATE: 2000-08-16
PRIORITY APPLICATION NUMBER: US 09/502,330
PRIORITY FILING DATE: 2000-02-11
PRIORITY APPLICATION NUMBER: US 60/133,200
PRIORITY FILING DATE: 1999-05-07
PRIORITY APPLICATION NUMBER: US 09/275,267
PRIORITY FILING DATE: 1998-03-23
PRIORITY APPLICATION NUMBER: US 60/119,917
PRIORITY FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 651
LENGTH: 20674
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 3124..3297
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 3871..4072
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 5758..5880
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 5996..6099
OTHER INFORMATION: exon 5
NAME/KEY: exon
LOCATION: 6349..6509
OTHER INFORMATION: exon 6
NAME/KEY: exon
LOCATION: 7379..7522
OTHER INFORMATION: exon 7
NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
NAME/KEY: exon
LOCATION: 12254..12340
OTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12854..13023
OTHER INFORMATION: exon 10
NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele

LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTTT
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2844
OTHER INFORMATION: 10-513-262 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2934
OTHER INFORMATION: 10-513-352 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 : deletion of C
NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 12-206-366 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6338
OTHER INFORMATION: 10-347-74 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6429
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OTHER INFORMATION: 10-347-165 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6467
OTHER INFORMATION: 10-347-203 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6534
OTHER INFORMATION: 10-347-271 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 6611
OTHER INFORMATION: 10-347-348 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 10-348-391 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 8658
OTHER INFORMATION: 10-349-97 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 8777
OTHER INFORMATION: 10-349-216 : deletion of CTG
NAME/KEY: allele
LOCATION: 8785
OTHER INFORMATION: 10-349-224 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 8926
OTHER INFORMATION: 10-349-368 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12171
OTHER INFORMATION: 10-350-72 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12429
OTHER INFORMATION: 10-350-332 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 13341
OTHER INFORMATION: 10-507-170 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 13492
OTHER INFORMATION: 10-507-321 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 13524
OTHER INFORMATION: 10-507-353 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 13535

Query Match 4.5% Score 56.8; DB 4; Length 20674;
Best Local Similarity 46.3%; Pred. No. 0.0021;
Matches 187; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 845 CATTATTGAGACTACCAATAATAATGCTTAATTTTCATTGCTACCTTTTAT 904
DB 11062 CTTTATTTTAAAGCTAAGAAATATTTAATTTAATTTAATTTAATTTA 11121
QY 905 TATGCCCTTGAATGCTTCACTTAATGACATTTTAAAGTTATGATACATCTGAT 964
DB 11122 TATTTAAATTTAAATTTTAAATTTAATTTAATTTAATTTAATTTAATTT 11181
QY 965 GAAAGCAAGCTAAATATGTTTACAGACAAAGTGATTTCACTGTTTAAATCT 1024
DB 11182 AAAATTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 11241
QY 1025 AGCATTAATCTTTTCTTCAATCAAAAGGTTTCAATTTTATTTAGTTGTTAGA 1084
DB 11242 TTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 11301
QY 1085 TACTTTCTTCATACATCTCTCAACCTAATAATTTGGAATATTTGTTGCTTTTG 1144
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DB 11302 TAATTTACTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 11361
QY 1145 TTTTCTCTTACGATACATTTTAAATAAATGTAAGCTCAATCTTTGCAAT 1204
DB 11362 TATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 11421
QY 1205 TGTAATGTTAGAAATTTTATATCTGTTAATAAATTA 1248
DB 11422 AATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 11465

RESULT 23
US-10-170-097-651
Sequence 651, Application US/10170097
Patent No. 6794143
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bouguetelerc, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIOMARKERS DERIVED FROM GENOMIC REGIONS CARRYING
FILE REFERENCE: GEN-T114XC2D1
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/10/170,097
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 651
LENGTH: 20674
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory region
FEATURE:
NAME/KEY: exon
LOCATION: 3124..3297
OTHER INFORMATION: exon 1
FEATURE:
NAME/KEY: exon
LOCATION: 3871..4072
OTHER INFORMATION: exon 2
FEATURE:
NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon 3
FEATURE:
NAME/KEY: exon
LOCATION: 5758..5880
OTHER INFORMATION: exon 4
FEATURE:
NAME/KEY: exon
LOCATION: 5966..6099
OTHER INFORMATION: exon 5
FEATURE:
NAME/KEY: exon
LOCATION: 6349..6509
OTHER INFORMATION: exon 6
FEATURE:
NAME/KEY: exon
LOCATION: 7379..7522
```

OTHER INFORMATION: exon 7  
FEATURE:  
NAME/KEY: exon  
LOCATION: 8645..8854  
OTHER INFORMATION: exon 8  
FEATURE:  
NAME/KEY: exon  
LOCATION: 12254..12340  
OTHER INFORMATION: exon 9  
FEATURE:  
NAME/KEY: exon  
LOCATION: 12854..13023  
OTHER INFORMATION: exon 10  
FEATURE:  
NAME/KEY: exon  
LOCATION: 13308..13429  
OTHER INFORMATION: exon 11  
FEATURE:  
NAME/KEY: exon  
LOCATION: 16775..16945  
OTHER INFORMATION: exon 12  
FEATURE:  
NAME/KEY: exon  
LOCATION: 16775..16945  
OTHER INFORMATION: exon 13  
FEATURE:  
NAME/KEY: exon  
LOCATION: 17063..17554  
OTHER INFORMATION: exon 14  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 17555..20674  
OTHER INFORMATION: 3'regulatory region  
FEATURE:  
NAME/KEY: allele  
LOCATION: 1128  
OTHER INFORMATION: 10-508-191 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 1182  
OTHER INFORMATION: 10-508-245 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 1559  
OTHER INFORMATION: 10-509-284 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 1570  
OTHER INFORMATION: 10-509-295 : deletion of C  
FEATURE:  
NAME/KEY: allele  
LOCATION: 1827  
OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTT  
FEATURE:  
NAME/KEY: allele  
LOCATION: 2048  
OTHER INFORMATION: 10-511-62 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 2323  
OTHER INFORMATION: 10-511-337 : insertion of T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 2341  
OTHER INFORMATION: 10-512-36 : polymorphic base G or C  
FEATURE:  
NAME/KEY: allele  
LOCATION: 2623  
OTHER INFORMATION: 10-512-318 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 2832  
OTHER INFORMATION: 10-513-250 : polymorphic base A or G

FEATURE:  
NAME/KEY: allele  
LOCATION: 2844  
OTHER INFORMATION: 10-513-262 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 2934  
OTHER INFORMATION: 10-513-352 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 2947  
OTHER INFORMATION: 10-513-365 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 3802  
OTHER INFORMATION: 12-206-81 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 4062  
OTHER INFORMATION: 10-343-231 : deletion of C  
FEATURE:  
NAME/KEY: allele  
LOCATION: 4088  
OTHER INFORMATION: 12-206-366 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 4109  
OTHER INFORMATION: 10-343-278 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 4170  
OTHER INFORMATION: 10-343-339 : polymorphic base G or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 5903  
OTHER INFORMATION: 10-346-23 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 6019  
OTHER INFORMATION: 10-346-141 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 6141  
OTHER INFORMATION: 10-346-263 : polymorphic base G or C  
FEATURE:  
NAME/KEY: allele  
LOCATION: 6183  
OTHER INFORMATION: 10-346-305 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 6338  
OTHER INFORMATION: 10-347-74 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 6375  
OTHER INFORMATION: 10-347-111 : polymorphic base G or C  
FEATURE:  
NAME/KEY: allele  
LOCATION: 6429  
OTHER INFORMATION: 10-347-165 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 6467  
OTHER INFORMATION: 10-347-203 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 6484  
OTHER INFORMATION: 10-347-220 : polymorphic base A or G

Query Match 4.5%; Score 56.8; DB 4; Length 20674;  
Best Local Similarity 46.3%; Pred. No. 0.0021;  
Matches 187; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 845 CATTATTGAAGACTACCAAAATTAATGCTTAATTTTCATTTGCTACCTCTTTTAT 904  
| | | | |  
Db 11062 CTTTATTAAATGATAGAAATAATTTAATATTTTAAATTAATTAATTTTAA 11121  
| | | | |  
QY 905 TATGCTTGGAATGTTCACTTAATGACATTTTAATAGTTATGTAATCACTGAAT 964  
| | | | |  
Db 11122 TATTAAATTAATTAATTTAATTTAATTAATTAATTTAATTTAATTAAT 11181  
| | | | |  
QY 965 GAAAGCAAGCTAATATGTTTACAGCAAGTGATGATTTACAGCTGTTTAAATCT 1024  
| | | | |  
Db 11182 AAAATTTAAATTAATTTAATTTAATTTAATTTAATTTAATTAATTTAATTT 11241  
| | | | |  
QY 1025 AGCATTAATCAATTTGCTTCAATCAAAAGTGCTTCAATATTTTAAAGTTAGTA 1084  
| | | | |  
Db 11242 TTAATTTAAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 11301  
| | | | |  
QY 1085 TACTTTCTCAATGACATTTCTCAACCTAATTTGGAATTTGTTGCTTTTG 1144  
| | | | |  
Db 11302 TAAATTTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 11361  
| | | | |  
QY 1145 TTTTCTCTTATAGTATGATTTTAAATTAATTAATTAATTAATTTGTAATTT 1204  
| | | | |  
Db 11362 TATTAAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTGCTTC 11421  
| | | | |  
QY 1205 TGTAAAGTTAAAGAAATTTTATTAATCTGTTAAATTAATTAATTAATTA 1248  
| | | | |  
Db 11422 AATTAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 11465  
| | | | |

RESULT 24  
US-09-370-838-153/c  
; Sequence 153, Application US/09370838  
; Patent No. 6444425  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Monamath, Raodon  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  
; FILE REFERENCE: 210121.475C1  
; CURRENT APPLICATION NUMBER: US/09/370,838  
; CURRENT FILING DATE: 1999-08-09  
; EARLIER FILING DATE: 1999-04-02  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 153  
; LENGTH: 2109  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-370-838-153

Query Match 4.4%; Score 55.2; DB 4; Length 2109;  
Best Local Similarity 51.2%; Pred. No. 0.0017;  
Matches 129; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 6 GAGGCGCGGGGTGAAGGCGCATGATGACAGCTGCGGCGGCGCTCGAGCGGCGGAG 65  
| | | | |  
Db 1140 GAGCGGACCGGGGCTGCTCGGCGCTCCGCGGCGCGCGCGCGCGCGCGCG 1081  
| | | | |  
QY 66 CCAAGCGCTGACCAAGTCTCTCTCTCGGTCCTCGGCTTCAGCTCGGCGCTCCGCG 125  
| | | | |  
Db 1080 CGCGCGCGCT 1021  
| | | | |  
QY 126 CAGCGCGGAGCGCATGCGACCCCGAGGCGCGCGCGCTCCCGCGAGCGGCTCGGCGCTC 185  
| | | | |  
Db 1020 CGGCGCGCGCGCTCCGCGCGCGCGCGCTCCCGCGAGCGCGCGCGCGCGCTC 961  
| | | | |  
QY 186 CTGCTGCTCTGCTGCTCAGAGTGCAGCGCGCGCTCGAGCGGCTCTGAATGCCCAAGGGG 245  
| | | | |  
Db 960 CCAAGCGGCG 901  
| | | | |

QY 246 AAGCAAAAGCGG 257  
| | | | |  
Db 900 CAGCGAGAGCGG 889  
| | | | |

RESULT 25  
US-09-854-133-153/c  
; Sequence 153, Application US/09854133  
; Patent No. 6759508  
; GENERAL INFORMATION:  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Monamath, Raodon  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 210121.475C10  
; CURRENT APPLICATION NUMBER: US/09/854,133  
; CURRENT FILING DATE: 2001-05-11  
; NUMBER OF SEQ ID NOS: 735  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 153  
; LENGTH: 2109  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-854-133-153

Query Match 4.4%; Score 55.2; DB 4; Length 2109;  
Best Local Similarity 51.2%; Pred. No. 0.0017;  
Matches 129; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 6 GAGGCGCGGGGTGAAGGCGCATGATGACAGCTGCGGCGGCGCTCGAGCGGCGGAG 65  
| | | | |  
Db 1140 GAGCGGACCGGGGCTGCTCGGCGCTCCGCGGCGCGCGCGCGCGCGCGCG 1081  
| | | | |  
QY 66 CCAAGCGCTGACCAAGTCTCTCTCTCGGTCCTCTCGGCTTCAGCTCGGCGCTCCGCG 125  
| | | | |  
Db 1080 CGCGCGCGCT 1021  
| | | | |  
QY 126 CAGCGCGGAGCGCATGCGACCCCGAGGCGCGCGCGCTCCCGCGAGCGGCTCGGCGCTC 185  
| | | | |  
Db 1020 CGGCGCGCGCGCTCCGCGCGCGCGCGCTCCCGCGAGCGCGCGCGCGCGCTC 961  
| | | | |  
QY 186 CTGCTGCTCTGCTGCTCAGAGTGCAGCGCGCGCTCGAGCGGCTCTGAATGCCCAAGGGG 245  
| | | | |  
Db 960 CCAAGCGGCG 901  
| | | | |  
QY 246 AAGCAAAAGCGG 257  
| | | | |  
Db 900 CAGCGAGAGCGG 889  
| | | | |

RESULT 26  
US-08-817-926-27  
; Sequence 27, Application US/08817926  
; Patent No. 6001590  
; GENERAL INFORMATION:  
; APPLICANT: Komeda, Toshinhiro  
; APPLICANT: Suda, Hisako  
; APPLICANT: Tamai, Yukio  
; APPLICANT: Iwamatsu, Akihiro  
; APPLICANT: Kato, No. 6001590uo  
; APPLICANT: Sakai, Yasuyoshi  
; TITLE OF INVENTION: PROMOTER/TERMINATOR FOR CANDIDA BOIDINI  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA

ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,926  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/02597  
FILING DATE: 12-SEP-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 234133/1995  
FILING DATE: 12-SEP-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 42536/1996  
FILING DATE: 29-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 081356/0112  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4818 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Candida boldinii  
US-08-817-926-27

Query Match 4.4%; Score 55; DB 3; Length 4818;

Best Local Similarity 45.5%; Pred. No. 0.0029; Mismatches 235; Indels 0; Gaps 0;

Matches 196; Conservative 0; Mismatches 235; Indels 0; Gaps 0;

QY 821 TGGATGGAATTCAGTTCTCGATCATTTATGGAAGACCAAAATTAATGCTTAAT 880  
DB 4077 TTGTTAATTTCTCATTAATTTATTTCTTAGATTTTAAATAATTTCTCTTTT 4136  
QY 881 TTCAATTTGCTACCTCTTTTATTAATGCTTGAATGTTCACTTAATGACATTTTA 940  
DB 4137 TTATTTTCTTCTTTCTTTCAATTTAAATGATGATGAAGAATTAATATATATA 4196  
QY 941 ATTAATTTATGATACATCTGAATGAAGCAAGCAATTAATGTTTACAGACCAAGTG 1000  
DB 4197 TTATTTTATTAATTAATTAAGTCAAGCGTTTAAAGAAAGTATTAATTAACATC 4256  
QY 1001 TGAATTCACAGCTGTTTAAATCTAGCATTAATCTTTGCTTCATCAAAAGTGTTTC 1060  
DB 4257 TTCTGAGTAAATAGTAATACAGATTTAATACCTTTTTCCTCAATTTTTC 4316  
QY 1061 AATATTTTATTAATGTTAGTAATCTTCTTCATAGTACATCTCTCAACCTTAAT 1120  
DB 4317 AATATTTATTAATTTGATTTGTTAATTAATGTAATTAAGAAATTAATTTCTGT 4376  
QY 1121 TTGGAATATTTGTTGAGTCTTTTCTTTCTTTGATAGATTTTAAAAAATAA 1180  
DB 4377 TTCTTTGTTGTTTATCTGTTTAAATTTTCTTTGATCAATCTTAAATTTAGTTT 4436  
QY 1181 AAGATCAACATCTTGTGCAATTTGAAATGTAAGATTTTAAATCTGTAAT 1240  
DB 4437 AATTTTATTAATTAATCTAATTTTAATTAATTAATTTGTTGAATTAATTTAATTA 4496  
QY 1241 AAAAAATTAATTT 1251  
DB 4497 ATTTCTAATTT 4507

RESULT 27

US-08-487-826B-13/C

Sequence 13, Application US/08487826B

Patent No. 5993827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan

APPLICANT: Miller, Louis H.

APPLICANT: Peterson, David S.

APPLICANT: Su, Xin-zhaun

APPLICANT: Wellens, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe Martens Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: California

COUNTRY: US

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,826B

FILING DATE: 10-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Israelisen, Ned

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH121.001CP1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 19124 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-487-826B-13

Query Match 4.3%; Score 54.2; DB 2; Length 19124;

Best Local Similarity 46.5%; Pred. No. 0.0085; Mismatches 238; Indels 2; Gaps 1;

Matches 209; Conservative 0; Mismatches 238; Indels 2; Gaps 1;

QY 788 TTGTTCAATTCACCAAGAGATGCTCTAGGAGGAATTCAGTTCTCGATCAT 847  
DB 15954 TTTTATTTTATTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 15895  
QY 848 TATTAAGACACTACCAATAATGCTTAATTTTCAATTTGCTACCTTTTATTAAT 907  
DB 15894 TTTTATTTTATTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 15835  
QY 908 GCCTTGAATGTTCACTTAATGACATTTTAAATGATTAATGATATGATGAA 967  
DB 15834 TTATTAATTTTATTTTATTAATTAATTTTATTTTATTTTATTTTATTTTATTTT 15777  
QY 968 AAGCAAGCTTAATTAATGTTTACAGCAAGGTGATTTTCACTGTTTAAATCTAGC 1027  
DB 15776 AACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 15717  
QY 1028 ATTAATTCATTTGCTTCATCAAAAGTGTTCATATTTTATTTTATTTTATTTTATTT 1087  
DB 15716 CTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTCTTCT 15657





US-10-204-708-2  
; Sequence 2, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; TITLE OF INVENTION: by Assessing DNA Methylation  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/204,708  
; CURRENT FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 2  
; LENGTH: 10467  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; US-10-204-708-2

Query Match  
Best Local Similarity 48.0%; Score 52.2; DB 4; Length 10467;  
Matches 182; Conservative 0; Mismatches 193; Indels 4; Gaps 1;

Qy 875 TTAATTTGATTTGCTACCTCTTTTATATGCTTGAAGTCTCACTTAATGACA 934  
Db 2464 TTTTGGATTTTATAGAGTGTGTTAGTTTATTTGTTGTTATTTGTTATG 2523

Qy 935 TTTTAAATAGTTTATGATATCATCTGATGAAAGCAAGCAATATGTTACAGACC 994  
Db 2524 TTTTAAATGCTTTTATTTTATGTTTATGTTTATTTATTTATTTGTTATG 2583

Qy 995 AAGTGATTTGACACTGTTTAAATCTAGACATTA---TTCATTTGCTCAATCA 1050  
Db 2584 GGTTTTAAATTTTATTTTATTTATGTTAATTTAGGTGATATTTTATTTAGT 2643

Qy 1051 AAGTGATTTCAATTTTATTTTATGTTAGTTAGATCTTTCTCATAGTCAATCTCTC 1110  
Db 2644 TATTTATTTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAG 2703

Qy 1111 AACCTAATTTGGAATATTTGTTGCTTTTCTTTTCTTTAGTATAGATTTTAA 1170  
Db 2704 GATTTTGAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 2763

Qy 1171 AAAAATATTAAGCTACCAATCTTTGATCAATTTGAAATGTTAAGATTTTATTA 1230  
Db 2764 TAGTATTTGTTAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 2823

Qy 1231 TCTGTTAAATTTAAATTTAT 1249  
Db 2824 TAGGTATATATATTTATTTGT 2842

RESULT 31  
US-09-056-075-1/c  
; Sequence 1, Application US/09056075  
; Patent No. 5955368  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Eric A.  
; APPLICANT: Bradshaw, Marilee  
; APPLICANT: Rood, Julian  
; TITLE OF INVENTION: Expression System for Clostridium

; TITLE OF INVENTION: Species  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056,075  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seay, Nicholas J.  
; REGISTRATION NUMBER: 27386  
; REFERENCE/DOCKET NUMBER: 960296.95238  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608-251-9166  
; TELEFAX: 608-251-9166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6243 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 3770..4013  
; OTHER INFORMATION: /note="RP4 origin of DNA transfer (orit)" from  
; OTHER INFORMATION: plasmid RP4"  
; US-09-056-075-1

Query Match  
Best Local Similarity 45.7%; Score 52.1; DB 2; Length 6243;  
Matches 181; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

Qy 850 TTGAAGAACTACCAAAATTAAGCTTATTTCAATTTGCTACCTTTTATTTATG 909  
Db 1488 TTATTAAGCTCATTTTATTTATTTCTTTCTTCAAGTTATATATATATTA 1429

Qy 910 CTGGAATGCTTCACTTAATGACATTTTAAATTAAGTTATGATATACATCTGA 969  
Db 1428 TTTTCAACTTTAATTAATTAATTTTATTTTATTTTATTTTATTTTATTT 1369

Qy 970 GCAAGCTAATATATGTTTACAGACCAAGCTGATTTACACTGTTTAAATCT 1029  
Db 1368 TTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1309

Qy 1030 TATTCATTTTGTCTCAATCAAAAGCTTCAATTTTATTTTATTTTATTTT 1089  
Db 1308 TTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1249

Qy 1090 TCTTCATGTCACATTTCTCAACCTAATATTTGGAATTTGTTGCTTTTGT 1149  
Db 1248 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1189

Qy 1150 TCTCTTAGTATAGCATTTTAAATAAATAAAGCTACCAATCTTTGATATTT 1209  
Db 1188 CCTCATTTTATTAAGCTGTATATTAAGGTATCTTGATCTGTTTATTTTGG 1129

Qy 1210 AGCTTAAAGATTTTATTTATCTGTTAATTAATAA 1245  
Db 1128 TTGTAAAGATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1093

RESULT 32

US-10-204-708-24/c  
; Sequence 24, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLER, Alexander  
; APPLICANT: PIEPERROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/204,708  
; PRIOR FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 24  
; LENGTH: 11049  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-24

Query Match 4.1%; Score 51.6; DB 4; Length 11049;  
Best Local Similarity 49.6%; Pred. No. 0.027;  
Matches 132; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 815 TTCTACGATGAGTGAATTCAGTTCTCGCATCTATTGAGACACCAATAATGCT 874  
DB 1427 TACACCTATATATATCTATCTCTAAATTAATCTTAATTTACTTAACAAATCAT 1368  
QY 875 TTAATTTTCATTTGCTACCTCTTTTATTTATGCTTGAATGCTTCACTTAATGACA 934  
DB 1367 ATACCTTTAATTTAATAATATTTACTTAATTTCCCTACAAAACTTTACTTAATTTATA 1308  
QY 935 TTTTAATTAAGTTTATGATATACATCTGAATGAAAGCAAGCTAATATGTTTACAGACC 994  
DB 1307 TTCTCAACACACATATATATAAAAAAATCTCTCTTATCTATATTAATTTATCTATTC 1248  
QY 995 AAAGTGAATTTCAACAGTCTTTTAAATCTAGCATTTATTTGCTTCAATCAAAAGT 1054  
DB 1247 AAACCTTAATTTCTTACTAACCCTAATTAATAAAAAATTAATTTACTATATTAATAAT 1188  
QY 1055 GGTTTCATATTTTCTTTTATGTTGTT 1080  
DB 1187 TTTTCTTTTATTTTCTTTTCTTTTCTTTT 1162

RESULT 33  
US-09-806-708B-23  
; Sequence 23, Application US/09806708B  
; Patent No. 6784342  
; GENERAL INFORMATION:  
; APPLICANT: The University of British Columbia  
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants  
; FILE REFERENCE: 4810-58741  
; CURRENT APPLICATION NUMBER: US/09/806,708B  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/147,133  
; PRIOR FILING DATE: 1999-08-04  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 1055  
; TYPE: DNA

ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(1055)  
; OTHER INFORMATION: consensus sequence of A.T. and L.A. PAB1 promoters  
US-09-806-708B-23

Query Match 4.1%; Score 51; DB 4; Length 1055;  
Best Local Similarity 22.8%; Pred. No. 0.013;  
Matches 100; Conservative 127; Mismatches 206; Indels 5; Gaps 2;

QY 816 TCTACTGATGAGTGAATTCAGTTCTCGCATCTATTGAGACCAATAATGCTT 875  
DB 42 TGKRCYARBMGMMTAYVMTATKGTGMAMRTWRMAMKKTIRMCMSTAMNNATMCT 101  
QY 876 TTAATTTTCATTTGCTACCTCTTTTATTTATGCTTGAATGCTTCACTTAATGACAT 935  
DB 102 AKKWTGTMMWTKNNNATGTRMMTGYMMTNNCSTMTABRRYKTRMMCYTAMMYGAS 161  
QY 936 TTTAATTAAGTTTATGATATACATCTGAATGAAAGCAAGCTAATATGTTTACAGCCA 995  
DB 162 MAGNASTRTTYTTRMKMKCKRSARARATRGARAYRATTAATTAATGTTKAMATTAAT 221  
QY 996 AAGTGTGATTTCAACAGTCTTTTAAATCTAGCATTTATTTGCTTCAATCAAAAGTG 1055  
DB 222 MNNNNNNNAK---ACKRATTGWRKSNCTCTAGGTTTKRATCGAATCGAMATKKW 277  
QY 1056 GTTTCATATTTTCTTTTATGTTGTTAGTAATACTTTCTCATAGCATCTCTCAACT 1115  
DB 278 KTWKTSAAKMTMNNNNNNNNNTTTKA-AMVAAAAMWMSATTTWMAAMSRKTMTYYGR 336  
QY 1116 ATAATTTGAATATGTTGCTTTGTTTCTTTCTTATGATATGATTTTAAATAA 1175  
DB 337 KTAAMNNNGTTCWTRMAMWTKMMKTKGTTTMMNNNGRITYGTWKATTTTAANN 396  
QY 1176 ATATTAAGCTACCAATCTTTGTAACAATTTGTAATGTAAGATTTTATTAATCTGT 1235  
DB 397 TTAAMKWTCTMNNNTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 456  
QY 1236 TAAATTAATAATTTATTTCC 1253  
DB 457 NNTTWTACCTWTTTKC 474

RESULT 34  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOXP2 VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:



```
QY      830 TTCAAGTTCTGCGCATCATTAATGAAGAACTACCAAAATAAGCTTAATTTTCATTGTC 889
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1122 KKAANNNNNNNGMDNMMDATKMSATGTAMWTHAKAGATMCWYWTGTNRRCMKT 1063
QY      890 TACCTCTTTTATTAATGACCTTGGATGGTTCACCTAAATGACATTTTAAATGAAGTTTA 949
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1062 YAMRTWYRSNANMSCATKBMWTKWYATKYRTMYAMWCAMRNMMCATNGYAKSCA 1003
QY      950 TGTATACATCTGAAGAAGAAAGCTAAATATGTTTACAGACCAAGAGTGATTCAC 1009
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1002 TNNAMWYATTAATAAATAAKMAMAGNNMMYGAAGANKGCMAAATMGBMWADTAGKNC 943
QY      1010 ACTGTTTAAATCTAGACATTAATTCATTTGCTTCATCAATAAGTGTTCAATATTTT 1069
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      942 NNNNNNNWTTDVRBMAMKAKNNNNNNAWYACYNBAATNNKATTHMKWTHGHSKRRIH 883
QY      1070 TTTAGTTGGTGAATACCTTTCTTCAATGTCACATTCCTCAACCTATTAATTTGAAGAT 1129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      882 HTRTCRTKRYNNNNNNNARTVYVYHHAARRMNAWYRTNNNNNNNNNNNACRTWRTWMAW 823
QY      1130 TGTGTGTGCTTTTGTCTTCTTCTAGATAGCATTTTAAATAAATAAGCTACC 1189
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      822 KHSNCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 763
QY      1190 AATCTTTGATCAATTTGTAATGTTAAGATTTTATATCTGTTAAATAAATTTAT 1249
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      762 TDMCYKTMWMTWYMDMTTMBTTRNNMTSTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 703
QY      1250 TTCCAACA 1257
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      702 ATNNWGCW 695
```

```
RESULT 37
US-09-801-861-3
; Sequence 3, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Human
US-09-801-861-3
```

```
Query Match      3.9%; Score 48.8; DB 4; Length 53332;
Best Local Similarity 49.1%; Pred. No. 0.27;
Matches 157; Conservative 0; Mismatches 162; Indels 1; Gaps 1;
```

```
QY      932 ACATTTTAAATAGTTATGTATACATCGAATGAAGAAAGCTAAATAGTTACAG 991
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31341 ATATTTTATATATTTATATATAGTTATATTTATATATATATATATATATATAT 31400
QY      992 ACCAAGTGATTTACACATGTTTTTAAATCTAGACATTTTCATTCATCAAA 1051
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31401 ATATTTGAATATATTAATA-TATTTATATATTTTATATATATTTATATATTTT 31459
QY      1052 AGTGTTTCAATTTTTTTTGTAGTTGTTAGAAATCTTCTCATAGTCACATTCCTCA 1111
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31460 ATATTTTATATATATATATATATTTTATATATATTTATATATATATATATAT 31519
QY      1112 ACCTATATTTGGAATATGTTGGTCTTTGTTTCTTCTAGATGCAATTTTAA 1171
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31520 ATTTATATATATTTATATATATTTATATATATTTATATATATATATATATTTAT 31579
```

```
QY      1172 AAAATATMAAGCTACCAATCTTGTGACATTTGTAAGTTAAGATTTTATAT 1231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31580 ATATTTATATATTTATATATATTTATATATTTATATATATTTATATATATTT 31639
QY      1232 CTGTTAAATMAAATTTATTT 1251
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31640 TATATATATATATATATGATTT 31659
```

```
RESULT 38
US-10-224-562-3
; Sequence 3, Application US/10224562
; Patent No. 6730506
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001098DIV
; CURRENT APPLICATION NUMBER: US/10/224,562
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-224-562-3
```

```
Query Match      3.9%; Score 48.8; DB 4; Length 53332;
Best Local Similarity 49.1%; Pred. No. 0.27;
Matches 157; Conservative 0; Mismatches 162; Indels 1; Gaps 1;
```

```
QY      932 ACATTTTAAATAGTTATGTATACATCGAATGAAGAAAGCTAAATAGTTACAG 991
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31341 ATATTTTATATATTTATATATAGTTATATTTATATATATATATATATATATAT 31400
QY      992 ACCAAGTGATTTACACATGTTTTTAAATCTAGACATTTTCATTCATCAAA 1051
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31401 ATATTTGATATATTTATA-TATTTATATATTTTATATATTTTATATATTTT 31459
QY      1052 AGTGTTTCAATTTTTTTTGTAGTTGTTAGAAATCTTCTCATAGTCACATTCCTCA 1111
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31460 ATATTTTATATATTTATATATATTTTATATATATTTATATATATATATATAT 31519
QY      1112 ACCTATATTTGGAATATGTTGGTCTTTGTTTCTTCTAGATGCAATTTTAA 1171
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31520 ATTTATATATATTTATATATATTTATATATTTTATATATATATATATATTTAT 31579
QY      1172 AAAATATMAAGCTACCAATCTTGTGACATTTGTAAGTTAAGATTTTATAT 1231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31580 ATATTTATATATTTATATATATTTTATATATTTTATATATATTTATATATTT 31639
QY      1232 CTGTTAAATMAAATTTATTT 1251
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      31640 TATATATATATATATGATTT 31659
```

```
RESULT 39
US-08-909-742-1/c
; Sequence 1, Application US/08909742
; Patent No. 6007991
; GENERAL INFORMATION:
; APPLICANT: Vimala S. Sivarmanan
; APPLICANT: Helen-yu Wang
; APPLICANT: Craig C. Malbon
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-
; TITLE OF INVENTION: ACTIVATED PROTEIN KINASES AS THERAPY FOR
; TITLE OF INVENTION: BREAST CANCER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
```

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Query Match 3.9%; Score 48.6; DB 3, Length 1866;
Best Local Similarity 55.0%; Pred. No. 0.061;
Matches 116; Conservative 0; Mismatches 94; Indels 1; Gaps 1.

Dy      45 CGGCTCTGGAGCGCGGCGGAGCGAGACGCTGACCAAGTTCCTCTCTCGATCTCTCCG 104
Db      210 CTGCAACTGCGGTGTAGCGCGGGCCACGTCGAAAGGCTGCCCCCTTCACCATCTCACCTG 151

Dy      105 CTCACGCTCCGGGCGTGGCCCGGCGAGCGGGAGCATGCAATCCCAAGGCCCCGCGCTTC 164
Db      150 CCGCGGAGACCCCGGGCGGACCCCTCGGTCTTAAAGGAGCTCCGCGCCCGCCCTCG 91

Dy      165 CGGACGAGGCTCCGGGCGCTCTGCTGCTCTGCTGACGCTCCGCGCGCTGAGAC 224
Db      90 AGCGCGCCCGCGCGCATCTCA-CTCCGCGTGTGCTGTGTGTGTGTGTGCGCGCTG 32

Dy      225 GCTCTGAGATCCCAAGGGGAGCAAAAG 255
Db      31 CCTCTGGGCGCCCGCGCGCGCGGAGAACG 1

RESULT 40
US-09-412-289-1/c
; Sequence 1, Application US/09412289
; Patent No. 6271210
; GENERAL INFORMATION:
; APPLICANT: Sivaraman, Vimala S.
; APPLICANT: Wang, Helen-Yu
; APPLICANT: Malden, Craig C.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-ACTIVATED
; FILE REFERENCE: Seq. 1-4 (178-225 CIP II/CON)
; CURRENT APPLICATION NUMBER: US/09/412,289
; CURRENT FILING DATE: 1999-10-05
; EARLIER APPLICATION NUMBER: 08/909,742
; EARLIER FILING DATE: 1997-08-12

```

	Query Match	Best Local Similarity	3.9%; 55.0%;	Score 48.6;	DB 3;	Length 1866;
	Matches	116;	Conservative	0;	Mismatches	94;
					Indels	1;
					Gaps	1;
OY	45	CGGCTTGGAGCGCGCGGAGCCAGAGCGTGCACGTTCTCTCTCGGCTTCCTCCGC	104			
Db	210	CTGCAACTGGGTGTAGAGCGCGGCGCCAGCTGGAAGGCTGCGCCCTTCAACATCTTCACCTC	151			
OY	105	CTCCAGCTCCGCGGTGCGGCCGCGAGCCGAGACCATGCGAACCCCAAGGAGCCCGCGCGCTCC	164			
Db	150	CCCCGGGACCCCGCGGGCGAACCCCTCGGTTCATAGGGGCTCCCCGCGCGCCCGCTG	91			
OY	165	CCGCAGGCGGCTCGCGGCGCTCTCTGCTCTCTGCTGTCAGACTGCCGCGCGCTCGAGC	224			
Db	90	AGCGCGCGCGCGCCCAATCTCCA-CTCCGCGTGTGCTGCTGCTGCTGTGTGCTGCGCTG	32			
OY	225	GCTCTGAGATCCCAAGGGGAACAAAG	255			
Db	31	CCCTCTGGGGCCCGCGCGCCCAAGAGC	1			

Query Match	3.9%	Score 48.4	DB 4	Length 6020
Best Local Similarity	43.3%	Pred. No. 0.12		
Matches	278	Conservative	0	Mismatches 361; Indels 3; Gaps 1;
607	GGATTTACACATTCATGAGCTGATATTTCAGGACCTTCACATTGAGCTATTAATT	666		

Db 2577 GGAATTAAAGTTGAGTAAGTGAATTTTGTAGAAATGAAATTAAGAAAAATTTTAAT 2636  
Qy 667 ATTGGACCAAGGAGCCCTGAATGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 726  
Db 2637 TTTTATATTTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2696  
Qy 727 TGAAGACCTTGTGAAGAAATGCTGTGATGATGATGATGATGATGATGATGATGATGATGAT 786  
Db 2697 GTAGATGAAAAATGAAAGTATTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2756  
Qy 787 CTGTTCAGATTAACCAAGAAAGAGATGCTTACAGATGATGATGATGATGATGATGATGATGAT 846  
Db 2757 TGTAAATTTGTAAATTTTATTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2816  
Qy 847 TTATGAGAACTACCAAAATTAATGCTTAAATTTTCACTTCTTCTTCTTCTTCTTCTTCTTCT 906  
Db 2817 TTGATAGAGGATGATTTTGTAAATTTTATTTTGTGATGATGATGATGATGATGATGATGATGAT 2876  
Qy 907 TGCCTGGAATGCTTCACTTAATGACATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 966  
Db 2877 TTTTATATAGGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2936  
Qy 967 AAAGCAAGCTAAATATGTTTACAGCAAGATGATTTCACTGTTTAAATTAATTAATTAAT 1026  
Db 2937 GAAATTTTGTAAATGAGGCTTTGAGTTTGTGATGATGATGATGATGATGATGATGATGATGAT 2996  
Qy 1027 CATTAATCAATTTGCTTCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1083  
Db 2997 AGTGAATTTTATTTTAAAGCTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 3056  
Qy 1084 ATACTTCTTCAATCACTTCTCAACCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1143  
Db 3057 GATATTTGTAAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3116  
Qy 1144 GTTTTCTCTTCAATCACTTCTCAACCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1203  
Db 3117 TATTTTCTTCAATCACTTCTCAACCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3176  
Qy 1204 TTGTAATGTTAAGAAATTTTATTAATCTGTTAAATTAATTAATTAATTAATTAATTAAT 1245  
Db 3177 GAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3218

RESULT 42  
US-10-204-708-35  
; Sequence 35, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPERBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/204,708  
; PRIOR FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 35  
; LENGTH: 9347  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-204-708-35  
Query Match 3.8%; Score 48.2; DB 4; Length 9347;  
Best Local Similarity 51.6%; Pred. No. 0.16; Mismatches 103; Indels 0; Gaps 0;  
Matches 110; Conservative 0; Mismatches 103; Indels 0; Gaps 0;  
Qy 1035 ATTTCCTTCAATCAAGATGCTTCAATTAATTTTGTAGTGAATTAATTTCTTC 1094  
Db 7491 AATTTAAGTTTATTTATTTGATTTTAAATTTTATTTTGTGAAGTAAATTAAGATTTA 7550  
Qy 1095 ATAGTCAATCTCTCAACCTAATTAATTTGGAATATGTTGTGCTTTGTTTCTCT 1154  
Db 7551 TTGTAATTTTGTGATTAATTAATTTTATTTTGTGATTAATTAATTTTATTTTAT 7610  
Qy 1155 TAGATACATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1214  
Db 7611 TAGATACAAATGCTTTTAAATTTTGTGTTTAAATTAATTTTGTGATTTATTTTAT 7670  
Qy 1215 AAGAAATTTTATTAATCTGTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1247  
Db 7671 TTTAGTTTATTTTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 7703

RESULT 43  
US-10-204-708-40  
; Sequence 40, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPERBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/204,708  
; PRIOR FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 40  
; LENGTH: 19513  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-204-708-40  
Query Match 3.8%; Score 48.2; DB 4; Length 19513;  
Best Local Similarity 49.3%; Pred. No. 0.23;  
Matches 181; Conservative 0; Mismatches 183; Indels 3; Gaps 2;  
Qy 865 AATAAGCTTAATTTTCAATTTGCTACCTTTTATTAATTAATTAATTAATTAATTAATTAAT 924  
Db 339 ATTGTAAGTTTATTTTGTAGTTAAGCAATTTTATTTTGTGATGATGATGATGATGATGATGAT 398  
Qy 925 TTAATGCAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 983  
Db 399 ATTATAGCGCTTATTTATTAATTAATTAATTTTGTGATGATGATGATGATGATGATGATGAT 458  
Qy 984 GTTTACAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1043  
Db 459 TGTATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 518  
Qy 1044 CAATCAAGT--CGTTCAATTTTATTTTGTGATGATGATGATGATGATGATGATGATGATGAT 1101

Db 519 TTTTAAGTGTGAGATATAGGTTGAGTTTCGGCTTCGTTTGGTAATTTTTTTA 578  
Qy 1102 CATCTCTCACTAATATTTGGATATTTGTTGCTTTTCTCTTCTAGTATA 1161  
Db 579 TTTTATAAATTTTGTTCGATATTTCTTATTAATTAATTTAGTTAT 638  
Qy 1162 GCATTTTAAAAAATATAAGCTACCAATCTTTGACAAATTTGTAAGAAAT 1221  
Db 639 TTGTATGGAATGATAAAAATGTAATATTTTGTATTAATTTTGAATA 698  
Qy 1222 TTTTATA 1228  
Db 699 ATTTTAA 705

## RESULT 44

US-09-790-988-1  
; Sequence 1, Application US/09790988  
; Patent No. 6632935  
; GENERAL INFORMATION:  
; APPLICANT: SHIGEMORU SHUJI  
; APPLICANT: MATANABE, HIDEKI  
; APPLICANT: HATTORI, MASAHIRA  
; APPLICANT: SAKAKI, YOSHIYUKI  
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
; FILE REFERENCE: 081356/0159  
; CURRENT APPLICATION NUMBER: US/09/790,988  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: JP2000-107160  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 640681  
; TYPE: DNA  
; ORGANISM: Buchnera sp.  
US-09-790-988-1

Query Match 3.8%; Score 47.8; DB 4; Length 640681;  
Best Local Similarity 47.9%; Pred. No. 1.5; Indels 3; Gaps 1;  
Matches 170; Conservative 0; Mismatches 182

Qy 897 TTTTATATATGCTTGAATGCTTCACTTAATGACATTTAATTAAGTTATGTATAC 956  
Db 88808 TTCTATATATTAAGTATTAATTTTCACTTAAGCAATTTTACGTATCATCAATTA 88867  
Qy 957 ATCTGAATGAAGCAAGCTAATATGTTTACAGACCAAGTGATTTCACTGTTT 1016  
Db 88868 AT--ATTAAATTAATCTCTAAGATTTATATATATGAAATTAATGTTAGTATTT 88924  
Qy 1017 TTTAACTAGCATATATTCATTTGCTTCATCAAAAGTGCTTCAATTTTTTTAGTT 1076  
Db 88925 TTTAAATTTTCAGATTAATCAATTTTATTAATAATTTACAGAGTGATTAATCTTGTA 88984  
Qy 1077 GGTAGAAATCTTCTTCATAGTACATCTCTCAACTATAATTTGGAATATGTTG 1136  
Db 88985 ATTAATAAATTAATTAATTAATTAATAAGTTTGATGCTTTTAAAGATATAT 89044  
Qy 1137 GCTCTTGTCTTCTCTAGTATAGCATTTTAAAAAATATTAAGCTACCAATCTTT 1196  
Db 89045 AATAATTAATTTTCTTTTAAATAATTTTACCTTACAGATTTGCTCCAAATTTTC 89104  
Qy 1197 GTACATTTGTAAATGTAAAGATTTTATATCTGTTAAATTAATTAATTT 1251  
Db 89105 ATTGATATTCAGGAGAGGTGATTTAAATATATTTTAAAAAATTAATTT 89159

## RESULT 45

US-08-397-653B-2  
; Sequence 2, Application US/08397653B  
; Patent No. 6328570  
; GENERAL INFORMATION:  
; APPLICANT: Martineau, Belinda

; TITLE OF INVENTION: COTTON MODIFICATION USING  
; TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calgene, Inc.  
; STREET: 1920 Fifth Street  
; CITY: Davis  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 95616

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.0  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/397,653B  
; FILING DATE: 28-FEB-1995  
; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth Lassen  
; REGISTRATION NUMBER: 31,845  
; NAME: Donna E. Scherer  
; REGISTRATION NUMBER: 34,719  
; NAME: Carl J. Schvedler  
; REGISTRATION NUMBER: 36,924  
; REFERENCE/DOCKET NUMBER: CGNE 112  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (916) 753-6313  
; TELEFAX: (916) 753-1510  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4383 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA

US-08-397-653B-2

Query Match 3.8%; Score 47.6; DB 3; Length 4383;  
Best Local Similarity 48.0%; Pred. No. 0.16;  
Matches 166; Conservative 0; Mismatches 179; Indels 1; Gaps 1;

Qy 843 ATCATATTTGAAGACTACCAAAATTAATGCTTTATTTTCACTTGTGCTACCTTTT 902  
Db 3351 ATGAATAATGATCGATCGATCTTAAATTTATGTTTACATTAATTAATCACTTCT 3410  
Qy 903 ATTGAGCTTGAATGCTTCACTTAATGACATTTTAAATAAGTTATGTATACATCTGA 962  
Db 3411 GTTACATTCATTTATCTAGTTATGATATGATATTAATTAATTAATTAATTAATTA 3470  
Qy 963 ATGAAGAAGCAAGCTAATATGTTTACAGACCAAGTGATTTGACACTGTTTAAAT 1022  
Db 3471 TCTTCAAAAGAGAGTACATATGTAACAAAGTAAAGGTAATTAACCTCTTTTATGA 3530  
Qy 1023 CTAGCATTTATGAT-TTTCCTTCAATCAAAAGTGCTTCAATATTTTGTAGTGT 1081  
Db 3531 TTCGATATATTCATATTTGATATCTCAAAATTAAGATTAATCATATTAATTTGTAG 3590  
Qy 1082 GAATCTTTCTTCATAGTACATCTCTCAACTATAATTTGGAATATGTTGCTGTT 1141  
Db 3591 AATTTAAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1187  
Qy 1142 TTGTTTCTCTTATAGTATGATTTTAAAAAATTAATTAATTAATTAATTAATTA 1187  
Db 3651 TAATATTAATGATTTCTTGTGCTGATTTATTAATTAATTAATTAATTAATTAAT 3696

## RESULT 46

US-08-397-653B-2  
; Patent No. 5175095  
; APPLICANT: Martineau, Belinda M.; Houck, Catherine M.

```

1  TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS
2
3  NUMBER OF SEQUENCES: 9
4
5  CURRENT APPLICATION DATA:
6
7  APPLICATION NUMBER: US/07/554,195
8
9  FILING DATE: 17-JUL-1990
10
11 SEQ ID NO.:4
12
13 LENGTH: 4383
14
15 5175095-4

```

Query Match	3.8%	Score 47.6;	DB 6;	Length 4303;
Best Local Similarity	48.0%;	Pred. No. 0.16;		
Matches 166;	Conservative 0;	Mismatches 179;	Indels 1;	Gaps 1

QY	843	ATCATTTATGGAAGACATCCAAATAATATGCTTAAATTTTCAATGCTACCTCTTTT	902
QY	843	ATCATTTATGGAAGACATCCAAATAATATGCTTAAATTTTCAATGCTACCTCTTTT	902
Db	3351	ATGAAAATATGATCGACTACGATCTTTAATTTTATCTTTTACATTTAATTAACCTTCT	3410
QY	903	ATTATGCTTGGAATGGTTCACCTTAATGACATTTTAATAATAGTTATGATACATCTGA	962
Db	3411	GTTACGATCTCAATTTATCTAGTTATGAATAAGAAATATAGAGTATTTGAAGTAGAGCTAG	3470
QY	963	ATGAAAGACAAGCTAAATATGTTATGACAGCAAAAGTGTGATTCACACTGTTTTAAAT	10222
Db	3471	TCTTCAACCAAGACGTCATATGTCACAAAGTAGGCTACTTTAACTCTTTTTTANGA	3530
QY	1023	CTAGCATTTATCAT-TTTGCTTCAATCAAAGTGGTTCAATATTTTTTTAGTTGGTTA	1081
Db	3531	TTTCGATATATTCATATTTTGGATATCTCAAAATTTGAGATTAATTCATATTAATTTTGAACGA	3590
QY	1082	GAATCACTTTCTTCAGTACATCTCTCCACCTTAATTTTGGAAATATTGTTGGTGCTT	1141
Db	3591	AATTTTAACATTAATTAATTAACCTCCCTATATAAAGTTTACTTCATGATTAAGAAATTA	3650
QY	1142	TTGTTTTTCTCTAGTATAGCATTTTTAAAAAATATAAAAAGCTA	1187
Db	3651	TAAATATTAAGAAATCTTGTTGCTGAATTAATTAATTAATGCTACGAA	3696

RESULT 47  
 US-07-867-106-2/c  
 ; Sequence 2, Application US/07867106  
 ; Patent No. 5389526  
 ; GENERAL INFORMATION:  
 APPLICANT: Slade, Martin B  
 APPLICANT: Chang, Andy C M  
 APPLICANT: Williams, Keith L  
 TITLE OF INVENTION: Improved Plasmid Vectors for Cellular  
 TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526r1s  
 STREET: One Liberty Place 46th Floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/867,106  
 FILING DATE: 19920625  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: AU PJ 7187  
 APPLICATION NUMBER: PCT/AU90/00530  
 FILING DATE: 02-NOV-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Peeney, Joanne Longo  
 REGISTRATION NUMBER: 35,134  
 REFERENCE/DOCKET NUMBER: RICE-0002  
 TELECOMMUNICATION INFORMATION:

```

1 TELEPHONE: 215-568-3100
2 TELEFAX: 215-568-3439
3 INFORMATION FOR SEQ ID NO: 2:
4
5 SEQUENCE CHARACTERISTICS:
6
7 LENGTH: 3852 base pairs
8
9 TYPE: NUCLEIC ACID
10 STRANDEDNESS: single
11 TOPOLOGY: linear
12 MOLECULE TYPE: DNA (genomic)
13
14 ANTI-SENSE: NO
15
16 FEATURE:
17
18 NAME/KEY: CDS
19 LOCATION: 2378..5038
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21 FEATURE:
22
23 NAME/KEY: CDS
24 LOCATION: 2378..5038
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Query Match 3.8%; Score 47.6; DB 1; Length 5852;  
Best Local Similarity 46.6%; Pred. No. 0.18;  
Matches 189; Conservative 0; Mismatches 214; Indels 3; Gaps 1;

Qy	843	CATATATGAAGAACACACAAAATAAAGCTTAATTTATTTGACACCTCTTTTAT	904
Db	497	CTTTTCTTTTTCATTTTCCACCTTTCACTTTTTTTCTTTTCTTTTCTTTT	438
Qy	905	TATGCTTGGAATGGTTCACCTTAATAGACATTTTAAATAGTTATGATCATCTGAT	964
Db	437	TTTAAAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATCTTCAT	378
Qy	965	GAAAGCAAGCTAATATGTTTACAGACCAAGTGTGATTCACACCTGTTTAAACT	1024
Db	377	GACCCATCTTTTCTTAAATTTATGATTAATTAATTAATTAATTAATTAATCT	318
Qy	1025	AGCATTAATCATTTGGCTTCATCAAAAGTGTTCACTTTTCTTTTATGTTGTTAAGA	1084
Db	317	ATACATATTTTAAATTAATTTTAAAGTATTAATAACAAAGATTTTTTTTATTTTTT	258
Qy	1085	TACTTCTTCATAGTCACATTCCTCA---ACCTATAATTTGGAATATGTTGGTCTT	1141
Db	257	TTTATTTTTTTTTTCAAGTTAAAGATTAATTAATTTTTTTTAAATCTTGATGACCT	198
Qy	1142	TTGGTTTTTCTCTAGTATAGCATTTTTTAAAAAATATAAAGCTACCAATCTTGTACA	1201
Db	197	TTATTTTTTATGCTTTTTCATGGTTATCTCTTAAAAAGTATCTATCGATCTATACG	138
Qy	1202	ATTGTAATGTTAAGAAATTTTTTTTATCTGTGTTAATAAATTT	1247
Db	137	ATTTTCATTTTGGAAAAATTAATTAATTAATTAATTAAGATTAAGT	92

```

/ RESULT 48
/ US-10-204-708-50
/ Sequence 50, Application US/10204708
/ Patent No. 6677731
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
/ TITLE OF INVENTION: by Assessing DNA Methylation
/ FILE REFERENCE: 5013.1012
/ CURRENT APPLICATION NUMBER: US/10/204,708
/ CURRENT FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: PCT/EP01/03971
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: DE 10019058.8
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/

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;; PRIOR FILING DATE: 2000-09-01  
;; NUMBER OF SEQ ID NOS: 98  
;; SEQ ID NO 50  
;; LENGTH: 6306  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-50

Query Match 3.8%; Score 47.6; DB 4; Length 6306;  
Best Local Similarity 45.5%; Pred. No. 0.19;  
Matches 211; Conservative 0; Mismatches 249; Indels 4; Gaps 1;

QY 788 TTGTCAGATTCACCAAGAGATGCTCTGATGGAATTCAGTTTCGCATCAT 847  
DB 4858 TTTTGTGTTATGTAAGAAAAATGATTTTAAATGCTGATTAAGTTATTTTAAAT 4917  
QY 848 TATTCAGAACTACCAAAATTAATGCTTAATTTTCACTTCTCTTTTATAT 907  
DB 4918 TGGAGTAAAGATAGTTTATAGTTATTTTGGTAATTTTGGAGTTT 4977  
QY 908 GCCTGGAATGCTTCACTTAATGACATTTTAAATAGTTATGATACCTGAATGA 967  
DB 4978 TTAATTTGATGATAGTAAGTGTGTTTTCGTCGATTTTAAATTTTGAATAT 5037  
QY 968 AAGCAAGCTAATATGTTTACAGACCAAGTGTATTCACAGCTTTTAAATCTAC 1027  
DB 5038 TGAAGGTTGATATTTTATTTTATGATTTTATGTTAT--TATAGTTATTTT 5093  
QY 1028 ATTATCATTTTCTTCAATCAAAAGTGTTCATATTTTATTTAGTTAGAAATAC 1087  
DB 5094 TTTTTCATTTTATTTTATTTTATGATTTTAAAGATTTTATAGTGAATTTGTA 5153  
QY 1088 TTTCTCAGTACATCTCTCAACCTATTAATTTGGAATTTGCTGCTTTGTT 1147  
DB 5154 TCGTATAGTGTGTTGTTTGTGTTTATTTTGTGTTTATTTTATTTATTTT 5213  
QY 1148 TTTCTCTGATAGATTTTAAAAAATATTAAGTACCAATCTTTGACATTTGT 1207  
DB 5214 TTTTATTTTATTTAGGAAGATTTTAAATATTAATTTTATTTTATTTTAAAGTT 5273  
QY 1208 AATATGTAAGATTTTATTTATCTGTTAAATTAATTAATTT 1251  
DB 5274 AATGTAAGAAAGTTTATTTAAATTTTATTTATGAAATTTT 5317

RESULT 49  
US-10-204-708-33  
;; Sequence 33, Application US/10204708  
;; Patent No. 6677731  
;; GENERAL INFORMATION:  
;; APPLICANT: OLEK, Alexander  
;; APPLICANT: PIEPENROCK, Christian  
;; APPLICANT: BERLIN, Kurt  
;; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
;; FILE REFERENCE: 5013.1012  
;; CURRENT APPLICATION NUMBER: US/10/204, 708  
;; CURRENT FILING DATE: 2003-05-06  
;; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
;; PRIOR FILING DATE: 2001-04-06  
;; PRIOR APPLICATION NUMBER: DE 10019058.8  
;; PRIOR FILING DATE: 2000-04-06  
;; PRIOR APPLICATION NUMBER: DE 10019173.8  
;; PRIOR FILING DATE: 2000-04-07  
;; PRIOR APPLICATION NUMBER: DE 10032529.7  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: DE 10043826.1  
;; PRIOR FILING DATE: 2000-09-01  
;; NUMBER OF SEQ ID NOS: 98  
;; SEQ ID NO 33  
;; LENGTH: 5455

;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-33

Query Match 3.8%; Score 47.4; DB 4; Length 5455;  
Best Local Similarity 48.1%; Pred. No. 0.2;  
Matches 195; Conservative 0; Mismatches 206; Indels 4; Gaps 2;

QY 847 TATTCAGAACTACCAAAATTAATGCTTTAATTTTCACTTCTCTTTTATTA 906  
DB 726 TTTTAAAGTTTATTTAATTTTATTTGTTTATTTTATGTTTATTTTAAATATGCTTT 785  
QY 907 TCCCTGGAATGCTTCACTTAATGACATTTTAAATTAATGTTATGATCATCTGAATGA 966  
DB 786 TTTTGAAGCGTTTATTTAT 844  
QY 967 AAGCAAGCTAATATGTTTACAGACCAAGTGTATTTCACTGTTTAAATCTAG 1026  
DB 845 TATTTTATTTATGATATTTATTTATTTTATTTAGATTTTGGAGATATATGTTTAAATGAG 904  
QY 1027 CATATTCATTTTCTTCAATCAAAAGTGTTCATATTTTATTTTATGTTGATGAATA 1086  
DB 905 TTTTATTTTGTGTTTATTTTAAATTTTGTGGGTTTATTTATTTTATTTATTTAGTTGCTTT 964  
QY 1087 CTTTCTCATCTCATCTCTCAACCTAATTTGGAATTTGTTGCTGCTTTGTT 1146  
DB 965 TTAATTTTATTTTATGTTTATTTTATTTTGGAAATTTTATTTTATTTTATTTTATTTT 1024  
QY 1147 TTTCTCTAGATAGATTTTAAAAAATTAAGTACCAATCTTTGACATTTG 1206  
DB 1025 GTTGTGTAAGATTTGATTTTATTAATTTTATTTAGGTTG--ATTTTAGAAATTTTAT 1081  
QY 1207 TAAATGTAAGATTTTATTTATCTGTTAAATTAATTAATTT 1251  
DB 1082 TATTTGTAAGTAAAGTTTATTTTATTTTAAATTAATTTT 1126

RESULT 50  
US-10-204-708-14  
;; Sequence 14, Application US/10204708  
;; Patent No. 6677731  
;; GENERAL INFORMATION:  
;; APPLICANT: OLEK, Alexander  
;; APPLICANT: PIEPENROCK, Christian  
;; APPLICANT: BERLIN, Kurt  
;; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
;; FILE REFERENCE: 5013.1012  
;; CURRENT APPLICATION NUMBER: US/10/204, 708  
;; CURRENT FILING DATE: 2003-05-06  
;; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
;; PRIOR FILING DATE: 2001-04-06  
;; PRIOR APPLICATION NUMBER: DE 10019058.8  
;; PRIOR FILING DATE: 2000-04-06  
;; PRIOR APPLICATION NUMBER: DE 10019173.8  
;; PRIOR FILING DATE: 2000-04-07  
;; PRIOR APPLICATION NUMBER: DE 10032529.7  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: DE 10043826.1  
;; PRIOR FILING DATE: 2000-09-01  
;; NUMBER OF SEQ ID NOS: 98  
;; SEQ ID NO 14  
;; LENGTH: 6113  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-14

Query Match 3.8%; Score 47.4; DB 4; Length 6113;  
Best Local Similarity 49.1%; Pred. No. 0.21;

